SEQUENCE LISTING

<110> OBSIDIAN THERAPEUTICS, INC.

<120> CA2 COMPOSITIONS AND METHODS FOR TUNABLE REGULATION

<130> 2095.1010PCT2/462540

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<151> 2019-04-18

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Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe
20 25 30

Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
35 40 45

Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
50 55 60

Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
65 70 75 80

Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa
85 90 95

Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys
100 105 110

Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp
115 120 125

Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu
130 135 140

Ser Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu
145 150 155 160

Lys Leu Glu Arg Ile
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Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe
            20                  25                  30

Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
        35                  40                  45

Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
    50                  55                  60

Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
65                  70                  75                  80

Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa
                85                  90                  95

Lys Leu Gly Arg Phe Pro Gln Val Gln Val Cys Pro Trp Phe Arg Pro
            100                 105                 110

Cys Ile Lys Ala Phe Gly Arg Gln Trp Glu His Cys
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Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe
            20                  25                  30

Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
        35                  40                  45

Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
    50                  55                  60

Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
65                  70                  75                  80

Glu Thr Lys Lys Tyr Ser Ser Ile Val Ser Lys Gln Glu Cys His His
                85                  90                  95

Ser Asn Cys Met Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp
            100                 105                 110

Glu Gly Ser Leu Lys Ser Lys Leu Leu Leu Gly Val Ile Asn Pro Asn
        115                 120                 125

Cys Ser Glu Asp Cys Lys Ser Ser Met Ser Val Val Gln Thr Leu Tyr
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Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe
            20                  25                  30


Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
        35                  40                  45


Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
    50                  55                  60


Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
65                  70                  75                  80


Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Lys
                85                  90                  95


Leu Gly Arg Phe Pro Gln Val Gln Val Cys Pro Trp Phe Arg Pro Cys
            100                 105                 110


Ile Lys Ala Phe Gly Arg Gln Trp Glu His Cys
        115                 120
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Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe
            20                  25                  30

Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
        35                  40                  45

Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
    50                  55                  60

Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
65                  70                  75                  80

Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Lys
                85                  90                  95

Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro
            100                 105                 110

Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro
        115                 120                 125

Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser
    130                 135                 140
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Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys
145 150 155 160

Leu Glu Arg Ile

<210> 6
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Glu Ala Gln Phe Glu Thr Lys Lys Tyr Ser Ser Ile Val Ser Lys Gln
20 25 30

Glu Cys His His Ser Asn Cys Met Gln Glu Leu Phe Leu Lys Phe Val
35 40 45

Asp Glu Asn Trp Glu Gly Ser Leu Lys Ser Lys Tyr Val Arg Gly Ser
50 55 60

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

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130   135   140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145   150   155   160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165   170   175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180   185   190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195   200   205

```
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
```

```
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270
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Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
85 90 95

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Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160
```

```
Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220
```

```
Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240


Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255


Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270


Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15


Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30


Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45
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```
Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
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275 280

<210> 14
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
85 90 95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
100 105 110

```
Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 15

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175
```

```
Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 16

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1               5                  10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
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```
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60
```

```
Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1   5   10   15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

```
Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 19

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                  10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
```

```
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240
```

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
245 250 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
260 265 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

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<400> 21
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

```
Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 22

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15


Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30


Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45


Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60


Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80


Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95


Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110


Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125


Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
```

```
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 23
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1   5   10   15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130   135   140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145   150   155   160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165   170   175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180   185   190

```
Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 24

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30
```

```
Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255
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Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
260 265 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

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<400> 25
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln

```
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 26

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15


Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30


Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45


Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60


Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80


Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95


Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110


Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125


Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140
```

```
Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130   135   140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145   150   155   160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165   170   175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180   185   190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195   200   205

```
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 28
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<400> 28

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
```

```
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270
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Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

<210> 29
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1-acylglycerol-3-phosphate O-acyltransferase 1; "

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
85 90 95

```
Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<223> /note="Uniprot ID: Q99943; "

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<400> 30

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

```
Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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<213> Homo sapiens

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<223> /note="ENSP ID: ENSP00000395613"

<400> 31

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                  10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220
```

```
Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240


Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255


Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270


Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


<210> 32
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<213> Homo sapiens

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<220>
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<223> /note="Uniprot ID:  Q99943; "

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<400> 32
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15


Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30


Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45
```

```
Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
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275 280

<210> 33
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<220>
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<400> 33
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
85 90 95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
100 105 110

```
Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 34
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<400> 34

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175
```

```
Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 35
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<400> 35

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                  10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
```

```
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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<220>
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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60
```

```
Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 37
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<212> PRT
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<220>
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<220>
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<400> 37
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1   5   10   15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

```
Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 38

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                  10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
```

```
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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<400> 39
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15
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Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240
```

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
245 250 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
260 265 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

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

<220>
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1-acylglycerol-3-phosphate O-acyltransferase 1; "

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

```
Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 41
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<213> Homo sapiens

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1-acylglycerol-3-phosphate O-acyltransferase 1; "

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<400> 41

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15


Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30


Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45


Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60


Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80


Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95


Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110


Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125


Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
```

```
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


<210> 42
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<223> /note="Gene Name:
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<220>
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<400> 42
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1   5   10   15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130   135   140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145   150   155   160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165   170   175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180   185   190

```
Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 43
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<212> PRT
<213> Homo sapiens

<220>
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<400> 43

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30
```

```
Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255
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Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
260 265 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

<210> 44
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<400> 44
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln

```
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<400> 45
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1   5   10   15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130   135   140

```
Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


<210> 46
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<400> 46
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1   5   10   15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20   25   30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
        35   40   45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50   55   60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65   70   75   80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85   90   95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100   105   110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115   120   125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130   135   140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145   150   155   160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165   170   175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180   185   190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195   200   205

```
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280
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<210> 47
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<400> 47

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Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1               5                   10                  15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
            20                  25                  30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
```

```
        35                  40                  45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
    50                  55                  60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65                  70                  75                  80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
                85                  90                  95

Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270
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Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
275 280

<210> 48
<211> 283
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 2; "

<220>
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<223> /note="Gene Symbol: AGPAT1; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 1; "

<220>
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<223> /note="Uniprot ID: Q99943; "

<220>
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<400> 48
Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
20 25 30

Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
35 40 45

Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
50 55 60

Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
85 90 95

```
Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
            100                 105                 110

Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
        115                 120                 125

Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
    130                 135                 140

Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
145                 150                 155                 160

Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


<210> 49
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<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<400> 49

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

```
Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
                165                 170                 175

Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
            180                 185                 190

Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
        195                 200                 205

Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
    210                 215                 220

Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
225                 230                 235                 240

Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
                245                 250                 255

Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
            260                 265                 270

Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
        275                 280


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

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O15120; "

<220>
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<223> /note="ENSP ID: ENSP00000360759"

<400> 50

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Met Glu Leu Trp Pro Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu
1               5                  10                  15

Leu Val Gln Leu Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu
            20                  25                  30

Tyr Cys Ala Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys
        35                  40                  45

Leu Leu Arg His Gly Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly
    50                  55                  60

Trp Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val
65                  70                  75                  80

Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val Ser
                85                  90                  95

Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val Leu Pro
            100                 105                 110

Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Leu Phe Leu Gly Pro
        115                 120                 125

Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe Phe Ile Asn Arg Gln
    130                 135                 140

Arg Ser Ser Thr Ala Met Thr Val Met Ala Asp Leu Gly Glu Arg Met
145                 150                 155                 160

Val Arg Glu Asn Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser
                165                 170                 175

Ser Phe Tyr Asn Thr Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr
            180                 185                 190

Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp
        195                 200                 205

Val Pro Ala Leu Val Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe
    210                 215                 220
```

```
Leu His Ile Ser Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser
225                 230                 235                 240


Gly Val Gln Pro Ala Gln
                245


<210> 51
<211> 278
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 3; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT2; "

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O15120; "

<220>
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<400> 51
Met Glu Leu Trp Pro Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu
1               5                   10                  15


Leu Val Gln Leu Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu
            20                  25                  30


Tyr Cys Ala Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys
        35                  40                  45


Leu Leu Arg His Gly Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly
    50                  55                  60


Trp Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val
65                  70                  75                  80
```

```
Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val Ser
                85                  90                  95

Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val Leu Pro
            100                 105                 110

Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Leu Phe Leu Gly Pro
        115                 120                 125

Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe Phe Ile Asn Arg Gln
    130                 135                 140

Arg Ser Ser Thr Ala Met Thr Val Met Ala Asp Leu Gly Glu Arg Met
145                 150                 155                 160

Val Arg Glu Asn Leu Lys Val Trp Ile Tyr Pro Glu Gly Thr Arg Asn
                165                 170                 175

Asp Asn Gly Asp Leu Leu Pro Phe Lys Lys Gly Ala Phe Tyr Leu Ala
            180                 185                 190

Val Gln Ala Gln Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser
        195                 200                 205

Ser Phe Tyr Asn Thr Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr
    210                 215                 220

Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp
225                 230                 235                 240

Val Pro Ala Leu Val Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe
                245                 250                 255

Leu His Ile Ser Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser
            260                 265                 270

Gly Val Gln Pro Ala Gln
        275
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<210> 52
<211> 278
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AGPAT2; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 2; "

<220>
<221> source
<223> /note="Uniprot ID: O15120; "

<220>
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<400> 52
Met Glu Leu Trp Pro Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu
1   5   10   15

Leu Val Gln Leu Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu
            20   25   30

Tyr Cys Ala Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys
        35   40   45

Leu Leu Arg His Gly Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly
    50   55   60

Trp Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val
65   70   75   80

Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val Ser
                85   90   95

Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val Leu Pro
            100   105   110

Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Leu Phe Leu Gly Pro
        115   120   125

Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe Phe Ile Asn Arg Gln
    130   135   140

```
Arg Ser Ser Thr Ala Met Thr Val Met Ala Asp Leu Gly Glu Arg Met
145                 150                 155                 160

Val Arg Glu Asn Leu Lys Val Trp Ile Tyr Pro Glu Gly Thr Arg Asn
                165                 170                 175

Asp Asn Gly Asp Leu Leu Pro Phe Lys Lys Gly Ala Phe Tyr Leu Ala
            180                 185                 190

Val Gln Ala Gln Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser
        195                 200                 205

Ser Phe Tyr Asn Thr Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr
    210                 215                 220

Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp
225                 230                 235                 240

Val Pro Ala Leu Val Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe
                245                 250                 255

Leu His Ile Ser Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser
            260                 265                 270

Gly Val Gln Pro Ala Gln
        275


<210> 53
<211> 376
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 4; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT3; "

<220>
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<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
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<223> /note="Uniprot ID: Q9NRZ7; "

<220>
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<223> /note="ENSP ID: ENSP00000291572"

<400> 53

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Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                  10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
        35                  40                  45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
65                  70                  75                  80

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

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
            100                 105                 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
        115                 120                 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205
```

```
Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

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

Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
        275                 280                 285

Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
    290                 295                 300

Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
305                 310                 315                 320

Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
                325                 330                 335

Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
            340                 345                 350

Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
        355                 360                 365

Asn Gln Glu Phe Lys Lys Lys Glu
    370                 375
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<210> 54
<211> 376
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AGPAT3; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
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<223> /note="Uniprot ID: Q9NRZ7; "

<220>
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<400> 54

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Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                   10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
        35                  40                  45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
65                  70                  75                  80

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

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
            100                 105                 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
        115                 120                 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
```

```
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

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

Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
        275                 280                 285

Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
    290                 295                 300

Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
305                 310                 315                 320

Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
                325                 330                 335

Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
            340                 345                 350

Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
        355                 360                 365

Asn Gln Glu Phe Lys Lys Lys Glu
    370                 375
```

<210> 55
<211> 376

<212> PRT
<213> Homo sapiens

<220>
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<220>
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1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NRZ7; "

<220>
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<223> /note="ENSP ID: ENSP00000381135"

<400> 55

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	Leu
1				5				10						15	

Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	Val	Gln
			20					25					30		

Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	Tyr	Arg	Arg
		35					40					45			

Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	Leu	Val	Met	Leu
	50					55					60				

Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	Phe	Thr	Asp	Gln	Ala
65					70					75					80

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

Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	Trp	Thr	Met	Cys	Glu	Arg	Phe
			100					105					110		

Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr
		115					120					125			

```
Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

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

Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
        275                 280                 285

Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
    290                 295                 300

Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
305                 310                 315                 320

Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
                325                 330                 335

Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
            340                 345                 350

Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
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        355                 360                 365

Asn Gln Glu Phe Lys Lys Lys Glu
    370                 375


<210> 56
<211> 376
<212> PRT
<213> Homo sapiens

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<220>
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<220>
<221> source
<223> /note="Uniprot ID:  Q9NRZ7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000381138"

<400> 56
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                   10                  15


Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30


Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
        35                  40                  45


Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60


Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
65                  70                  75                  80


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

```
Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
            100                 105                 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
        115                 120                 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

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

Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
        275                 280                 285

Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
    290                 295                 300

Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
305                 310                 315                 320
```

```
Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
                325                 330                 335

Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
            340                 345                 350

Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
        355                 360                 365

Asn Gln Glu Phe Lys Lys Lys Glu
    370                 375


<210> 57
<211> 376
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 4; "

<220>
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<220>
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<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NRZ7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000381140"

<400> 57
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                   10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
        35                  40                  45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60
```

```
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
65                  70                  75                  80

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

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
            100                 105                 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
        115                 120                 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

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

Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
        275                 280                 285
```

```
Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
    290                 295                 300

Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
305                 310                 315                 320

Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
                325                 330                 335

Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
            340                 345                 350

Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
        355                 360                 365

Asn Gln Glu Phe Lys Lys Lys Glu
    370                 375


<210> 58
<211> 79
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
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<223> /note="ENSP ID: ENSP00000389318"

<400> 58
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                   10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
```

```
        35                  40                  45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln
65                  70                  75


<210> 59
<211> 38
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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      1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
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<223> /note="ENSP ID: ENSP00000394102"

<400> 59
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                   10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu
        35


<210> 60
<211> 128
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AGPAT3; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
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<223> /note="ENSP ID: ENSP00000412079"

<400> 60
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1 5 10 15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
20 25 30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
35 40 45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
50 55 60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
65 70 75 80

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

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
100 105 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
115 120 125

<210> 61
<211> 255
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AGPAT3; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413906"

<400> 61

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Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                  10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
        35                  40                  45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
65                  70                  75                  80

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

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
            100                 105                 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
        115                 120                 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190
```

```
Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
                245                 250                 255


<210> 62
<211> 255
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
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<223> /note="ENSP ID: ENSP00000414440"

<400> 62
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
1               5                   10                  15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
            20                  25                  30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
        35                  40                  45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
    50                  55                  60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
```

```
65                  70                  75                  80

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

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
            100                 105                 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
        115                 120                 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
    130                 135                 140

Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
145                 150                 155                 160

Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
                245                 250                 255


<210> 63
<211> 376
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<221> source
<223> /note="Gene Symbol: AGPAT3; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NRZ7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443510"

<400> 63

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

```
Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
                165                 170                 175

Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
            180                 185                 190

Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
        195                 200                 205

Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
    210                 215                 220

Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
225                 230                 235                 240

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

Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
        275                 280                 285

Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
    290                 295                 300

Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
305                 310                 315                 320

Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
                325                 330                 335

Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
            340                 345                 350

Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
        355                 360                 365

Asn Gln Glu Phe Lys Lys Lys Glu
    370                 375
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<210> 64

<211> 378
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 5; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT4; "

<220>
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<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NRZ5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000314036"

<400> 64

Met	Asp	Leu	Ala	Gly	Leu	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val
1				5					10					15	

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

Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys
		35					40					45			

Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu
	50					55					60				

Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg
65				70					75					80	

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

Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	Trp	Ser	Leu	Ser	Glu	Arg	Phe
			100					105					110		

Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr
		115					120					125			

```
Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys
    130                 135                 140

Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln
145                 150                 155                 160

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

Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala
            180                 185                 190

Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr
        195                 200                 205

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

Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
225                 230                 235                 240

Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg
                245                 250                 255

Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala
            260                 265                 270

Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr
        275                 280                 285

Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg
    290                 295                 300

Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr
305                 310                 315                 320

Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu
                325                 330                 335

Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val
            340                 345                 350
```

```
Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly
        355                 360                 365

Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp
    370                 375

<210> 65
<211> 159
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 5; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT4; "

<220>
<221> source
<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355872"

<400> 65
Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
1               5                   10                  15

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

Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
        35                  40                  45

Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu
    50                  55                  60

Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg
65                  70                  75                  80

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

Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe
            100                 105                 110
```

```
Gly Leu Leu Gly Val Ser Gln Lys Cys Ile Pro Pro Cys Leu Thr His
        115                 120                 125

Phe Ser Gly Ser Ala Pro Pro Leu Val Phe Leu Leu Leu Val Ile Gln
    130                 135                 140

Asn Leu Gln Lys Asn Gln Gln Ser Phe Tyr Leu Met Lys Trp Ser
145                 150                 155


<210> 66
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 5; "

<220>
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<223> /note="Gene Symbol: AGPAT4; "

<220>
<221> source
<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355878"

<400> 66
Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
1               5                   10                  15

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

Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
        35                  40                  45

Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Arg Leu Gln Gly Pro
    50                  55                  60

Gly Gln Glu Arg Ala Gly Leu Cys Pro Asn Tyr Arg Leu Asp Val Val
65                  70                  75                  80
```

```
Leu His Arg Asp Gly Leu Leu Phe Ala Gln Val Gly Ala Gly Ser Gln
                85                  90                  95


Asp Gly Cys His Gln Phe Ala Ala Pro Pro Gly Leu Pro Arg Glu Val
            100                 105                 110


Phe Phe Pro Asp Ser Leu
        115


<210> 67
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 5; "

<220>
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<223> /note="Gene Symbol: AGPAT4; "

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<220>
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<223> /note="ENSP ID: ENSP00000400211"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 67
Xaa Ser Ala Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn
1               5                   10                  15


Pro Thr Leu Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu
            20                  25                  30


Tyr Val Arg Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu
        35                  40                  45


Cys Ser Ala Trp Leu His Lys Leu Tyr Gln Glu Lys Gly Trp Gly Asp
    50                  55                  60
```

```
Thr Glu Phe Ser Lys Gln Tyr Val Ser Val Ser Arg Pro Gly Arg Leu
65                  70                  75                  80


Ala Leu Cys Pro Ser Glu Lys Ile Ala Glu Gln Gln Val Glu Val Val
                85                  90                  95


His Gly Phe Ser Lys Gln Ser Gly Glu
            100                 105


<210> 68
<211> 133
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AGPAT4; "

<220>
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      1-acylglycerol-3-phosphate O-acyltransferase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413901"

<400> 68
Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
1               5                   10                  15


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


Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
        35                  40                  45


Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu
    50                  55                  60


Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg
65                  70                  75                  80


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

```
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe
            100                 105                 110

Gly Leu Leu Gly Phe Asp Leu Leu His Val Ala Cys Met Pro Leu Glu
        115                 120                 125

Leu Gly Leu Phe Ser
    130


<210> 69
<211> 364
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 6; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT5; "

<220>
<221> source
<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NUQ2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000285518"

<400> 69
Met Leu Leu Ser Leu Val Leu His Thr Tyr Ser Met Arg Tyr Leu Leu
1               5                   10                  15

Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp
            20                  25                  30

Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln
        35                  40                  45

Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe
    50                  55                  60
```

```
Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu
65                  70                  75                  80

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

Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu
            100                 105                 110

Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu
        115                 120                 125

Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser
    130                 135                 140

Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val
145                 150                 155                 160

Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg
                165                 170                 175

Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala
            180                 185                 190

Ala Gln Arg Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg Ile
        195                 200                 205

Lys Ala Thr His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp Ala
    210                 215                 220

Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys Asp Asp Gly Gly Gln
225                 230                 235                 240

Arg Arg Glu Ser Pro Thr Met Thr Glu Phe Leu Cys Lys Glu Cys Pro
                245                 250                 255

Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu
            260                 265                 270

Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys
        275                 280                 285

Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg
```

```
    290                 295                 300

Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys
305                 310                 315                 320

Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu
                325                 330                 335

Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly
            340                 345                 350

Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala
        355                 360


<210> 70
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 6; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT5; "

<220>
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<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428152"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 70
Xaa Phe Phe Glu Asn Tyr Thr Gly Val Gln Val Ser Arg Leu Pro Leu
1               5                   10                  15

Pro Gly Leu Gly Val His Pro Ser Ser Arg Gly Arg Gly Pro Leu Arg
            20                  25                  30

Ser Pro Thr Ala Gly Glu Gly His Pro Ala Gly Pro Ala Asp Pro Ala
```

```
        35                  40                  45

Arg Arg Ala Arg Ala Ala Ser Pro Pro Ser Ser Pro His Ala Ser Cys
    50                  55                  60

Arg Ser Ala Glu Ile Ala Leu
65                  70


<210> 71
<211> 88
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 6; "

<220>
<221> source
<223> /note="Gene Symbol: AGPAT5; "

<220>
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<223> /note="Gene Name:
      1-acylglycerol-3-phosphate O-acyltransferase 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430016"

<400> 71
Met Leu Leu Ser Leu Val Leu His Thr Tyr Ser Met Arg Tyr Leu Leu
1               5                   10                  15

Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp
            20                  25                  30

Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln
        35                  40                  45

Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe
    50                  55                  60

Phe Phe Glu Asn Tyr Thr Gly Val Gln Leu Thr Gly Leu Leu Leu Thr
65                  70                  75                  80

Ser Trp Pro Ser Gly Arg Met Arg
                85
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<210> 72
<211> 181
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AGPAT5; "

<220>
<221> source
<223> /note="Gene Name:
1-acylglycerol-3-phosphate O-acyltransferase 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430751"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 72
Xaa Val Leu His Ala Leu Pro Ala Ala Gln Arg Arg Ala Pro Gly His
1 5 10 15

Gly Ala His Leu Arg Val Gly Leu Gly Gly Leu Ala Ala Ala Leu Arg
20 25 30

Leu Pro Ala Arg Pro Leu Leu Pro Ser Ala Gly Arg Pro Ala Leu Leu
35 40 45

Arg Leu Pro Glu His Gly Ala Leu Leu Leu Arg Glu Leu His Arg Gly
50 55 60

Pro Glu Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp
65 70 75 80

Arg Ile Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg
85 90 95

Trp Leu His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe
100 105 110

```
Tyr Glu Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser
        115                 120                 125

Val Asn Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile
    130                 135                 140

Leu Ser Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys
145                 150                 155                 160

Leu Tyr Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp
                165                 170                 175

Val Thr Ile Lys Ala
            180


<210> 73
<211> 501
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 7; "

<220>
<221> source
<223> /note="Gene Symbol: ACCS; "

<220>
<221> source
<223> /note="Gene Name:
      1-aminocyclopropane-1-carboxylate synthase homolog
      (Arabidopsis)
      (non-functional); "

<220>
<221> source
<223> /note="Uniprot ID:  Q96QU6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000263776"

<400> 73
Met Phe Thr Leu Pro Gln Lys Asp Phe Arg Ala Pro Thr Thr Cys Leu
1               5                   10                  15

Gly Pro Thr Cys Met Gln Asp Leu Gly Ser Ser His Gly Glu Asp Leu
            20                  25                  30
```

```
Glu Gly Glu Cys Ser Arg Lys Leu Asp Gln Lys Leu Pro Glu Leu Arg
        35                  40                  45

Gly Val Gly Asp Pro Ala Met Ile Ser Ser Asp Thr Ser Tyr Leu Ser
    50                  55                  60

Ser Arg Gly Arg Met Ile Lys Trp Phe Trp Asp Ser Ala Glu Glu Gly
65                  70                  75                  80

Tyr Arg Thr Tyr His Met Asp Glu Tyr Asp Glu Asp Lys Asn Pro Ser
                85                  90                  95

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

Leu Ser Trp Arg Leu Ser Gln Arg Asp Met Gln Arg Val Glu Pro Ser
        115                 120                 125

Leu Leu Gln Tyr Ala Asp Trp Arg Gly His Leu Phe Leu Arg Glu Glu
    130                 135                 140

Val Ala Lys Phe Leu Ser Phe Tyr Cys Lys Ser Pro Val Pro Leu Arg
145                 150                 155                 160

Pro Glu Asn Val Val Val Leu Asn Gly Gly Ala Ser Leu Phe Ser Ala
                165                 170                 175

Leu Ala Thr Val Leu Cys Glu Ala Gly Glu Ala Phe Leu Ile Pro Thr
            180                 185                 190

Pro Tyr Tyr Gly Ala Ile Thr Gln His Val Cys Leu Tyr Gly Asn Ile
        195                 200                 205

Arg Leu Ala Tyr Val Tyr Leu Asp Ser Glu Val Thr Gly Leu Asp Thr
    210                 215                 220

Arg Pro Phe Gln Leu Thr Val Glu Lys Leu Glu Met Ala Leu Arg Glu
225                 230                 235                 240

Ala His Ser Glu Gly Val Lys Val Lys Gly Leu Ile Leu Ile Ser Pro
                245                 250                 255
```

```
Gln Asn Pro Leu Gly Asp Val Tyr Ser Pro Glu Glu Leu Gln Glu Tyr
            260                 265                 270

Leu Val Phe Ala Lys Arg His Arg Leu His Val Ile Val Asp Glu Val
        275                 280                 285

Tyr Met Leu Ser Val Phe Glu Lys Ser Val Gly Tyr Arg Ser Val Leu
    290                 295                 300

Ser Leu Glu Arg Leu Pro Asp Pro Gln Arg Thr His Val Met Trp Ala
305                 310                 315                 320

Thr Ser Lys Asp Phe Gly Met Ser Gly Leu Arg Phe Gly Thr Leu Tyr
                325                 330                 335

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

His Gly Leu Ser Gly Leu Val Gln Tyr Gln Met Ala Gln Leu Leu Arg
        355                 360                 365

Asp Arg Asp Trp Ile Asn Gln Val Tyr Leu Pro Glu Asn His Ala Arg
    370                 375                 380

Leu Lys Ala Ala His Thr Tyr Val Ser Glu Glu Leu Arg Ala Leu Gly
385                 390                 395                 400

Ile Pro Phe Leu Ser Arg Gly Ala Gly Phe Phe Ile Trp Val Asp Leu
                405                 410                 415

Arg Lys Tyr Leu Pro Lys Gly Thr Phe Glu Glu Glu Met Leu Leu Trp
            420                 425                 430

Arg Arg Phe Leu Asp Asn Lys Val Leu Leu Ser Phe Gly Lys Ala Phe
        435                 440                 445

Glu Cys Lys Glu Pro Gly Trp Phe Arg Phe Val Phe Ser Asp Gln Val
    450                 455                 460

His Arg Leu Cys Leu Gly Met Gln Arg Val Gln Gln Val Leu Ala Gly
465                 470                 475                 480

Lys Ser Gln Val Ala Glu Asp Pro Arg Pro Ser Gln Ser Gln Glu Pro
```

485 490 495

Ser Asp Gln Arg Arg
500

<210> 74
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 7; "

<220>
<221> source
<223> /note="Gene Symbol: ACCS; "

<220>
<221> source
<223> /note="Gene Name:
1-aminocyclopropane-1-carboxylate synthase homolog
(Arabidopsis)
(non-functional); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434156"

<400> 74
Met Phe Thr Leu Pro Gln Lys Asp Phe Arg Ala Pro Thr Thr Cys Leu
1 5 10 15

Gly Pro Thr Cys Met Gln Asp Leu Gly Ser Ser His Gly Glu Asp Leu
20 25 30

Glu Gly Glu Cys Ser Arg Lys Leu Asp Gln Lys Leu Pro Glu Leu Arg
35 40 45

Gly Val Gly Asp Pro Ala Met Ile Ser Ser Asp Thr Ser Tyr Leu Ser
50 55 60

Ser Arg Gly Arg Met Ile Lys Trp Phe Trp Asp Ser Ala Glu Glu Gly
65 70 75 80

Tyr Arg Thr Tyr His Met Asp Glu Tyr Asp Glu Asp Lys Asn Pro Ser
85 90 95

Gly Ile Ile Asn Leu Gly Thr Ser Glu Asn Lys Leu Cys Phe Asp Leu

100 105 110

Leu Ser Trp Arg Leu Ser Gln Arg Asp Met Gln Arg Val Glu Pro Ser
115 120 125

Leu Leu Gln Tyr Ala Asp Trp Arg Gly His Leu
130 135

<210> 75
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 7; "

<220>
<221> source
<223> /note="Gene Symbol: ACCS; "

<220>
<221> source
<223> /note="Gene Name:
1-aminocyclopropane-1-carboxylate synthase homolog
(Arabidopsis)
(non-functional); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435919"

<400> 75
Met Phe Thr Leu Pro Gln Lys Asp Phe Arg Ala Pro Thr Thr Cys Leu
1 5 10 15

Gly Pro Thr Cys Met Gln Asp Leu Gly Ser Ser His Gly Glu Asp Leu
20 25 30

Glu Gly Glu Cys Ser Arg Lys Leu Asp Gln Lys Leu Pro Glu Leu Arg
35 40 45

Gly Val Gly Asp Pro Ala Met Ile Ser Ser Asp Thr Ser Tyr Leu Ser
50 55 60

Ser Arg Gly Arg Met Ile Lys Trp Phe Trp Asp Ser Ala
65 70 75

<210> 76

<211> 568
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 8; "

<220>
<221> source
<223> /note="Gene Symbol: ACCSL; "

<220>
<221> source
<223> /note="Gene Name:
1-aminocyclopropane-1-carboxylate synthase homolog
(Arabidopsis) (non-functional)-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q4AC99; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000368109"

<400> 76
Met Ser His Arg Ser Asp Thr Leu Pro Val Pro Ser Gly Gln Arg Arg
1   5   10   15

Gly Arg Val Pro Arg Asp His Ser Ile Tyr Thr Gln Leu Leu Glu Ile
            20   25   30

Thr Leu His Leu Gln Gln Ala Met Thr Glu His Phe Val Gln Leu Thr
        35   40   45

Ser Arg Gln Gly Leu Ser Leu Glu Glu Arg Arg His Thr Glu Ala Ile
    50   55   60

Cys Glu His Glu Ala Leu Leu Ser Arg Leu Ile Cys Arg Met Ile Asn
65   70   75   80

Leu Leu Gln Ser Gly Ala Ala Ser Gly Leu Glu Leu Gln Val Pro Leu
                85   90   95

Pro Ser Glu Asp Ser Arg Gly Asp Val Arg Tyr Gly Gln Arg Ala Gln
            100   105   110

Leu Ser Gly Gln Pro Asp Pro Val Pro Gln Leu Ser Asp Cys Glu Ala
        115   120   125

```
Ala Phe Val Asn Arg Asp Leu Ser Ile Arg Gly Ile Asp Ile Ser Val
    130                 135                 140

Phe Tyr Gln Ser Ser Phe Gln Asp Tyr Asn Ala Tyr Gln Lys Asp Lys
145                 150                 155                 160

Tyr His Lys Asp Lys Asn Thr Leu Gly Phe Ile Asn Leu Gly Thr Ser
                165                 170                 175

Glu Asn Lys Leu Cys Met Asp Leu Met Thr Glu Arg Leu Gln Glu Ser
            180                 185                 190

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

Gly Gln Pro Phe Leu Arg Glu Glu Val Ala Arg Phe Leu Thr Tyr Tyr
    210                 215                 220

Cys Arg Ala Pro Thr Arg Leu Asp Pro Glu Asn Val Val Val Leu Asn
225                 230                 235                 240

Gly Cys Cys Ser Val Phe Cys Ala Leu Ala Met Val Leu Cys Asp Pro
                245                 250                 255

Gly Glu Ala Phe Leu Val Pro Ala Pro Phe Tyr Gly Gly Phe Ala Phe
            260                 265                 270

Ser Ser Arg Leu Tyr Ala Lys Val Glu Leu Ile Pro Val His Leu Glu
        275                 280                 285

Ser Glu Val Thr Val Thr Asn Thr His Pro Phe Gln Leu Thr Val Asp
    290                 295                 300

Lys Leu Glu Glu Ala Leu Leu Glu Ala Arg Leu Glu Gly Lys Lys Val
305                 310                 315                 320

Arg Gly Leu Val Leu Ile Asn Pro Gln Asn Pro Leu Gly Asp Ile Tyr
                325                 330                 335

Ser Pro Asp Ser Leu Met Lys Tyr Leu Glu Phe Ala Lys Arg Tyr Asn
            340                 345                 350
```

```
Leu His Val Ile Ile Asp Glu Ile Tyr Met Leu Ser Val Phe Asp Glu
        355                 360                 365

Ser Ile Thr Phe His Ser Ile Leu Ser Met Lys Ser Leu Pro Asp Ser
    370                 375                 380

Asn Arg Thr His Val Ile Trp Gly Thr Ser Lys Asp Phe Gly Ile Ser
385                 390                 395                 400

Gly Phe Arg Phe Gly Ala Leu Tyr Thr His Asn Lys Glu Val Ala Ser
                405                 410                 415

Ala Val Ser Ala Phe Gly Tyr Leu His Ser Ile Ser Gly Ile Thr Gln
            420                 425                 430

His Lys Leu Cys Gln Leu Leu Gln Asn Thr Glu Trp Ile Asp Lys Val
        435                 440                 445

Tyr Leu Pro Thr Asn Cys Tyr Arg Leu Arg Glu Ala His Lys Tyr Ile
    450                 455                 460

Thr Ala Glu Leu Lys Ala Leu Glu Ile Pro Phe His Asn Arg Ser Ser
465                 470                 475                 480

Gly Leu Tyr Val Trp Ile Asn Leu Lys Lys Tyr Leu Asp Pro Cys Thr
                485                 490                 495

Phe Glu Glu Glu Arg Leu Leu Tyr Cys Arg Phe Leu Asp Asn Lys Leu
            500                 505                 510

Leu Leu Ser Arg Gly Lys Thr Tyr Met Cys Lys Glu Pro Gly Trp Phe
        515                 520                 525

Cys Leu Ile Phe Ala Asp Glu Leu Pro Arg Leu Lys Leu Ala Met Arg
    530                 535                 540

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

Gln Leu Glu Asp Ala Met Arg Glu
                565
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<210> 77
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 8; "

<220>
<221> source
<223> /note="Gene Symbol: ACCSL; "

<220>
<221> source
<223> /note="Gene Name:
1-aminocyclopropane-1-carboxylate synthase homolog
(Arabidopsis) (non-functional)-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436505"

<400> 77

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

```
    130                 135                 140

Phe Tyr Gln Ser Ser Phe Gln Asp Tyr Asn Ala Tyr Gln Lys Asp Lys
145                 150                 155                 160

Tyr His Lys Asp Lys Asn Thr Leu Gly Gly Ala Arg Gly Leu Thr
                165                 170                 175


<210> 78
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 9; "

<220>
<221> source
<223> /note="Gene Symbol: BPGM; "

<220>
<221> source
<223> /note="Gene Name:
      2,3-bisphosphoglycerate mutase; "

<220>
<221> source
<223> /note="Uniprot ID:  P07738; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000342032"

<400> 78
Met Ser Lys Tyr Lys Leu Ile Met Leu Arg His Gly Glu Gly Ala Trp
1               5                   10                  15

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

Glu Gly Met Glu Glu Ala Arg Asn Cys Gly Lys Gln Leu Lys Ala Leu
        35                  40                  45

Asn Phe Glu Phe Asp Leu Val Phe Thr Ser Val Leu Asn Arg Ser Ile
    50                  55                  60

His Thr Ala Trp Leu Ile Leu Glu Glu Leu Gly Gln Glu Trp Val Pro
65                  70                  75                  80
```

```
Val Glu Ser Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Ile
                85                  90                  95

Gly Leu Asn Arg Glu Gln Met Ala Leu Asn His Gly Glu Glu Gln Val
            100                 105                 110

Arg Leu Trp Arg Arg Ser Tyr Asn Val Thr Pro Pro Pro Ile Glu Glu
        115                 120                 125

Ser His Pro Tyr Tyr Gln Glu Ile Tyr Asn Asp Arg Arg Tyr Lys Val
    130                 135                 140

Cys Asp Val Pro Leu Asp Gln Leu Pro Arg Ser Glu Ser Leu Lys Asp
145                 150                 155                 160

Val Leu Glu Arg Leu Leu Pro Tyr Trp Asn Glu Arg Ile Ala Pro Glu
                165                 170                 175

Val Leu Arg Gly Lys Thr Ile Leu Ile Ser Ala His Gly Asn Ser Ser
            180                 185                 190

Arg Ala Leu Leu Lys His Leu Glu Gly Ile Ser Asp Glu Asp Ile Ile
        195                 200                 205

Asn Ile Thr Leu Pro Thr Gly Val Pro Ile Leu Leu Glu Leu Asp Glu
    210                 215                 220

Asn Leu Arg Ala Val Gly Pro His Gln Phe Leu Gly Asp Gln Glu Ala
225                 230                 235                 240

Ile Gln Ala Ala Ile Lys Lys Val Glu Asp Gln Gly Lys Val Lys Gln
                245                 250                 255

Ala Lys Lys
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<210> 79
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 9; "

<220>
<221> source
<223> /note="Gene Symbol: BPGM; "

<220>
<221> source
<223> /note="Gene Name:
2,3-bisphosphoglycerate mutase; "

<220>
<221> source
<223> /note="Uniprot ID: P07738; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376840"

<400> 79
Met Ser Lys Tyr Lys Leu Ile Met Leu Arg His Gly Glu Gly Ala Trp
1   5   10   15

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

Glu Gly Met Glu Glu Ala Arg Asn Cys Gly Lys Gln Leu Lys Ala Leu
        35   40   45

Asn Phe Glu Phe Asp Leu Val Phe Thr Ser Val Leu Asn Arg Ser Ile
    50   55   60

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

Val Glu Ser Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Ile
                85   90   95

Gly Leu Asn Arg Glu Gln Met Ala Leu Asn His Gly Glu Glu Gln Val
            100   105   110

Arg Leu Trp Arg Arg Ser Tyr Asn Val Thr Pro Pro Pro Ile Glu Glu
        115   120   125

Ser His Pro Tyr Tyr Gln Glu Ile Tyr Asn Asp Arg Arg Tyr Lys Val
    130   135   140

Cys Asp Val Pro Leu Asp Gln Leu Pro Arg Ser Glu Ser Leu Lys Asp
145   150   155   160

```
Val Leu Glu Arg Leu Leu Pro Tyr Trp Asn Glu Arg Ile Ala Pro Glu
                165                 170                 175

Val Leu Arg Gly Lys Thr Ile Leu Ile Ser Ala His Gly Asn Ser Ser
            180                 185                 190

Arg Ala Leu Leu Lys His Leu Glu Gly Ile Ser Asp Glu Asp Ile Ile
        195                 200                 205

Asn Ile Thr Leu Pro Thr Gly Val Pro Ile Leu Leu Glu Leu Asp Glu
    210                 215                 220

Asn Leu Arg Ala Val Gly Pro His Gln Phe Leu Gly Asp Gln Glu Ala
225                 230                 235                 240

Ile Gln Ala Ala Ile Lys Lys Val Glu Asp Gln Gly Lys Val Lys Gln
                245                 250                 255

Ala Lys Lys
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<210> 80
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 9; "

<220>
<221> source
<223> /note="Gene Symbol: BPGM; "

<220>
<221> source
<223> /note="Gene Name:
2,3-bisphosphoglycerate mutase; "

<220>
<221> source
<223> /note="Uniprot ID: P07738; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399838"

<400> 80

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Met Ser Lys Tyr Lys Leu Ile Met Leu Arg His Gly Glu Gly Ala Trp
1               5                  10                  15

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

Glu Gly Met Glu Glu Ala Arg Asn Cys Gly Lys Gln Leu Lys Ala Leu
        35                  40                  45

Asn Phe Glu Phe Asp Leu Val Phe Thr Ser Val Leu Asn Arg Ser Ile
    50                  55                  60

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

Val Glu Ser Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Ile
                85                  90                  95

Gly Leu Asn Arg Glu Gln Met Ala Leu Asn His Gly Glu Glu Gln Val
            100                 105                 110

Arg Leu Trp Arg Arg Ser Tyr Asn Val Thr Pro Pro Pro Ile Glu Glu
        115                 120                 125

Ser His Pro Tyr Tyr Gln Glu Ile Tyr Asn Asp Arg Arg Tyr Lys Val
    130                 135                 140

Cys Asp Val Pro Leu Asp Gln Leu Pro Arg Ser Glu Ser Leu Lys Asp
145                 150                 155                 160

Val Leu Glu Arg Leu Leu Pro Tyr Trp Asn Glu Arg Ile Ala Pro Glu
                165                 170                 175

Val Leu Arg Gly Lys Thr Ile Leu Ile Ser Ala His Gly Asn Ser Ser
            180                 185                 190

Arg Ala Leu Leu Lys His Leu Glu Gly Ile Ser Asp Glu Asp Ile Ile
        195                 200                 205

Asn Ile Thr Leu Pro Thr Gly Val Pro Ile Leu Leu Glu Leu Asp Glu
    210                 215                 220

Asn Leu Arg Ala Val Gly Pro His Gln Phe Leu Gly Asp Gln Glu Ala
```

225 230 235 240

Ile Gln Ala Ala Ile Lys Lys Val Glu Asp Gln Gly Lys Val Lys Gln
245 250 255

Ala Lys Lys

<210> 81
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 9; "

<220>
<221> source
<223> /note="Gene Symbol: BPGM; "

<220>
<221> source
<223> /note="Gene Name:
2,3-bisphosphoglycerate mutase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403050"

<400> 81
Met Ser Lys Tyr Lys Leu Ile Met Leu Arg His Gly Glu Gly Ala Trp
1 5 10 15

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

Glu Gly Met Glu Glu Ala Arg Asn Cys Gly Lys Gln Leu Lys Ala Leu
35 40 45

Asn Phe Glu Phe Asp Leu Val Phe Thr Ser Val Leu Asn Arg Ser Ile
50 55 60

His Thr Ala Trp Leu Ile Leu Glu Glu Leu Gly Gln Glu Trp
65 70 75

<210> 82
<211> 401
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 10; "

<220>
<221> source
<223> /note="Gene Symbol: CNP; "

<220>
<221> source
<223> /note="Gene Name:
2',3'-cyclic nucleotide 3' phosphodiesterase; "

<220>
<221> source
<223> /note="Uniprot ID: P09543; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377466"

<400> 82

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Met Ser Ser Ser Gly Ala Lys Asp Lys Pro Glu Leu Gln Phe Pro Phe
1               5                  10                  15


Leu Gln Asp Glu Asp Thr Val Ala Thr Leu Leu Glu Cys Lys Thr Leu
            20                  25                  30


Phe Ile Leu Arg Gly Leu Pro Gly Ser Gly Lys Ser Thr Leu Ala Arg
        35                  40                  45


Val Ile Val Asp Lys Tyr Arg Asp Gly Thr Lys Met Val Ser Ala Asp
    50                  55                  60


Ala Tyr Lys Ile Thr Pro Gly Ala Arg Gly Ala Phe Ser Glu Glu Tyr
65                  70                  75                  80


Lys Arg Leu Asp Glu Asp Leu Ala Ala Tyr Cys Arg Arg Arg Asp Ile
                85                  90                  95


Arg Ile Leu Val Leu Asp Asp Thr Asn His Glu Arg Glu Arg Leu Glu
            100                 105                 110


Gln Leu Phe Glu Met Ala Asp Gln Tyr Gln Tyr Gln Val Val Leu Val
        115                 120                 125


Glu Pro Lys Thr Ala Trp Arg Leu Asp Cys Ala Gln Leu Lys Glu Lys
```

```
    130                 135                 140

Asn Gln Trp Gln Leu Ser Ala Asp Asp Leu Lys Lys Leu Lys Pro Gly
145                 150                 155                 160

Leu Glu Lys Asp Phe Leu Pro Leu Tyr Phe Gly Trp Phe Leu Thr Lys
                165                 170                 175

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

Leu Gly Asn His Lys Ala Phe Lys Lys Glu Leu Arg Gln Phe Val Pro
        195                 200                 205

Gly Asp Glu Pro Arg Glu Lys Met Asp Leu Val Thr Tyr Phe Gly Lys
    210                 215                 220

Arg Pro Pro Gly Val Leu His Cys Thr Thr Lys Phe Cys Asp Tyr Gly
225                 230                 235                 240

Lys Ala Pro Gly Ala Glu Glu Tyr Ala Gln Gln Asp Val Leu Lys Lys
                245                 250                 255

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

Pro Lys Thr Thr Gly Ala Arg Val Glu Leu Ser Glu Gln Gln Leu Gln
        275                 280                 285

Leu Trp Pro Ser Asp Val Asp Lys Leu Ser Pro Thr Asp Asn Leu Pro
    290                 295                 300

Arg Gly Ser Arg Ala His Ile Thr Leu Gly Cys Ala Ala Asp Val Glu
305                 310                 315                 320

Ala Val Gln Thr Gly Leu Asp Leu Leu Glu Ile Leu Arg Gln Glu Lys
                325                 330                 335

Gly Gly Ser Arg Gly Glu Glu Val Gly Glu Leu Ser Arg Gly Lys Leu
            340                 345                 350

Tyr Ser Leu Gly Asn Gly Arg Trp Met Leu Thr Leu Ala Lys Asn Met
        355                 360                 365
```

```
Glu Val Arg Ala Ile Phe Thr Gly Tyr Tyr Gly Lys Gly Lys Pro Val
    370                 375                 380

Pro Thr Gln Gly Ser Arg Lys Gly Gly Ala Leu Gln Ser Cys Thr Ile
385                 390                 395                 400

Ile
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<210> 83
<211> 421
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 10; "

<220>
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<223> /note="Gene Symbol: CNP; "

<220>
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<223> /note="Gene Name:
2',3'-cyclic nucleotide 3' phosphodiesterase; "

<220>
<221> source
<223> /note="Uniprot ID: P09543; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377470"

<400> 83

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Met Asn Arg Gly Phe Ser Arg Lys Ser His Thr Phe Leu Pro Lys Ile
1               5                   10                  15

Phe Phe Arg Lys Met Ser Ser Ser Gly Ala Lys Asp Lys Pro Glu Leu
            20                  25                  30

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

Cys Lys Thr Leu Phe Ile Leu Arg Gly Leu Pro Gly Ser Gly Lys Ser
    50                  55                  60
```

```
Thr Leu Ala Arg Val Ile Val Asp Lys Tyr Arg Asp Gly Thr Lys Met
65                  70                  75                  80

Val Ser Ala Asp Ala Tyr Lys Ile Thr Pro Gly Ala Arg Gly Ala Phe
                85                  90                  95

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

Arg Arg Asp Ile Arg Ile Leu Val Leu Asp Asp Thr Asn His Glu Arg
        115                 120                 125

Glu Arg Leu Glu Gln Leu Phe Glu Met Ala Asp Gln Tyr Gln Tyr Gln
    130                 135                 140

Val Val Leu Val Glu Pro Lys Thr Ala Trp Arg Leu Asp Cys Ala Gln
145                 150                 155                 160

Leu Lys Glu Lys Asn Gln Trp Gln Leu Ser Ala Asp Asp Leu Lys Lys
                165                 170                 175

Leu Lys Pro Gly Leu Glu Lys Asp Phe Leu Pro Leu Tyr Phe Gly Trp
            180                 185                 190

Phe Leu Thr Lys Lys Ser Ser Glu Thr Leu Arg Lys Ala Gly Gln Val
        195                 200                 205

Phe Leu Glu Glu Leu Gly Asn His Lys Ala Phe Lys Lys Glu Leu Arg
    210                 215                 220

Gln Phe Val Pro Gly Asp Glu Pro Arg Glu Lys Met Asp Leu Val Thr
225                 230                 235                 240

Tyr Phe Gly Lys Arg Pro Pro Gly Val Leu His Cys Thr Thr Lys Phe
                245                 250                 255

Cys Asp Tyr Gly Lys Ala Pro Gly Ala Glu Glu Tyr Ala Gln Gln Asp
            260                 265                 270

Val Leu Lys Lys Ser Tyr Ser Lys Ala Phe Thr Leu Thr Ile Ser Ala
        275                 280                 285

Leu Phe Val Thr Pro Lys Thr Thr Gly Ala Arg Val Glu Leu Ser Glu
```

```
    290                 295                 300

Gln Gln Leu Gln Leu Trp Pro Ser Asp Val Asp Lys Leu Ser Pro Thr
305                 310                 315                 320

Asp Asn Leu Pro Arg Gly Ser Arg Ala His Ile Thr Leu Gly Cys Ala
                325                 330                 335

Ala Asp Val Glu Ala Val Gln Thr Gly Leu Asp Leu Leu Glu Ile Leu
            340                 345                 350

Arg Gln Glu Lys Gly Gly Ser Arg Gly Glu Glu Val Gly Glu Leu Ser
        355                 360                 365

Arg Gly Lys Leu Tyr Ser Leu Gly Asn Gly Arg Trp Met Leu Thr Leu
    370                 375                 380

Ala Lys Asn Met Glu Val Arg Ala Ile Phe Thr Gly Tyr Tyr Gly Lys
385                 390                 395                 400

Gly Lys Pro Val Pro Thr Gln Gly Ser Arg Lys Gly Gly Ala Leu Gln
                405                 410                 415

Ser Cys Thr Ile Ile
            420


<210> 84
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 10; "

<220>
<221> source
<223> /note="Gene Symbol: CNP; "

<220>
<221> source
<223> /note="Gene Name:
      2',3'-cyclic nucleotide 3' phosphodiesterase; "

<220>
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<223> /note="ENSP ID: ENSP00000413104"
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<400> 84
Met Ser Ser Ser Gly Ala Lys Asp Lys Pro Glu Leu Gln Phe Pro Phe
1   5   10   15

Leu Gln Asp Glu Asp Thr Val Ala Thr Leu Leu Glu Cys Lys Thr Leu
            20   25   30

Phe Ile Leu Arg Gly Leu Pro Gly Ser Gly Lys Ser Thr Leu Ala Arg
        35   40   45

Val Ile Val Asp Lys Tyr Arg Asp Gly Thr Lys Met Val Ser Ala Asp
    50   55   60

Ala Tyr Lys Ile Thr Pro Gly Ala Arg Gly Ala Phe Ser Glu Glu Tyr
65   70   75   80

Lys Arg Leu Asp Glu Asp Leu Ala Ala Tyr Cys Arg Arg Arg Asp Ile
                85   90   95

Arg Ile Leu Val Leu Asp Asp Thr Asn His Glu Arg Glu Arg Leu Glu
            100   105   110

Gln Leu Phe Glu Met Ala Asp Gln Tyr Gln Tyr Gln Val Val Leu Val
        115   120   125

Glu Pro Lys Thr Ala Trp Arg Leu Asp Cys Ala Gln Leu Lys Glu Lys
    130   135   140

<210> 85
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 10; "

<220>
<221> source
<223> /note="Gene Symbol: CNP; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source

<223> /note="ENSP ID: ENSP00000466807"

<400> 85
Met Ser Ser Ser Gly Ala Lys Asp Lys Pro Glu Leu Gln Phe Pro Phe
1   5   10   15

Leu Gln Asp Glu Asp Thr Val Ala Thr Leu Leu Glu Cys Lys Thr Leu
            20   25   30

Phe Ile Leu Arg Gly Leu Pro Gly Ser Gly Lys Ser Thr Leu Ala Arg
        35   40   45

Val Ile Val Asp Lys Tyr Arg Asp Gly Thr Lys Met Val Ser Ala Asp
    50   55   60

Ala Tyr Lys Ile Thr Pro Gly Ala Arg Gly Ala Phe Ser Glu Glu Tyr
65   70   75   80

Lys Arg Leu Asp Glu Asp Leu Ala Ala Tyr Cys Arg Arg Arg Asp Ile
                85   90   95

Arg Ile Leu Val Leu Asp Asp Thr Asn His Glu Arg Glu Arg Leu Glu
            100   105   110

Gln Leu Phe Glu Met Ala Asp Gln
        115   120

<210> 86
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 10; "

<220>
<221> source
<223> /note="Gene Symbol: CNP; "

<220>
<221> source
<223> /note="Gene Name:
      2',3'-cyclic nucleotide 3' phosphodiesterase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467641"

<400> 86
Met Ser Ser Leu Gly Met Ser Pro Gly Arg Arg Trp Thr Trp Ser Pro
1 5 10 15

Thr Leu Glu Arg Asp Pro Gln Ala Cys Cys Ile Ala Gln Pro Ser Phe
20 25 30

Val Thr Thr Gly Arg Leu Pro Gly Gln Arg Ser Thr Leu Asn Lys Met
35 40 45

Cys

<210> 87
<211> 164
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 10; "

<220>
<221> source
<223> /note="Gene Symbol: CNP; "

<220>
<221> source
<223> /note="Gene Name:
2',3'-cyclic nucleotide 3' phosphodiesterase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468198"

<400> 87
Met Asp Glu Asp Thr Val Ala Thr Leu Leu Glu Cys Lys Thr Leu Phe
1 5 10 15

Ile Leu Arg Gly Leu Pro Gly Ser Gly Lys Ser Thr Leu Ala Arg Val
20 25 30

Ile Val Asp Lys Tyr Arg Asp Gly Thr Lys Met Val Ser Ala Asp Ala
35 40 45

Tyr Lys Ile Thr Pro Gly Ala Arg Gly Ala Phe Ser Glu Glu Tyr Lys
50 55 60

Arg Leu Asp Glu Asp Leu Ala Ala Tyr Cys Arg Arg Arg Asp Ile Arg

65 70 75 80

Ile Leu Val Leu Asp Asp Thr Asn His Glu Arg Glu Arg Leu Glu Gln
85 90 95

Leu Phe Glu Met Ala Asp Gln Tyr Gln Tyr Gln Val Val Leu Val Glu
100 105 110

Pro Lys Thr Ala Trp Arg Leu Asp Cys Ala Gln Leu Lys Glu Lys Asn
115 120 125

Gln Trp Gln Leu Ser Ala Asp Asp Leu Lys Lys Leu Lys Pro Gly Leu
130 135 140

Glu Lys Asp Phe Leu Pro Leu Tyr Phe Gly Trp Phe Leu Thr Lys Lys
145 150 155 160

Ser Ser Glu Thr

<210> 88
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 10; "

<220>
<221> source
<223> /note="Gene Symbol: CNP; "

<220>
<221> source
<223> /note="Gene Name:
2',3'-cyclic nucleotide 3' phosphodiesterase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468471"

<400> 88
Met Ser Ser Ser Gly Ala Lys Asp Lys Pro Glu Leu Gln Phe Pro Phe
1 5 10 15

Leu Gln Asp Glu Asp Thr Val Ala Thr Leu Leu Glu Cys Lys Thr Leu
20 25 30

```
Phe Ile Leu Arg Gly Leu Pro Gly Ser Gly Lys Ser Thr Leu Ala Arg
        35                  40                  45

Val Ile Val Asp Lys Tyr Arg Asp Gly Thr Lys Met Val Ser Ala Asp
    50                  55                  60

Ala Tyr Lys Ile Thr Pro Gly Ala Arg Gly Ala Phe Ser Glu Glu Tyr
65                  70                  75                  80

Lys Arg Leu Asp Glu Asp Leu Ala Ala Tyr Cys Arg Arg Arg Asp Ile
                85                  90                  95

Arg Ile Leu Val Leu Asp Asp Thr Asn His Glu Arg Glu Arg Leu Glu
            100                 105                 110

Gln Leu Phe Glu Met Ala Asp Gln Tyr Gln Tyr Gln Val Val Leu Val
        115                 120                 125

Glu Pro Lys Thr Ala Trp Arg Leu Asp Cys Ala Gln Leu Lys Glu Lys
    130                 135                 140

Asn Gln Trp Gln Leu Ser Ala Asp Asp
145                 150


<210> 89
<211> 335
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 1,
      mitochondrial; "

<220>
<221> source
<223> /note="Uniprot ID:  Q16698; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000220764"

<400> 89
Met Lys Leu Pro Ala Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro
1 5 10 15

Cys Gly Leu Ala Pro Arg Arg Phe Phe Ser Tyr Gly Thr Lys Ile Leu
20 25 30

Tyr Gln Asn Thr Glu Ala Leu Gln Ser Lys Phe Phe Ser Pro Leu Gln
35 40 45

Lys Ala Met Leu Pro Pro Asn Ser Phe Gln Gly Lys Val Ala Phe Ile
50 55 60

Thr Gly Gly Gly Thr Gly Leu Gly Lys Gly Met Thr Thr Leu Leu Ser
65 70 75 80

Ser Leu Gly Ala Gln Cys Val Ile Ala Ser Arg Lys Met Asp Val Leu
85 90 95

Lys Ala Thr Ala Glu Gln Ile Ser Ser Gln Thr Gly Asn Lys Val His
100 105 110

Ala Ile Gln Cys Asp Val Arg Asp Pro Asp Met Val Gln Asn Thr Val
115 120 125

Ser Glu Leu Ile Lys Val Ala Gly His Pro Asn Ile Val Ile Asn Asn
130 135 140

Ala Ala Gly Asn Phe Ile Ser Pro Thr Glu Arg Leu Ser Pro Asn Ala
145 150 155 160

Trp Lys Thr Ile Thr Asp Ile Val Leu Asn Gly Thr Ala Phe Val Thr
165 170 175

Leu Glu Ile Gly Lys Gln Leu Ile Lys Ala Gln Lys Gly Ala Ala Phe
180 185 190

Leu Ser Ile Thr Thr Ile Tyr Ala Glu Thr Gly Ser Gly Phe Val Val
195 200 205

Pro Ser Ala Ser Ala Lys Ala Gly Val Glu Ala Met Ser Lys Ser Leu

```
    210                 215                 220

Ala Ala Glu Trp Gly Lys Tyr Gly Met Arg Phe Asn Val Ile Gln Pro
225                 230                 235                 240

Gly Pro Ile Lys Thr Lys Gly Ala Phe Ser Arg Leu Asp Pro Thr Gly
                245                 250                 255

Thr Phe Glu Lys Glu Met Ile Gly Arg Ile Pro Cys Gly Arg Leu Gly
            260                 265                 270

Thr Val Glu Glu Leu Ala Asn Leu Ala Ala Phe Leu Cys Ser Asp Tyr
        275                 280                 285

Ala Ser Trp Ile Asn Gly Ala Val Ile Lys Phe Asp Gly Gly Glu Glu
    290                 295                 300

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

Gln Trp Asp Thr Ile Glu Glu Leu Ile Arg Lys Thr Lys Gly Ser
                325                 330                 335


<210> 90
<211> 205
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 1,
      mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427936"

<400> 90
Met Thr Ala Tyr Leu Ala Thr Gly Ile Leu Trp Lys Glu Met Phe Phe
1               5                   10                  15
```

```
Ser Tyr Gly Thr Lys Ile Leu Tyr Gln Asn Thr Glu Ala Leu Gln Ser
            20                  25                  30

Lys Phe Phe Ser Pro Leu Gln Lys Ala Met Leu Pro Pro Asn Ser Phe
        35                  40                  45

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

Gly Met Thr Thr Leu Leu Ser Ser Leu Gly Ala Gln Cys Val Ile Ala
65                  70                  75                  80

Ser Arg Lys Met Asp Val Leu Lys Ala Thr Ala Glu Gln Ile Ser Ser
                85                  90                  95

Gln Thr Gly Asn Lys Val His Ala Ile Gln Cys Asp Val Arg Asp Pro
            100                 105                 110

Asp Met Val Gln Asn Thr Val Ser Glu Leu Ile Lys Val Ala Gly His
        115                 120                 125

Pro Asn Ile Val Ile Asn Asn Ala Ala Gly Asn Phe Ile Ser Pro Thr
    130                 135                 140

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

Asn Gly Thr Ala Phe Val Thr Leu Glu Ile Gly Lys Gln Leu Ile Lys
                165                 170                 175

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

Thr Gly Ser Gly Phe Val Val Pro Ser Ala Ser Ala Lys
        195                 200                 205


<210> 91
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428162"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 91
Xaa Ala Ala Glu Trp Gly Lys Tyr Gly Met Arg Phe Asn Val Ile Gln
1 5 10 15

Pro Gly Pro Ile Lys Thr Lys Glu Cys Val Trp Gly Arg Glu Val Cys
20 25 30

Cys Gly Thr Asn Pro Asp Asn Ala Glu Cys His
35 40

<210> 92
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428533"

<400> 92
Met Lys Leu Pro Ala Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro
1   5   10   15

Cys Gly Leu Ala Pro Arg Arg Arg Cys Tyr His Leu Ile Val Phe Lys
            20   25   30

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

<210> 93
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 1,
      mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428701"

<400> 93
Met Lys Leu Pro Ala Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro
1   5   10   15

Cys Gly Leu Ala Pro Arg Arg Glu Asp Gly Cys Phe Glu Ser Tyr Arg
            20   25   30

Arg Thr Asn Phe Phe Ser Asn Trp Lys
        35   40

<210> 94
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429096"

<400> 94

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Met Leu Pro Pro Asn Ser Phe Gln Gly Lys Val Ala Phe Ile Thr Gly
1               5                  10                  15

Gly Gly Thr Gly Leu Gly Lys Gly Met Thr Thr Leu Leu Ser Ser Leu
            20                  25                  30

Gly Ala Gln Cys Val Ile Ala Ser Arg Lys Met Asp Val Leu Lys Ala
        35                  40                  45

Thr Ala Glu Gln Ile Ser Ser Gln Thr Gly Asn Lys Val His Ala Ile
    50                  55                  60

Gln Cys Asp Val Arg Asp Pro Asp Met Val Gln Asn Thr Val Ser Glu
65                  70                  75                  80

Leu Ile Lys Val Ala Gly His Pro Asn Ile Val Ile Asn Asn Ala Ala
                85                  90                  95

Gly Asn Phe Ile Ser Pro Thr Glu Arg Leu Ser Pro Asn Ala Trp Lys
            100                 105                 110

Thr Ile Thr Asp Ile Val Leu Asn Gly Thr Ala Phe Val Thr Leu Glu
        115                 120                 125

Ile Gly Lys Gln Leu Ile Lys Ala Gln Lys Gly Ala Ala Phe Leu Ser
    130                 135                 140

Ile Thr Thr Ile Tyr Ala Glu
145                 150
```

<210> 95
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
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<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429551"

<400> 95
Met Lys Leu Pro Ala Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro
1 5 10 15

Cys Gly Leu Ala Pro Arg Arg Glu Asp Gly Cys Phe Glu Ser Tyr Arg
20 25 30

Arg Thr Asn Phe Phe Ser Asn Trp Lys
35 40

<210> 96
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,
mitochondrial; "

<220>
<221> source

<223> /note="Uniprot ID: Q16698; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429779"

<400> 96
Met Ser Gly Leu Gly Lys Lys His Leu Leu Leu Met Gly Glu Phe Phe
1   5   10   15

Ser Tyr Gly Thr Lys Ile Leu Tyr Gln Asn Thr Glu Ala Leu Gln Ser
            20   25   30

Lys Phe Phe Ser Pro Leu Gln Lys Ala Met Leu Pro Pro Asn Ser Phe
        35   40   45

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

Gly Met Thr Thr Leu Leu Ser Ser Leu Gly Ala Gln Cys Val Ile Ala
65   70   75   80

Ser Arg Lys Met Asp Val Leu Lys Ala Thr Ala Glu Gln Ile Ser Ser
                85   90   95

Gln Thr Gly Asn Lys Val His Ala Ile Gln Cys Asp Val Arg Asp Pro
            100   105   110

Asp Met Val Gln Asn Thr Val Ser Glu Leu Ile Lys Val Ala Gly His
        115   120   125

Pro Asn Ile Val Ile Asn Asn Ala Ala Gly Asn Phe Ile Ser Pro Thr
    130   135   140

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

Asn Gly Thr Ala Phe Val Thr Leu Glu Ile Gly Lys Gln Leu Ile Lys
                165   170   175

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

Thr Gly Ser Gly Phe Val Val Pro Ser Ala Ser Ala Lys Ala Gly Val
        195   200   205

```
Glu Ala Met Ser Lys Ser Leu Ala Ala Glu Trp Gly Lys Tyr Gly Met
    210                 215                 220

Arg Phe Asn Val Ile Gln Pro Gly Pro Ile Lys Thr Lys Gly Ala Phe
225                 230                 235                 240

Ser Arg Leu Asp Pro Thr Gly Thr Phe Glu Lys Glu Met Ile Gly Arg
                245                 250                 255

Ile Pro Cys Gly Arg Leu Gly Thr Val Glu Glu Leu Ala Asn Leu Ala
            260                 265                 270

Ala Phe Leu Cys Ser Asp Tyr Ala Ser Trp Ile Asn Gly Ala Val Ile
        275                 280                 285

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

Leu Arg Lys Val Thr Lys Glu Gln Trp Asp Thr Ile Glu Glu Leu Ile
305                 310                 315                 320

Arg Lys Thr Lys Gly Ser
                325


<210> 97
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 1,
      mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430561"
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<400> 97
Met Phe Phe Ser Tyr Gly Thr Lys Ile Leu Tyr Gln Asn Thr Glu Ala
1 5 10 15

Leu Gln Ser Lys Phe Phe Ser Pro Leu Gln Lys Ala Met Leu Pro Pro
20 25 30

Asn Ser Phe Gln Gly Lys Val Ala Phe Ile Thr Gly Gly Gly Thr Gly
35 40 45

Leu Gly Lys Gly Met Thr Thr Leu Leu Ser Ser Leu Gly Ala Gln Cys
50 55 60

Val Ile Ala Ser Arg Lys Met Asp Val Leu Lys Ala Thr Ala Glu Gln
65 70 75 80

Ile Ser Ser Gln Thr Gly Asn Lys Val His Ala Ile Gln Cys Asp Val
85 90 95

Arg Asp Pro Asp Met Val Gln Asn Thr Val Ser Glu Leu Ile Lys Val
100 105 110

Ala Gly His Pro Asn Ile Val Ile Asn Asn Ala Ala Gly Asn Phe Ile
115 120 125

Ser Pro Thr Glu Arg Leu Ser Pro Asn Ala Trp Lys Thr Ile Thr Asp
130 135 140

Ile Val Leu Asn Gly Thr Ala Phe Val Thr Leu Glu Ile Gly Lys Gln
145 150 155 160

Leu Ile Lys Ala Gln Lys Gly Ala Ala Phe Leu Ser Ile Thr Thr Ile
165 170 175

Tyr Ala Glu Thr Gly
180

<210> 98
<211> 95
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430759"

<400> 98
Met Lys Leu Pro Ala Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro
1 5 10 15

Cys Gly Leu Ala Pro Arg Arg Phe Phe Ser Tyr Gly Thr Lys Ile Leu
20 25 30

Tyr Gln Asn Thr Glu Ala Leu Gln Ser Lys Phe Phe Ser Pro Leu Gln
35 40 45

Lys Ala Met Leu Pro Pro Asn Ser Phe Gln Gly Lys Val Ala Phe Ile
50 55 60

Thr Gly Gly Gly Thr Gly Leu Gly Lys Gly Met Thr Thr Leu Leu Ser
65 70 75 80

Ser Leu Gly Ala Gln Cys Val Ile Ala Ser Arg Asn Ala Phe Leu
85 90 95

<210> 99
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 11; "

<220>
<221> source
<223> /note="Gene Symbol: DECR1; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 1,

mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431045"

<400> 99
Met Lys Leu Pro Ala Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro
1   5   10   15

Cys Gly Leu Ala Pro Arg Arg Glu Asp Gly Cys Phe Glu Ser Tyr Arg
            20   25   30

Arg Thr Asn Phe Phe Ser Asn Trp Lys
        35   40

<210> 100
<211> 292
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
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<223> /note="Gene Symbol: DECR2; "

<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
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<223> /note="Uniprot ID: Q9NUI1; "

<220>
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<223> /note="ENSP ID: ENSP00000219481"

<400> 100
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1   5   10   15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20   25   30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35   40   45

```
Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60

Val Leu Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr Gly Arg Arg Cys
65                  70                  75                  80

Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala Val Met Ala Ala
                85                  90                  95

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

Cys Ala Ala Gly Asn Phe Leu Cys Pro Ala Gly Ala Leu Ser Phe Asn
        115                 120                 125

Ala Phe Lys Thr Val Met Asp Ile Asp Thr Ser Gly Thr Phe Asn Val
    130                 135                 140

Ser Arg Val Leu Tyr Glu Lys Phe Phe Arg Asp His Gly Gly Val Ile
145                 150                 155                 160

Val Asn Ile Thr Ala Thr Leu Gly Asn Arg Gly Gln Ala Leu Gln Val
                165                 170                 175

His Ala Gly Ser Ala Lys Ala Ala Val Asp Ala Met Thr Arg His Leu
            180                 185                 190

Ala Val Glu Trp Gly Pro Gln Asn Ile Arg Val Asn Ser Leu Ala Pro
        195                 200                 205

Gly Pro Ile Ser Gly Thr Glu Gly Leu Arg Arg Leu Gly Gly Pro Gln
    210                 215                 220

Ala Ser Leu Ser Thr Lys Val Thr Ala Ser Pro Leu Gln Arg Leu Gly
225                 230                 235                 240

Asn Lys Thr Glu Ile Ala His Ser Val Leu Tyr Leu Ala Ser Pro Leu
                245                 250                 255

Ala Ser Tyr Val Thr Gly Ala Val Leu Val Ala Asp Gly Gly Ala Trp
            260                 265                 270
```

```
Leu Thr Phe Pro Asn Gly Val Lys Gly Leu Pro Asp Phe Ala Ser Phe
        275                 280                 285


Ser Ala Lys Leu
    290


<210> 101
<211> 94
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000393382"


<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 101
Xaa Ala Arg Lys Leu Ala Gly Ala Thr Gly Arg Arg Cys Leu Pro Leu
1               5                   10                  15


Ser Met Asp Val Arg Ala Pro Pro Ala Val Met Ala Ala Val Asp Gln
            20                  25                  30


Ala Leu Lys Glu Phe Gly Arg Ile Asp Ile Leu Ile Asn Cys Ala Ala
        35                  40                  45


Gly Asn Phe Leu Cys Pro Ala Gly Ala Leu Ser Phe Asn Ala Phe Lys
    50                  55                  60


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

```
Leu Tyr Glu Lys Phe Phe Arg Val Gly Ala Ser Cys Ala Leu
                85                  90


<210> 102
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
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<223> /note="ENSP ID: ENSP00000395913"

<400> 102
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                  10                  15


Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30


Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45


Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60


Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65                  70                  75                  80


Ser



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

<220>
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<221> source
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<220>
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2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
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<223> /note="Uniprot ID: Q9NUI1; "

<220>
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<223> /note="ENSP ID: ENSP00000399697"

<400> 103

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Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                  10                  15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg Ala Ser Glu Asp Gln Met Gly His Cys Ser Ser Ser Gly Thr
    50                  55                  60

Cys Leu Ala Gly Val Ala Thr Phe Met Val Ile Val Gly Lys Gln Pro
65                  70                  75                  80

Pro Asn Gln Lys Ser Arg Glu Thr Lys Glu Gln Gly Arg Gln Ile Pro
                85                  90                  95

Phe Val Cys Val Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser
            100                 105                 110

Leu Pro Arg Val Leu Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr Gly
        115                 120                 125

Arg Arg Cys Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala Val
    130                 135                 140
```

```
Met Ala Ala Val Asp Gln Ala Leu Lys Glu Phe Gly Arg Ile Asp Ile
145                 150                 155                 160

Leu Ile Asn Cys Ser Ser Ser Ser Cys Gly Leu Pro Phe Cys Arg Cys
                165                 170                 175

Gly Arg Glu Leu Pro Val Pro Arg Trp Arg Leu Val Leu Gln Arg Leu
            180                 185                 190

Gln Asp Arg Asp Gly His Arg Tyr Gln Arg His Leu Gln Cys Val Ser
        195                 200                 205

Cys Ala Leu
    210


<210> 104
<211> 280
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
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<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000400374"

<400> 104
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                   10                  15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg His Gly Cys His Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr
    50                  55                  60
```

```
Gly Arg Arg Cys Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala
65                  70                  75                  80

Val Met Ala Ala Val Asp Gln Ala Leu Lys Glu Phe Gly Arg Ile Asp
                85                  90                  95

Ile Leu Ile Asn Cys Ala Ala Gly Asn Phe Leu Cys Pro Ala Gly Ala
            100                 105                 110

Leu Ser Phe Asn Ala Phe Lys Thr Val Met Asp Ile Asp Thr Ser Gly
        115                 120                 125

Thr Phe Asn Val Ser Arg Val Leu Tyr Glu Lys Phe Phe Arg Asp His
    130                 135                 140

Gly Gly Val Ile Val Asn Ile Thr Ala Thr Leu Gly Asn Arg Gly Gln
145                 150                 155                 160

Ala Leu Gln Val His Ala Gly Ser Ala Lys Ala Ala Val Asp Ala Met
                165                 170                 175

Thr Arg His Leu Ala Val Glu Trp Gly Pro Gln Asn Ile Arg Val Asn
            180                 185                 190

Ser Leu Ala Pro Gly Pro Ile Ser Gly Thr Glu Gly Leu Arg Arg Leu
        195                 200                 205

Gly Gly Pro Gln Ala Ser Leu Ser Thr Lys Val Thr Ala Ser Pro Leu
    210                 215                 220

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

Ala Ser Pro Leu Ala Ser Tyr Val Thr Gly Ala Val Leu Val Ala Asp
                245                 250                 255

Gly Gly Ala Trp Leu Thr Phe Pro Asn Gly Val Lys Gly Leu Pro Asp
            260                 265                 270

Phe Ala Ser Phe Ser Ala Lys Leu
        275                 280
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<210> 105
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402180"

<400> 105
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
50 55 60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65 70 75 80

Ser

<210> 106
<211> 292
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUI1; "

<220>
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<223> /note="ENSP ID: ENSP00000481547"

<400> 106

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

```
Val Asn Ile Thr Ala Thr Leu Gly Asn Arg Gly Gln Ala Leu Gln Val
                165                 170                 175

His Ala Gly Ser Ala Lys Ala Ala Val Asp Ala Met Thr Arg His Leu
            180                 185                 190

Ala Val Glu Trp Gly Pro Gln Asn Ile Arg Val Asn Ser Leu Ala Pro
        195                 200                 205

Gly Pro Ile Ser Gly Thr Glu Gly Leu Arg Arg Leu Gly Gly Pro Gln
    210                 215                 220

Ala Ser Leu Ser Thr Lys Val Thr Ala Ser Pro Leu Gln Arg Leu Gly
225                 230                 235                 240

Asn Lys Thr Glu Ile Ala His Ser Val Leu Tyr Leu Ala Ser Pro Leu
                245                 250                 255

Ala Ser Tyr Val Thr Gly Ala Val Leu Val Ala Asp Gly Gly Ala Trp
            260                 265                 270

Leu Thr Phe Pro Asn Gly Val Lys Gly Leu Pro Asp Phe Ala Ser Phe
        275                 280                 285

Ser Ala Lys Leu
    290


<210> 107
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
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<220>
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<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000486613"

<400> 107
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1   5   10   15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20   25   30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35   40   45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50   55   60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65   70   75   80

Ser

<210> 108
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
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<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486679"

<400> 108
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1   5   10   15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20   25   30

```
Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65                  70                  75                  80

Ser
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<210> 109
<211> 280
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487756"

<400> 109

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Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                   10                  15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg His Gly Cys His Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr
    50                  55                  60

Gly Arg Arg Cys Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala
```

65 70 75 80

Val Met Ala Ala Val Asp Gln Ala Leu Lys Glu Phe Gly Arg Ile Asp
85 90 95

Ile Leu Ile Asn Cys Ala Ala Gly Asn Phe Leu Cys Pro Ala Gly Ala
100 105 110

Leu Ser Phe Asn Ala Phe Lys Thr Val Met Asp Ile Asp Thr Ser Gly
115 120 125

Thr Phe Asn Val Ser Arg Val Leu Tyr Glu Lys Phe Phe Arg Asp His
130 135 140

Gly Gly Val Ile Val Asn Ile Thr Ala Thr Leu Gly Asn Arg Gly Gln
145 150 155 160

Ala Leu Gln Val His Ala Gly Ser Ala Lys Ala Ala Val Asp Ala Met
165 170 175

Thr Arg His Leu Ala Val Glu Trp Gly Pro Gln Asn Ile Arg Val Asn
180 185 190

Ser Leu Ala Pro Gly Pro Ile Ser Gly Thr Glu Gly Leu Arg Arg Leu
195 200 205

Gly Gly Pro Gln Ala Ser Leu Ser Thr Lys Val Thr Ala Ser Pro Leu
210 215 220

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

Ala Ser Pro Leu Ala Ser Tyr Val Thr Gly Ala Val Leu Val Ala Asp
245 250 255

Gly Gly Ala Trp Leu Thr Phe Pro Asn Gly Val Lys Gly Leu Pro Asp
260 265 270

Phe Ala Ser Phe Ser Ala Lys Leu
275 280

<210> 110
<211> 142

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
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<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487776"

<400> 110
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg Ile Gln Val Pro Ala Arg Gly Thr Gly Glu Arg Ser Arg Ile
50 55 60

Ala Leu Gly Gly Val Arg Thr Ser Arg Pro Leu Gln Ala Ala Arg Lys
65 70 75 80

Leu Ala Gly Ala Thr Gly Arg Arg Cys Leu Pro Leu Ser Met Asp Val
85 90 95

Arg Ala Pro Pro Ala Val Met Ala Ala Val Asp Gln Ala Leu Lys Glu
100 105 110

Phe Gly Arg Ile Asp Ile Leu Ile Asn Cys Ala Ala Gly Asn Phe Leu
115 120 125

Cys Pro Ala Gly Ala Leu Ser Phe Asn Ala Phe Lys Thr Val
130 135 140

<210> 111
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
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<223> /note="Gene Symbol: DECR2; "

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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487820"

<400> 111
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
50 55 60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65 70 75 80

Ser

<210> 112
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<220>

<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487947"

<400> 112
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
50 55 60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65 70 75 80

Ser

<210> 113
<211> 238
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
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<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
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<223> /note="ENSP ID: ENSP00000487969"

<400> 113
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
50 55 60

Val Leu Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr Gly Arg Arg Cys
65 70 75 80

Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala Val Met Ala Ala
85 90 95

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

Cys Glu Ser Val Leu Ser Glu Ala Pro Ala Ala Pro Ala Val Ser His
115 120 125

Ser Ala Gly Ala Ala Gly Asn Phe Leu Cys Pro Ala Gly Ala Leu Ser
130 135 140

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

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

Val Ile Val Asn Ile Thr Ala Thr Leu Gly Asn Arg Gly Gln Ala Leu
180 185 190

Gln Val His Ala Gly Ser Ala Lys Ala Ala Val Asp Ala Met Thr Arg
195 200 205

His Leu Ala Val Glu Trp Gly Pro Gln Asn Ile Arg Val Asn Ser Leu
210 215 220

Ala Pro Gly Pro Ile Ser Gly Thr Glu Gly Leu Arg Arg Leu
225 230 235

<210> 114
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488142"

<400> 114
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
50 55 60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65 70 75 80

Ser

<210> 115
<211> 238
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488501"

<400> 115

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Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                  10                  15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60

Val Leu Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr Gly Arg Arg Cys
65                  70                  75                  80

Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala Val Met Ala Ala
                85                  90                  95

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

Cys Glu Ser Val Leu Ser Glu Ala Pro Ala Ala Pro Ala Val Ser His
        115                 120                 125

Ser Ala Gly Ala Ala Gly Asn Phe Leu Cys Pro Ala Gly Ala Leu Ser
    130                 135                 140

Phe Asn Ala Phe Lys Thr Val Met Asp Ile Asp Thr Ser Gly Thr Phe
145                 150                 155                 160
```

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

Val Ile Val Asn Ile Thr Ala Thr Leu Gly Asn Arg Gly Gln Ala Leu
            180                 185                 190

Gln Val His Ala Gly Ser Ala Lys Ala Ala Val Asp Ala Met Thr Arg
        195                 200                 205

His Leu Ala Val Glu Trp Gly Pro Gln Asn Ile Arg Val Asn Ser Leu
    210                 215                 220

Ala Pro Gly Pro Ile Ser Gly Thr Glu Gly Leu Arg Arg Leu
225                 230                 235


<210> 116
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
      2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488619"

<400> 116
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                   10                  15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45
```

```
Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60

Val Leu Thr Val Ile Arg Pro Pro Gln Pro Pro Lys Val Pro Gly Leu
65                  70                  75                  80

Gln Val
```

<210> 117
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488728"

<400> 117

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Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1               5                   10                  15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
            20                  25                  30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60

Val Leu Thr Arg Trp Val Phe Thr Thr Leu Thr Arg Leu Val Ser Asn
65                  70                  75                  80

Ser
```

<210> 118
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488732"

<400> 118
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg Ile Gln Val Pro Ala Arg Gly Thr Gly Glu Arg Ser Arg Ile
50 55 60

Ala Leu Gly Gly Val Arg Thr Ser Arg Pro Leu Gln Ala Ala Arg Lys
65 70 75 80

Leu Ala Gly Ala Thr Gly Arg Arg Cys Leu Pro Leu Ser Met Asp Val
85 90 95

Arg Ala Pro Pro Ala Val Met Ala Ala Val Asp Gln Ala Leu Lys Glu
100 105 110

Phe Gly Arg Ile Asp Ile Leu Ile Asn Cys Ala Ala Gly Asn Phe Leu
115 120 125

Cys Pro Ala Gly Ala Leu Ser Phe Asn Ala Phe Lys Thr Val
130 135 140

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

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUI1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488824"

<400> 119
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
35 40 45

Met Arg Ala Ser Glu Asp Gln Met Gly His Cys Ser Ser Ser Gly Thr
50 55 60

Cys Leu Ala Gly Val Ala Thr Phe Met Val Ile Val Gly Lys Gln Pro
65 70 75 80

Pro Asn Gln Lys Ser Arg Glu Thr Lys Glu Gln Gly Arg Gln Ile Pro
85 90 95

Phe Val Cys Val Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser
100 105 110

```
Leu Pro Arg Val Leu Thr Ala Ala Arg Lys Leu Ala Gly Ala Thr Gly
        115                 120                 125

Arg Arg Cys Leu Pro Leu Ser Met Asp Val Arg Ala Pro Pro Ala Val
    130                 135                 140

Met Ala Ala Val Asp Gln Ala Leu Lys Glu Phe Gly Arg Ile Asp Ile
145                 150                 155                 160

Leu Ile Asn Cys Ser Ser Ser Ser Cys Gly Leu Pro Phe Cys Arg Cys
                165                 170                 175

Gly Arg Glu Leu Pro Val Pro Arg Trp Arg Leu Val Leu Gln Arg Leu
            180                 185                 190

Gln Asp Arg Asp Gly His Arg Tyr Gln Arg His Leu Gln Cys Val Ser
        195                 200                 205

Cys Ala Leu
    210
```

<210> 120
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488844"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 120
Xaa Ala Arg Lys Leu Ala Gly Ala Thr Gly Arg Arg Cys Leu Pro Leu
1 5 10 15

Ser Met Asp Val Arg Ala Pro Pro Ala Val Met Ala Ala Val Asp Gln
20 25 30

Ala Leu Lys Glu Phe Gly Arg Ile Asp Ile Leu Ile Asn Cys Ala Ala
35 40 45

Gly Asn Phe Leu Cys Pro Ala Gly Ala Leu Ser Phe Asn Ala Phe Lys
50 55 60

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

Leu Tyr Glu Lys Phe Phe Arg Val Gly Ala Ser Cys Ala Leu
85 90

<210> 121
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 12; "

<220>
<221> source
<223> /note="Gene Symbol: DECR2; "

<220>
<221> source
<223> /note="Gene Name:
2,4-dienoyl CoA reductase 2, peroxisomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488859"

<400> 121
Met Ala Gln Pro Pro Pro Asp Val Glu Gly Asp Asp Cys Leu Pro Ala
1 5 10 15

Tyr Arg His Leu Phe Cys Pro Asp Leu Leu Arg Asp Lys Val Ala Phe
20 25 30

```
Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Arg Ile Ala Glu Ile Phe
        35                  40                  45

Met Arg His Gly Cys His Thr Val Ile Ala Ser Arg Ser Leu Pro Arg
    50                  55                  60

Val Leu Thr Val Ile Arg Pro Pro Gln Pro Pro Lys Val Pro Gly Leu
65                  70                  75                  80

Gln Val
```

<210> 122
<211> 516
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 13; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR24; "

<220>
<221> source
<223> /note="Gene Name:
24-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="Uniprot ID: Q15392; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000360316"

<400> 122

```
Met Glu Pro Ala Val Ser Leu Ala Val Cys Ala Leu Leu Phe Leu Leu
1               5                  10                  15

Trp Val Arg Leu Lys Gly Leu Glu Phe Val Leu Ile His Gln Arg Trp
            20                  25                  30

Val Phe Val Cys Leu Phe Leu Leu Pro Leu Ser Leu Ile Phe Asp Ile
        35                  40                  45

Tyr Tyr Tyr Val Arg Ala Trp Val Val Phe Lys Leu Ser Ser Ala Pro
    50                  55                  60
```

```
Arg Leu His Glu Gln Arg Val Arg Asp Ile Gln Lys Gln Val Arg Glu
65                  70                  75                  80

Trp Lys Glu Gln Gly Ser Lys Thr Phe Met Cys Thr Gly Arg Pro Gly
                85                  90                  95

Trp Leu Thr Val Ser Leu Arg Val Gly Lys Tyr Lys Lys Thr His Lys
            100                 105                 110

Asn Ile Met Ile Asn Leu Met Asp Ile Leu Glu Val Asp Thr Lys Lys
        115                 120                 125

Gln Ile Val Arg Val Glu Pro Leu Val Thr Met Gly Gln Val Thr Ala
    130                 135                 140

Leu Leu Thr Ser Ile Gly Trp Thr Leu Pro Val Leu Pro Glu Leu Asp
145                 150                 155                 160

Asp Leu Thr Val Gly Gly Leu Ile Met Gly Thr Gly Ile Glu Ser Ser
                165                 170                 175

Ser His Lys Tyr Gly Leu Phe Gln His Ile Cys Thr Ala Tyr Glu Leu
            180                 185                 190

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

Asp Leu Phe Tyr Ala Val Pro Trp Ser Cys Gly Thr Leu Gly Phe Leu
    210                 215                 220

Val Ala Ala Glu Ile Arg Ile Ile Pro Ala Lys Lys Tyr Val Lys Leu
225                 230                 235                 240

Arg Phe Glu Pro Val Arg Gly Leu Glu Ala Ile Cys Ala Lys Phe Thr
                245                 250                 255

His Glu Ser Gln Arg Gln Glu Asn His Phe Val Glu Gly Leu Leu Tyr
            260                 265                 270

Ser Leu Asp Glu Ala Val Ile Met Thr Gly Val Met Thr Asp Glu Ala
        275                 280                 285
```

```
Glu Pro Ser Lys Leu Asn Ser Ile Gly Asn Tyr Tyr Lys Pro Trp Phe
    290                 295                 300

Phe Lys His Val Glu Asn Tyr Leu Lys Thr Asn Arg Glu Gly Leu Glu
305                 310                 315                 320

Tyr Ile Pro Leu Arg His Tyr Tyr His Arg His Thr Arg Ser Ile Phe
                325                 330                 335

Trp Glu Leu Gln Asp Ile Ile Pro Phe Gly Asn Asn Pro Ile Phe Arg
            340                 345                 350

Tyr Leu Phe Gly Trp Met Val Pro Pro Lys Ile Ser Leu Leu Lys Leu
        355                 360                 365

Thr Gln Gly Glu Thr Leu Arg Lys Leu Tyr Glu Gln His His Val Val
    370                 375                 380

Gln Asp Met Leu Val Pro Met Lys Cys Leu Gln Gln Ala Leu His Thr
385                 390                 395                 400

Phe Gln Asn Asp Ile His Val Tyr Pro Ile Trp Leu Cys Pro Phe Ile
                405                 410                 415

Leu Pro Ser Gln Pro Gly Leu Val His Pro Lys Gly Asn Glu Ala Glu
            420                 425                 430

Leu Tyr Ile Asp Ile Gly Ala Tyr Gly Glu Pro Arg Val Lys His Phe
        435                 440                 445

Glu Ala Arg Ser Cys Met Arg Gln Leu Glu Lys Phe Val Arg Ser Val
    450                 455                 460

His Gly Phe Gln Met Leu Tyr Ala Asp Cys Tyr Met Asn Arg Glu Glu
465                 470                 475                 480

Phe Trp Glu Met Phe Asp Gly Ser Leu Tyr His Lys Leu Arg Glu Lys
                485                 490                 495

Leu Gly Cys Gln Asp Ala Phe Pro Glu Val Tyr Asp Lys Ile Cys Lys
            500                 505                 510
```

Ala Ala Arg His
515

<210> 123
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 13; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR24; "

<220>
<221> source
<223> /note="Gene Name:
24-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416585"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 123
Xaa Ser Leu Leu Lys Leu Thr Gln Gly Glu Thr Leu Arg Lys Leu Tyr
1 5 10 15

Glu Gln His His Val Val Gln Asp Met Leu Val Pro Met Lys Cys Leu
20 25 30

Gln Gln Ala Leu His Thr Phe Gln Asn Asp Ile His Val Tyr Pro Ile
35 40 45

Trp Leu Cys Pro Phe Ile Leu Pro Ser Gln Pro Gly Leu Val His Pro
50 55 60

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

Pro Arg Val Lys His Phe Glu Ala Arg Ser Cys Met Arg Gln Leu Glu
85 90 95

```
Lys Phe Val Arg Ser Val His Gly Phe Gln Met Leu Tyr Ala Asp Cys
            100                 105                 110

Tyr Met Asn Arg Glu Glu Phe Trp Glu Met Phe Asp Gly Ser Leu Tyr
        115                 120                 125

His Lys Leu Arg Glu Lys Leu Gly Cys Gln Asp Ala Phe Pro Glu Val
    130                 135                 140

Tyr Asp Lys Ile Cys Lys Ala Ala Arg His
145                 150
```

<210> 124
<211> 427
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 13; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR24; "

<220>
<221> source
<223> /note="Gene Name:
24-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000440191"

<400> 124

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Met Cys Thr Gly Arg Pro Gly Trp Leu Thr Val Ser Leu Arg Val Gly
1               5                   10                  15

Lys Tyr Lys Lys Thr His Lys Asn Ile Met Ile Asn Leu Met Asp Ile
            20                  25                  30

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

Thr Met Gly Gln Val Thr Ala Leu Leu Thr Ser Ile Gly Trp Thr Leu
    50                  55                  60

Pro Val Leu Pro Glu Leu Asp Asp Leu Thr Val Gly Gly Leu Ile Met
65                  70                  75                  80
```

```
Gly Thr Gly Ile Glu Ser Ser Ser His Lys Tyr Gly Leu Phe Gln His
                85                  90                  95

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

Cys Thr Pro Ser Glu Asn Ser Asp Leu Phe Tyr Ala Val Pro Trp Ser
        115                 120                 125

Cys Gly Thr Leu Gly Phe Leu Val Ala Ala Glu Ile Arg Ile Ile Pro
    130                 135                 140

Ala Lys Lys Tyr Val Lys Leu Arg Phe Glu Pro Val Arg Gly Leu Glu
145                 150                 155                 160

Ala Ile Cys Ala Lys Phe Thr His Glu Ser Gln Arg Gln Glu Asn His
                165                 170                 175

Phe Val Glu Gly Leu Leu Tyr Ser Leu Asp Glu Ala Val Ile Met Thr
            180                 185                 190

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

Asn Tyr Tyr Lys Pro Trp Phe Phe Lys His Val Glu Asn Tyr Leu Lys
    210                 215                 220

Thr Asn Arg Glu Gly Leu Glu Tyr Ile Pro Leu Arg His Tyr Tyr His
225                 230                 235                 240

Arg His Thr Arg Ser Ile Phe Trp Glu Leu Gln Asp Ile Ile Pro Phe
                245                 250                 255

Gly Asn Asn Pro Ile Phe Arg Tyr Leu Phe Gly Trp Met Val Pro Pro
            260                 265                 270

Lys Ile Ser Leu Leu Lys Leu Thr Gln Gly Glu Thr Leu Arg Lys Leu
        275                 280                 285

Tyr Glu Gln His His Val Val Gln Asp Met Leu Val Pro Met Lys Cys
    290                 295                 300
```

```
Leu Gln Gln Ala Leu His Thr Phe Gln Asn Asp Ile His Val Tyr Pro
305                 310                 315                 320

Ile Trp Leu Cys Pro Phe Ile Leu Pro Ser Gln Pro Gly Leu Val His
                325                 330                 335

Pro Lys Gly Asn Glu Ala Glu Leu Tyr Ile Asp Ile Gly Ala Tyr Gly
            340                 345                 350

Glu Pro Arg Val Lys His Phe Glu Ala Arg Ser Cys Met Arg Gln Leu
        355                 360                 365

Glu Lys Phe Val Arg Ser Val His Gly Phe Gln Met Leu Tyr Ala Asp
    370                 375                 380

Cys Tyr Met Asn Arg Glu Glu Phe Trp Glu Met Phe Asp Gly Ser Leu
385                 390                 395                 400

Tyr His Lys Leu Arg Glu Lys Leu Gly Cys Gln Asp Ala Phe Pro Glu
                405                 410                 415

Val Tyr Asp Lys Ile Cys Lys Ala Ala Arg His
            420                 425


<210> 125
<211> 400
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="Uniprot ID:  P00973; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000202917"

<400> 125

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Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
1               5                  10                  15

Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His
            20                  25                  30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
        35                  40                  45

Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
    50                  55                  60

Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65                  70                  75                  80

Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
                85                  90                  95

Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
            100                 105                 110

Arg Ala Phe Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
        115                 120                 125

Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
    130                 135                 140

Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
145                 150                 155                 160

Gly Gly Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
                165                 170                 175

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

Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
        195                 200                 205

Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
    210                 215                 220
```

```
Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
225                 230                 235                 240

Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
                245                 250                 255

Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
            260                 265                 270

Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
        275                 280                 285

Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
    290                 295                 300

Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
305                 310                 315                 320

Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
                325                 330                 335

Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Ala Glu Ser Asn Ser Ala
            340                 345                 350

Asp Asp Glu Thr Asp Asp Pro Arg Arg Tyr Gln Lys Tyr Gly Tyr Ile
        355                 360                 365

Gly Thr His Glu Tyr Pro His Phe Ser His Arg Pro Ser Thr Leu Gln
    370                 375                 380

Ala Ala Ser Thr Pro Gln Ala Glu Glu Asp Trp Thr Cys Thr Ile Leu
385                 390                 395                 400


<210> 126
<211> 414
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
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<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="Uniprot ID: P00973; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388001"

<400> 126

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Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
1               5                   10                  15


Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His
            20                  25                  30


Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
        35                  40                  45


Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
    50                  55                  60


Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65                  70                  75                  80


Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
                85                  90                  95


Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
            100                 105                 110


Arg Ala Phe Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
        115                 120                 125


Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
    130                 135                 140


Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
145                 150                 155                 160


Gly Gly Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
```

```
                165                 170                 175

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

Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
        195                 200                 205

Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
    210                 215                 220

Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
225                 230                 235                 240

Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
                245                 250                 255

Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
            260                 265                 270

Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
        275                 280                 285

Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
    290                 295                 300

Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
305                 310                 315                 320

Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
                325                 330                 335

Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Thr Gln His Thr Pro Gly
            340                 345                 350

Ser Ile His Pro Thr Gly Arg Arg Gly Leu Asp Leu His His Pro Leu
        355                 360                 365

Asn Ala Ser Ala Ser Trp Gly Lys Gly Leu Gln Cys Tyr Leu Asp Gln
    370                 375                 380

Phe Leu His Phe Gln Val Gly Leu Leu Ile Gln Arg Gly Gln Ser Ser
385                 390                 395                 400
```

Ser Val Ser Trp Cys Ile Ile Gln Asp Arg Thr Gln Val Ser
405 410

<210> 127
<211> 364
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="Uniprot ID: P00973; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000415721"

<400> 127
Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
1 5 10 15

Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His
20 25 30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
35 40 45

Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
50 55 60

Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65 70 75 80

Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
85 90 95

```
Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
            100                 105                 110

Arg Ala Phe Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
        115                 120                 125

Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
    130                 135                 140

Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
145                 150                 155                 160

Gly Gly Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
                165                 170                 175

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

Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
        195                 200                 205

Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
    210                 215                 220

Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
225                 230                 235                 240

Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
                245                 250                 255

Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
            260                 265                 270

Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
        275                 280                 285

Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
    290                 295                 300

Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
305                 310                 315                 320

Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
```

```
                325                 330                 335

Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Val Arg Pro Pro Ala Ser
            340                 345                 350

Ser Leu Pro Phe Ile Pro Ala Pro Leu His Glu Ala
        355                 360


<210> 128
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448001"

<400> 128
Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
1               5                   10                  15

Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His
            20                  25                  30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
        35                  40                  45

Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
    50                  55                  60

Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65                  70                  75                  80

Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
                85                  90                  95
```

```
Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
            100                 105                 110

Arg Ala Phe Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
        115                 120                 125

Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
    130                 135                 140

Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Glu Ser Ser
145                 150                 155                 160

Gln Leu Leu Phe Leu Pro Leu Pro Ile Ser Glu Gln Lys Ser Pro Thr
                165                 170                 175

Val
```

<210> 129
<211> 302
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448348"

<400> 129

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

Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His Ala Ile Asp Ile
            20                  25                  30

Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly Ser Ser Tyr Pro
```

```
        35                  40                  45

Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser Gly Lys Gly Thr
    50                  55                  60

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

Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly Glu Phe Ile Gln
                85                  90                  95

Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu Arg Ala Phe Ser
            100                 105                 110

Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn Pro Arg Ala Leu
        115                 120                 125

Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly Val Glu Phe Asp
    130                 135                 140

Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr Gly Gly Tyr Lys
145                 150                 155                 160

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

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

Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu Ile Arg Leu Val
        195                 200                 205

Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly Lys Leu Pro Pro
    210                 215                 220

Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp Glu Arg Gly Ser
225                 230                 235                 240

Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg Thr Val Leu Glu
                245                 250                 255

Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp Thr Lys Tyr Tyr
            260                 265                 270
```

```
Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg Arg Gln Leu Thr
        275                 280                 285

Lys Pro Arg Tyr Ala Ile Pro Thr Trp Leu Ser Ser Pro Met
    290                 295                 300


<210> 130
<211> 360
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448790"

<400> 130
Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
1               5                   10                  15

Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His
            20                  25                  30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
        35                  40                  45

Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
    50                  55                  60

Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65                  70                  75                  80

Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
                85                  90                  95
```

```
Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
            100                 105                 110

Arg Ala Phe Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
        115                 120                 125

Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
    130                 135                 140

Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
145                 150                 155                 160

Gly Gly Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
                165                 170                 175

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

Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
        195                 200                 205

Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
    210                 215                 220

Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
225                 230                 235                 240

Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
                245                 250                 255

Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
            260                 265                 270

Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
        275                 280                 285

Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
    290                 295                 300

Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
305                 310                 315                 320

Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
```

```
                325                 330                 335

Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Val Asn Leu Thr Leu Val
            340                 345                 350

Gly Arg Arg Asn Tyr Thr Asn Asn
        355                 360


<210> 131
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000449053"

<400> 131
Phe Arg Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile
1               5                   10                  15

Tyr Trp Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr
            20                  25                  30

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

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

Leu Ala Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn
65                  70                  75                  80

Trp Asp Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Met Arg Gln Arg
                85                  90                  95
```

```
Leu Arg Glu Val Arg Ser Leu Ala Gln Gly His Gln Leu Thr Ser Gly
            100                 105                 110

Gly Asn Gly Ile Gln Ala Gln Trp Thr Leu Lys Pro Val Leu Met Ser
        115                 120                 125

Leu Cys
    130


<210> 132
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450286"

<400> 132
Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
1               5                   10                  15

Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His
            20                  25                  30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
        35                  40                  45

Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Cys Lys Lys Lys
    50                  55                  60

Leu Gly Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr
65                  70                  75                  80

Ala Trp Glu
```

<210> 133
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000474083"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 133
Xaa Pro Ser Thr Leu Gln Ala Ala Ser Thr Pro Gln Ala Glu Glu Asp
1 5 10 15

Trp Thr Cys Thr Ile Leu
20

<210> 134
<211> 15
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 14; "

<220>
<221> source
<223> /note="Gene Symbol: OAS1; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 1, 40/46kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475139"

<400> 134
Ala Glu Ser Asn Ser Ala Asp Asp Glu Thr Asp Asp Pro Arg Arg
1   5   10   15

<210> 135
<211> 719
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 15; "

<220>
<221> source
<223> /note="Gene Symbol: OAS2; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 2, 69/71kDa; "

<220>
<221> source
<223> /note="Uniprot ID: P29728; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000342278"

<400> 135
Met Gly Asn Gly Glu Ser Gln Leu Ser Ser Val Pro Ala Gln Lys Leu
1   5   10   15

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

Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Leu Gln Glu Pro
        35   40   45

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

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

```
Phe Ser Asp Leu Lys Gln Phe Gln Asp Gln Lys Arg Ser Gln Arg Asp
                85                  90                  95

Ile Leu Asp Lys Thr Gly Asp Lys Leu Lys Phe Cys Leu Phe Thr Lys
            100                 105                 110

Trp Leu Lys Asn Asn Phe Glu Ile Gln Lys Ser Leu Asp Gly Phe Thr
        115                 120                 125

Ile Gln Val Phe Thr Lys Asn Gln Arg Ile Ser Phe Glu Val Leu Ala
    130                 135                 140

Ala Phe Asn Ala Leu Ser Leu Asn Asp Asn Pro Ser Pro Trp Ile Tyr
145                 150                 155                 160

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

Phe Ala Val Cys Phe Thr Glu Leu Gln Gln Lys Phe Phe Asp Asn Arg
            180                 185                 190

Pro Gly Lys Leu Lys Asp Leu Ile Leu Leu Ile Lys His Trp His Gln
        195                 200                 205

Gln Cys Gln Lys Lys Ile Lys Asp Leu Pro Ser Leu Ser Pro Tyr Ala
    210                 215                 220

Leu Glu Leu Leu Thr Val Tyr Ala Trp Glu Gln Gly Cys Arg Lys Asp
225                 230                 235                 240

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

Cys Gln Glu Lys Leu Cys Ile Tyr Trp Met Val Asn Tyr Asn Phe Glu
            260                 265                 270

Asp Glu Thr Ile Arg Asn Ile Leu Leu His Gln Leu Gln Ser Ala Arg
        275                 280                 285

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

Lys Ile Cys Trp Gln Trp Leu Lys Lys Glu Ala Gln Thr Trp Leu Thr
```

305 310 315 320

Ser Pro Asn Leu Asp Asn Glu Leu Pro Ala Pro Ser Trp Asn Val Leu
325 330 335

Pro Ala Pro Leu Phe Thr Thr Pro Gly His Leu Leu Asp Lys Phe Ile
340 345 350

Lys Glu Phe Leu Gln Pro Asn Lys Cys Phe Leu Glu Gln Ile Asp Ser
355 360 365

Ala Val Asn Ile Ile Arg Thr Phe Leu Lys Glu Asn Cys Phe Arg Gln
370 375 380

Ser Thr Ala Lys Ile Gln Ile Val Arg Gly Gly Ser Thr Ala Lys Gly
385 390 395 400

Thr Ala Leu Lys Thr Gly Ser Asp Ala Asp Leu Val Val Phe His Asn
405 410 415

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

Lys Glu Ile His Glu Gln Leu Lys Ala Phe Trp Arg Glu Lys Glu Glu
435 440 445

Glu Leu Glu Val Ser Phe Glu Pro Pro Lys Trp Lys Ala Pro Arg Val
450 455 460

Leu Ser Phe Ser Leu Lys Ser Lys Val Leu Asn Glu Ser Val Ser Phe
465 470 475 480

Asp Val Leu Pro Ala Phe Asn Ala Leu Gly Gln Leu Ser Ser Gly Ser
485 490 495

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

Ser Asp Leu Pro Gly Gly Glu Phe Ser Thr Cys Phe Thr Val Leu Gln
515 520 525

Arg Asn Phe Ile Arg Ser Arg Pro Thr Lys Leu Lys Asp Leu Ile Arg
530 535 540

```
Leu Val Lys His Trp Tyr Lys Glu Cys Glu Arg Lys Leu Lys Pro Lys
545                 550                 555                 560

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

Trp Glu Gln Gly Ser Gly Val Pro Asp Phe Asp Thr Ala Glu Gly Phe
            580                 585                 590

Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Gln Gln Leu Cys Ile Phe
        595                 600                 605

Trp Lys Val Asn Tyr Asn Phe Glu Asp Glu Thr Val Arg Lys Phe Leu
    610                 615                 620

Leu Ser Gln Leu Gln Lys Thr Arg Pro Val Ile Leu Asp Pro Ala Glu
625                 630                 635                 640

Pro Thr Gly Asp Val Gly Gly Gly Asp Arg Trp Cys Trp His Leu Leu
                645                 650                 655

Ala Lys Glu Ala Lys Glu Trp Leu Ser Ser Pro Cys Phe Lys Asp Gly
            660                 665                 670

Thr Gly Asn Pro Ile Pro Pro Trp Lys Val Pro Thr Met Gln Thr Pro
        675                 680                 685

Gly Ser Cys Gly Ala Arg Ile His Pro Ile Val Asn Glu Met Phe Ser
    690                 695                 700

Ser Arg Ser His Arg Ile Leu Asn Asn Asn Ser Lys Arg Asn Phe
705                 710                 715


<210> 136
<211> 687
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 15; "

<220>
<221> source
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<223> /note="Gene Symbol: OAS2; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 2, 69/71kDa; "

<220>
<221> source
<223> /note="Uniprot ID: P29728; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376362"

<400> 136

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Met Gly Asn Gly Glu Ser Gln Leu Ser Ser Val Pro Ala Gln Lys Leu
1               5                  10                  15

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

Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Leu Gln Glu Pro
        35                  40                  45

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

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

Phe Ser Asp Leu Lys Gln Phe Gln Asp Gln Lys Arg Ser Gln Arg Asp
                85                  90                  95

Ile Leu Asp Lys Thr Gly Asp Lys Leu Lys Phe Cys Leu Phe Thr Lys
            100                 105                 110

Trp Leu Lys Asn Asn Phe Glu Ile Gln Lys Ser Leu Asp Gly Phe Thr
        115                 120                 125

Ile Gln Val Phe Thr Lys Asn Gln Arg Ile Ser Phe Glu Val Leu Ala
    130                 135                 140

Ala Phe Asn Ala Leu Ser Leu Asn Asp Asn Pro Ser Pro Trp Ile Tyr
145                 150                 155                 160

Arg Glu Leu Lys Arg Ser Leu Asp Lys Thr Asn Ala Ser Pro Gly Glu
```

```
                165                 170                 175

Phe Ala Val Cys Phe Thr Glu Leu Gln Gln Lys Phe Phe Asp Asn Arg
            180                 185                 190

Pro Gly Lys Leu Lys Asp Leu Ile Leu Leu Ile Lys His Trp His Gln
        195                 200                 205

Gln Cys Gln Lys Lys Ile Lys Asp Leu Pro Ser Leu Ser Pro Tyr Ala
    210                 215                 220

Leu Glu Leu Leu Thr Val Tyr Ala Trp Glu Gln Gly Cys Arg Lys Asp
225                 230                 235                 240

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

Cys Gln Glu Lys Leu Cys Ile Tyr Trp Met Val Asn Tyr Asn Phe Glu
            260                 265                 270

Asp Glu Thr Ile Arg Asn Ile Leu Leu His Gln Leu Gln Ser Ala Arg
        275                 280                 285

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

Lys Ile Cys Trp Gln Trp Leu Lys Lys Glu Ala Gln Thr Trp Leu Thr
305                 310                 315                 320

Ser Pro Asn Leu Asp Asn Glu Leu Pro Ala Pro Ser Trp Asn Val Leu
                325                 330                 335

Pro Ala Pro Leu Phe Thr Thr Pro Gly His Leu Leu Asp Lys Phe Ile
            340                 345                 350

Lys Glu Phe Leu Gln Pro Asn Lys Cys Phe Leu Glu Gln Ile Asp Ser
        355                 360                 365

Ala Val Asn Ile Ile Arg Thr Phe Leu Lys Glu Asn Cys Phe Arg Gln
    370                 375                 380

Ser Thr Ala Lys Ile Gln Ile Val Arg Gly Gly Ser Thr Ala Lys Gly
385                 390                 395                 400
```

Thr Ala Leu Lys Thr Gly Ser Asp Ala Asp Leu Val Val Phe His Asn
405 410 415

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

Lys Glu Ile His Glu Gln Leu Lys Ala Phe Trp Arg Glu Lys Glu Glu
435 440 445

Glu Leu Glu Val Ser Phe Glu Pro Pro Lys Trp Lys Ala Pro Arg Val
450 455 460

Leu Ser Phe Ser Leu Lys Ser Lys Val Leu Asn Glu Ser Val Ser Phe
465 470 475 480

Asp Val Leu Pro Ala Phe Asn Ala Leu Gly Gln Leu Ser Ser Gly Ser
485 490 495

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

Ser Asp Leu Pro Gly Gly Glu Phe Ser Thr Cys Phe Thr Val Leu Gln
515 520 525

Arg Asn Phe Ile Arg Ser Arg Pro Thr Lys Leu Lys Asp Leu Ile Arg
530 535 540

Leu Val Lys His Trp Tyr Lys Glu Cys Glu Arg Lys Leu Lys Pro Lys
545 550 555 560

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

Trp Glu Gln Gly Ser Gly Val Pro Asp Phe Asp Thr Ala Glu Gly Phe
580 585 590

Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Gln Gln Leu Cys Ile Phe
595 600 605

Trp Lys Val Asn Tyr Asn Phe Glu Asp Glu Thr Val Arg Lys Phe Leu
610 615 620

```
Leu Ser Gln Leu Gln Lys Thr Arg Pro Val Ile Leu Asp Pro Ala Glu
625                 630                 635                 640


Pro Thr Gly Asp Val Gly Gly Gly Asp Arg Trp Cys Trp His Leu Leu
                645                 650                 655


Ala Lys Glu Ala Lys Glu Trp Leu Ser Ser Pro Cys Phe Lys Asp Gly
            660                 665                 670


Thr Gly Asn Pro Ile Pro Pro Trp Lys Val Pro Val Lys Val Ile
        675                 680                 685


<210> 137
<211> 172
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 15; "

<220>
<221> source
<223> /note="Gene Symbol: OAS2; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 2, 69/71kDa; "

<220>
<221> source
<223> /note="Uniprot ID:  P29728; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000411763"

<400> 137
Met Gly Asn Gly Glu Ser Gln Leu Ser Ser Val Pro Ala Gln Lys Leu
1               5                   10                  15


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


Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Leu Gln Glu Pro
        35                  40                  45


Glu Gln Phe Pro Leu Val Gln Gly Val Ala Ile Gly Gly Ser Tyr Gly
```

```
    50                  55                  60

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

Phe Ser Asp Leu Lys Gln Phe Gln Asp Gln Lys Arg Ser Gln Arg Asp
                85                  90                  95

Ile Leu Asp Lys Thr Gly Asp Lys Leu Lys Phe Cys Leu Phe Thr Lys
            100                 105                 110

Trp Leu Lys Asn Asn Phe Glu Ile Gln Lys Ser Leu Asp Gly Phe Thr
        115                 120                 125

Ile Gln Val Phe Thr Lys Asn Gln Arg Ile Ser Phe Glu Val Leu Ala
    130                 135                 140

Ala Phe Asn Ala Leu Ser Lys His Cys Trp Val Ser Gly Glu Lys Ser
145                 150                 155                 160

Gln Arg Ser Gly Cys Gln Thr Ala Leu Cys Asn Leu
                165                 170


<210> 138
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 15; "

<220>
<221> source
<223> /note="Gene Symbol: OAS2; "

<220>
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<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 2, 69/71kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446977"

<400> 138
Met Gly Asn Gly Glu Ser Gln Leu Ser Ser Val Pro Ala Gln Lys Leu
1               5                   10                  15
```

```
Gly Trp Phe Ile Gln Glu Tyr Leu Lys Pro Tyr Glu Glu Cys Gln Thr
            20                  25                  30

Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Leu Gln Glu Pro
        35                  40                  45

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

Arg Lys Thr Val Leu Arg Gly Asn Ser Asp Gly Leu Asn Asp Asn Pro
65                  70                  75                  80

Ser Pro Trp Ile Tyr Arg Glu Leu Lys Arg Ser Leu Asp Lys Thr Asn
                85                  90                  95

Ala Ser Pro Gly Glu Phe Ala Val Cys Phe Thr Glu Leu Gln Gln Lys
            100                 105                 110

Phe Phe Asp Asn Arg Pro Gly Lys Leu Lys Asp Leu Ile Leu Leu Ile
        115                 120                 125

Lys His Trp His Gln Gln Cys Gln Lys Lys Ile Lys Asp Leu Pro Ser
    130                 135                 140

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

Gly Cys Arg Lys Asp Asn Phe Asp Ile Ala Glu Gly Val Arg Thr Val
                165                 170                 175

Leu Glu Leu Ile Lys Cys Gln Glu Lys Leu Cys Ile Tyr Trp Met Val
            180                 185                 190

Asn Tyr Asn Phe Glu Asp Glu Thr Ile Arg Asn Ile Leu Leu His Gln
        195                 200                 205

Leu Gln Ser Ala Arg Pro Val Ile Leu Asp Pro Val Asp Pro Thr Asn
    210                 215                 220

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

```
Gln Thr Trp Leu Thr Ser Pro Asn Leu Asp Asn Glu Leu Pro Ala Pro
                245                 250                 255


Ser Trp Asn Val Leu Pro Ala Pro Leu Phe Thr Thr Pro Gly
            260                 265                 270


<210> 139
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 15; "

<220>
<221> source
<223> /note="Gene Symbol: OAS2; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 2, 69/71kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450307"

<400> 139
Met Gly Asn Gly Glu Ser Gln Leu Ser Ser Val Pro Ala Gln Lys Leu
1               5                   10                  15


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


Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Leu Gln Glu Pro
        35                  40                  45


Glu Gln Phe Pro Leu Val Gln Gly Val Ala Ile Ala
    50                  55                  60


<210> 140
<211> 726
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 15; "

<220>
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<221> source
<223> /note="Gene Symbol: OAS2; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 2, 69/71kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483679"

<400> 140

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Met Gly Asn Gly Glu Ser Gln Leu Ser Ser Val Pro Ala Gln Lys Leu
1               5                  10                  15

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

Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Leu Gln Glu Pro
        35                  40                  45

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

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

Phe Ser Asp Leu Lys Gln Phe Gln Asp Gln Lys Arg Ser Gln Arg Asp
                85                  90                  95

Ile Leu Asp Lys Thr Gly Asp Lys Leu Lys Phe Cys Leu Phe Thr Lys
            100                 105                 110

Trp Leu Lys Asn Asn Phe Glu Ile Gln Lys Ser Leu Asp Gly Phe Thr
        115                 120                 125

Ile Gln Val Phe Thr Lys Asn Gln Arg Ile Ser Phe Glu Val Leu Ala
    130                 135                 140

Ala Phe Asn Ala Leu Ser Leu Asn Asp Asn Pro Ser Pro Trp Ile Tyr
145                 150                 155                 160

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

```
Phe Ala Val Cys Phe Thr Glu Leu Gln Gln Lys Phe Phe Asp Asn Arg
            180                 185                 190

Pro Gly Lys Leu Lys Asp Leu Ile Leu Leu Ile Lys His Trp His Gln
        195                 200                 205

Gln Cys Gln Lys Lys Ile Lys Asp Leu Pro Ser Leu Ser Pro Tyr Ala
    210                 215                 220

Leu Glu Leu Leu Thr Val Tyr Ala Trp Glu Gln Gly Cys Arg Lys Asp
225                 230                 235                 240

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

Cys Gln Glu Lys Leu Cys Ile Tyr Trp Met Val Asn Tyr Asn Phe Glu
            260                 265                 270

Asp Glu Thr Ile Arg Asn Ile Leu Leu His Gln Leu Gln Ser Ala Arg
        275                 280                 285

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

Lys Ile Cys Trp Gln Trp Leu Lys Lys Glu Ala Gln Thr Trp Leu Thr
305                 310                 315                 320

Ser Pro Asn Leu Asp Asn Glu Leu Pro Ala Pro Ser Trp Asn Val Leu
                325                 330                 335

Pro Ala Pro Leu Phe Thr Thr Pro Gly His Leu Leu Asp Lys Phe Ile
            340                 345                 350

Lys Glu Phe Leu Gln Pro Asn Lys Cys Phe Leu Glu Gln Ile Asp Ser
        355                 360                 365

Ala Val Asn Ile Ile Arg Thr Phe Leu Lys Glu Asn Cys Phe Arg Gln
    370                 375                 380

Ser Thr Ala Lys Ile Gln Ile Val Arg Gly Gly Ser Thr Ala Lys Gly
385                 390                 395                 400

Thr Ala Leu Lys Thr Gly Ser Asp Ala Asp Leu Val Val Phe His Asn
```

```
                405                 410                 415

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

Lys Glu Ile His Glu Gln Leu Lys Ala Phe Trp Arg Glu Lys Glu Glu
        435                 440                 445

Glu Leu Glu Val Ser Phe Glu Pro Pro Lys Trp Lys Ala Pro Arg Val
    450                 455                 460

Leu Ser Phe Ser Leu Lys Ser Lys Val Leu Asn Glu Ser Val Ser Phe
465                 470                 475                 480

Asp Val Leu Pro Ala Phe Asn Ala Leu Gly Gln Leu Ser Ser Gly Ser
                485                 490                 495

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

Ser Asp Leu Pro Gly Gly Glu Phe Ser Thr Cys Phe Thr Val Leu Gln
        515                 520                 525

Arg Asn Phe Ile Arg Ser Arg Pro Thr Lys Leu Lys Asp Leu Ile Arg
    530                 535                 540

Leu Val Lys His Trp Tyr Lys Glu Cys Glu Arg Lys Leu Lys Pro Lys
545                 550                 555                 560

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

Trp Glu Gln Gly Ser Gly Val Pro Asp Phe Asp Thr Ala Glu Gly Phe
            580                 585                 590

Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Gln Gln Leu Cys Ile Phe
        595                 600                 605

Trp Lys Val Asn Tyr Asn Phe Glu Asp Glu Thr Val Arg Lys Phe Leu
    610                 615                 620

Leu Ser Gln Leu Gln Lys Thr Arg Pro Val Ile Leu Asp Pro Ala Glu
625                 630                 635                 640
```

```
Pro Thr Gly Asp Val Gly Gly Gly Asp Arg Trp Cys Trp His Leu Leu
                645                 650                 655

Ala Lys Glu Ala Lys Glu Trp Leu Ser Ser Pro Cys Phe Lys Asp Gly
            660                 665                 670

Thr Gly Asn Pro Ile Pro Pro Trp Lys Val Pro Thr Met Gln Thr Pro
        675                 680                 685

Gly Ser Cys Gly Ala Arg Ile His Pro Ile Val Asn Glu Met Phe Ser
    690                 695                 700

Ser Arg Ser His Arg Ile Leu Asn Asn Asn Ser Lys Arg Asn Phe Arg
705                 710                 715                 720

Ser Ser Gly Asn Arg Phe
                725
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<210> 141
<211> 1087
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 16; "

<220>
<221> source
<223> /note="Gene Symbol: OAS3; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 3, 100kDa; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y6K5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000228928"

<400> 141

```
Met Asp Leu Tyr Ser Thr Pro Ala Ala Ala Leu Asp Arg Phe Val Ala
1               5                   10                  15
```

```
Arg Arg Leu Gln Pro Arg Lys Glu Phe Val Glu Lys Ala Arg Arg Ala
            20                  25                  30

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

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

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

Leu Asp Cys Phe Lys Ser Tyr Val Asp Gln Arg Ala Arg Arg Ala Glu
                85                  90                  95

Ile Leu Ser Glu Met Arg Ala Ser Leu Glu Ser Trp Trp Gln Asn Pro
            100                 105                 110

Val Pro Gly Leu Arg Leu Thr Phe Pro Glu Gln Ser Val Pro Gly Ala
        115                 120                 125

Leu Gln Phe Arg Leu Thr Ser Val Asp Leu Glu Asp Trp Met Asp Val
    130                 135                 140

Ser Leu Val Pro Ala Phe Asn Val Leu Gly Gln Ala Gly Ser Gly Val
145                 150                 155                 160

Lys Pro Lys Pro Gln Val Tyr Ser Thr Leu Leu Asn Ser Gly Cys Gln
                165                 170                 175

Gly Gly Glu His Ala Ala Cys Phe Thr Glu Leu Arg Arg Asn Phe Val
            180                 185                 190

Asn Ile Arg Pro Ala Lys Leu Lys Asn Leu Ile Leu Leu Val Lys His
        195                 200                 205

Trp Tyr His Gln Val Cys Leu Gln Gly Leu Trp Lys Glu Thr Leu Pro
    210                 215                 220

Pro Val Tyr Ala Leu Glu Leu Leu Thr Ile Phe Ala Trp Glu Gln Gly
225                 230                 235                 240

Cys Lys Lys Asp Ala Phe Ser Leu Ala Glu Gly Leu Arg Thr Val Leu
```

```
                245                 250                 255

Gly Leu Ile Gln Gln His Gln His Leu Cys Val Phe Trp Thr Val Asn
            260                 265                 270

Tyr Gly Phe Glu Asp Pro Ala Val Gly Gln Phe Leu Gln Arg Gln Leu
        275                 280                 285

Lys Arg Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro Thr Trp Asp
    290                 295                 300

Leu Gly Asn Gly Ala Ala Trp His Trp Asp Leu Leu Ala Gln Glu Ala
305                 310                 315                 320

Ala Ser Cys Tyr Asp His Pro Cys Phe Leu Arg Gly Met Gly Asp Pro
                325                 330                 335

Val Gln Ser Trp Lys Gly Pro Gly Leu Pro Arg Ala Gly Cys Ser Gly
            340                 345                 350

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

Ser Lys Ser Leu Asn Ala Val Tyr Pro Arg Ala Gly Ser Lys Pro Pro
    370                 375                 380

Ser Cys Pro Ala Pro Gly Pro Thr Gly Ala Ala Ser Ile Val Pro Ser
385                 390                 395                 400

Val Pro Gly Met Ala Leu Asp Leu Ser Gln Ile Pro Thr Lys Glu Leu
                405                 410                 415

Asp Arg Phe Ile Gln Asp His Leu Lys Pro Ser Pro Gln Phe Gln Glu
            420                 425                 430

Gln Val Lys Lys Ala Ile Asp Ile Ile Leu Arg Cys Leu His Glu Asn
        435                 440                 445

Cys Val His Lys Ala Ser Arg Val Ser Lys Gly Gly Ser Phe Gly Arg
    450                 455                 460

Gly Thr Asp Leu Arg Asp Gly Cys Asp Val Glu Leu Ile Ile Phe Leu
465                 470                 475                 480
```

```
Asn Cys Phe Thr Asp Tyr Lys Asp Gln Gly Pro Arg Arg Ala Glu Ile
                485                 490                 495

Leu Asp Glu Met Arg Ala Gln Leu Glu Ser Trp Trp Gln Asp Gln Val
            500                 505                 510

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

Gln Phe Gln Leu Val Ser Thr Ala Leu Lys Ser Trp Thr Asp Val Ser
    530                 535                 540

Leu Leu Pro Ala Phe Asp Ala Val Gly Gln Leu Ser Ser Gly Thr Lys
545                 550                 555                 560

Pro Asn Pro Gln Val Tyr Ser Arg Leu Leu Thr Ser Gly Cys Gln Glu
                565                 570                 575

Gly Glu His Lys Ala Cys Phe Ala Glu Leu Arg Arg Asn Phe Met Asn
            580                 585                 590

Ile Arg Pro Val Lys Leu Lys Asn Leu Ile Leu Leu Val Lys His Trp
        595                 600                 605

Tyr Arg Gln Val Ala Ala Gln Asn Lys Gly Lys Gly Pro Ala Pro Ala
    610                 615                 620

Ser Leu Pro Pro Ala Tyr Ala Leu Glu Leu Leu Thr Ile Phe Ala Trp
625                 630                 635                 640

Glu Gln Gly Cys Arg Gln Asp Cys Phe Asn Met Ala Gln Gly Phe Arg
                645                 650                 655

Thr Val Leu Gly Leu Val Gln Gln His Gln Gln Leu Cys Val Tyr Trp
            660                 665                 670

Thr Val Asn Tyr Ser Thr Glu Asp Pro Ala Met Arg Met His Leu Leu
        675                 680                 685

Gly Gln Leu Arg Lys Pro Arg Pro Leu Val Leu Asp Pro Ala Asp Pro
    690                 695                 700
```

```
Thr Trp Asn Val Gly His Gly Ser Trp Glu Leu Leu Ala Gln Glu Ala
705                 710                 715                 720

Ala Ala Leu Gly Met Gln Ala Cys Phe Leu Ser Arg Asp Gly Thr Ser
                725                 730                 735

Val Gln Pro Trp Asp Val Met Pro Ala Leu Leu Tyr Gln Thr Pro Ala
            740                 745                 750

Gly Asp Leu Asp Lys Phe Ile Ser Glu Phe Leu Gln Pro Asn Arg Gln
        755                 760                 765

Phe Leu Ala Gln Val Asn Lys Ala Val Asp Thr Ile Cys Ser Phe Leu
    770                 775                 780

Lys Glu Asn Cys Phe Arg Asn Ser Pro Ile Lys Val Ile Lys Val Val
785                 790                 795                 800

Lys Gly Gly Ser Ser Ala Lys Gly Thr Ala Leu Arg Gly Arg Ser Asp
                805                 810                 815

Ala Asp Leu Val Val Phe Leu Ser Cys Phe Ser Gln Phe Thr Glu Gln
            820                 825                 830

Gly Asn Lys Arg Ala Glu Ile Ile Ser Glu Ile Arg Ala Gln Leu Glu
        835                 840                 845

Ala Cys Gln Gln Glu Arg Gln Phe Glu Val Lys Phe Glu Val Ser Lys
    850                 855                 860

Trp Glu Asn Pro Arg Val Leu Ser Phe Ser Leu Thr Ser Gln Thr Met
865                 870                 875                 880

Leu Asp Gln Ser Val Asp Phe Asp Val Leu Pro Ala Phe Asp Ala Leu
                885                 890                 895

Gly Gln Leu Val Ser Gly Ser Arg Pro Ser Ser Gln Val Tyr Val Asp
            900                 905                 910

Leu Ile His Ser Tyr Ser Asn Ala Gly Glu Tyr Ser Thr Cys Phe Thr
        915                 920                 925
```

```
Glu Leu Gln Arg Asp Phe Ile Ile Ser Arg Pro Thr Lys Leu Lys Ser
    930                 935                 940

Leu Ile Arg Leu Val Lys His Trp Tyr Gln Gln Cys Thr Lys Ile Ser
945                 950                 955                 960

Lys Gly Arg Gly Ser Leu Pro Pro Gln His Gly Leu Glu Leu Leu Thr
                965                 970                 975

Val Tyr Ala Trp Glu Gln Gly Gly Lys Asp Ser Gln Phe Asn Met Ala
            980                 985                 990

Glu Gly Phe Arg Thr Val Leu Glu  Leu Val Thr Gln Tyr  Arg Gln
Leu
        995                 1000                1005

Cys Ile  Tyr Trp Thr Ile Asn  Tyr Asn Ala Lys Asp  Lys Thr Val
    1010                1015                1020

Gly Asp  Phe Leu Lys Gln Gln  Leu Gln Lys Pro Arg  Pro Ile Ile
    1025                1030                1035

Leu Asp  Pro Ala Asp Pro Thr  Gly Asn Leu Gly His  Asn Ala Arg
    1040                1045                1050

Trp Asp  Leu Leu Ala Lys Glu  Ala Ala Ala Cys Thr  Ser Ala Leu
    1055                1060                1065

Cys Cys  Met Gly Arg Asn Gly  Ile Pro Ile Gln Pro  Trp Pro Val
    1070                1075                1080

Lys Ala  Ala Val
    1085
```

<210> 142
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 16; "

<220>
<221> source
<223> /note="Gene Symbol: OAS3; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase 3, 100kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000447323"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 142
Xaa Thr Ile Cys Ser Phe Leu Lys Glu Asn Cys Phe Arg Asn Ser Pro
1 5 10 15

Ile Lys Val Ile Lys Val Val Lys Glu Arg Gln Phe Glu Val Lys Phe
20 25 30

Glu Val Ser Lys Trp Glu Asn Pro Arg Val Leu Ser Phe Ser Leu Thr
35 40 45

Ser Gln Thr Met Leu Asp Gln Ser Val Asp Phe Asp Val Leu Pro Ala
50 55 60

Phe Asp Ala Leu Gly Gln Leu Val Ser Gly Ser Arg Pro Ser Ser Gln
65 70 75 80

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

Thr Cys Phe Thr Glu Leu Gln Arg Asp Phe Ile Ile Ser Arg Pro Thr
100 105 110

Lys Leu Lys Ser Leu Ile Arg Leu Val Lys His Trp Tyr Gln Gln Cys
115 120 125

Thr Lys Ile Ser Lys Gly Arg Gly Ser Leu Pro Pro Gln His Gly Leu
130 135 140

Glu Leu Leu Thr Val Tyr Ala Trp Glu Gln Gly Gly Lys Asp Ser Gln
145 150 155 160

```
Phe Asn Met Ala Glu Gly
                165


<210> 143
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 16; "

<220>
<221> source
<223> /note="Gene Symbol: OAS3; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 3, 100kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448388"

<400> 143
Met Asp Leu Tyr Ser Thr Pro Ala Ala Ala Leu Asp Arg Phe Val Ala
1               5                  10                  15


Arg Arg Leu Gln Pro Arg Lys Glu Phe Val Glu Lys Ala Arg Arg Ala
            20                  25                  30


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


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


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


Leu Asp Cys Phe Lys Ser Tyr Val Asp Gln Arg Ala Arg Arg Ala Glu
                85                  90                  95


Ile Leu Ser Glu Met Arg Ala Ser Leu Glu Ser Trp Trp Gln Asn Pro
            100                 105                 110


Val Pro Gly Leu Arg Leu Thr Phe Pro Glu Gln Ser Val Pro Gly Ala
        115                 120                 125
```

```
Leu Gln Phe Arg Leu Thr Ser Val Asp Leu Glu Asp Trp Met Asp Val
    130                 135                 140

Ser Leu Val Pro Ala Phe Asn Val Leu Gly Gln Ala Gly Ser Gly Val
145                 150                 155                 160

Lys Pro Lys Pro Gln Val Tyr Ser Thr Leu Leu Asn Ser Gly Cys Gln
                165                 170                 175

Gly Gly Glu His Ala Ala Cys Phe Thr Glu Leu Arg Arg Asn Phe Val
            180                 185                 190

Asn Ile Arg Pro Ala Lys Leu Lys Asn Leu Ile Leu Leu Val Lys His
        195                 200                 205

Trp Tyr His Gln Val Lys Pro Leu Gly Arg Val Ser Pro Asp Met
    210                 215                 220


<210> 144
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 16; "

<220>
<221> source
<223> /note="Gene Symbol: OAS3; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase 3, 100kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000449299"

<400> 144
Met Asp Leu Tyr Ser Thr Pro Ala Ala Ala Leu Asp Arg Phe Val Ala
1               5                   10                  15

Arg Arg Leu Gln Pro Arg Lys Glu Phe Val Glu Lys Ala Arg Arg Ala
            20                  25                  30
```

```
Leu Gly Ala Leu Ala Ala Ala Leu Arg Glu Arg Gly Gly Arg Leu Gly
        35                  40                  45

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

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

Leu Asp Cys Phe Lys Ser Tyr Val Asp Gln Arg Ala Arg Arg Ala Glu
                85                  90                  95

Ile Leu Ser Glu Met Arg Ala Ser Leu Glu Ser Trp Trp Gln Asn Pro
            100                 105                 110

Val Pro Gly Leu Arg Leu Thr Phe Pro Glu Gln Ser Val Pro Gly Ala
        115                 120                 125

Leu Gln Phe Arg Leu Thr Ser Val Asp Leu Glu Asp Trp Met Asp Val
    130                 135                 140

Ser Leu Val Pro Ala Phe Asn Val Leu Gly Glu Gly Phe Leu Asp His
145                 150                 155                 160

Ser Arg Val Gly Gly Lys Arg Ser Leu Gly Thr Thr Gln Asp Phe Gln
                165                 170                 175

Phe
```

<210> 145
<211> 514
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 17; "

<220>
<221> source
<223> /note="Gene Symbol: OASL; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q15646; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000257570"

<400> 145
Met Ala Leu Met Gln Glu Leu Tyr Ser Thr Pro Ala Ser Arg Leu Asp
1   5   10   15

Ser Phe Val Ala Gln Trp Leu Gln Pro His Arg Glu Trp Lys Glu Glu
            20   25   30

Val Leu Asp Ala Val Arg Thr Val Glu Glu Phe Leu Arg Gln Glu His
        35   40   45

Phe Gln Gly Lys Arg Gly Leu Asp Gln Asp Val Arg Val Leu Lys Val
    50   55   60

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

Glu Val Glu Leu Val Ala Phe Leu Ser Cys Phe His Ser Phe Gln Glu
                85   90   95

Ala Ala Lys His His Lys Asp Val Leu Arg Leu Ile Trp Lys Thr Met
            100   105   110

Trp Gln Ser Gln Asp Leu Leu Asp Leu Gly Leu Glu Asp Leu Arg Met
        115   120   125

Glu Gln Arg Val Pro Asp Ala Leu Val Phe Thr Ile Gln Thr Arg Gly
    130   135   140

Thr Ala Glu Pro Ile Thr Val Thr Ile Val Pro Ala Tyr Arg Ala Leu
145   150   155   160

Gly Pro Ser Leu Pro Asn Ser Gln Pro Pro Pro Glu Val Tyr Val Ser
                165   170   175

Leu Ile Lys Ala Cys Gly Gly Pro Gly Asn Phe Cys Pro Ser Phe Ser
            180   185   190

```
Glu Leu Gln Arg Asn Phe Val Lys His Arg Pro Thr Lys Leu Lys Ser
        195                 200                 205

Leu Leu Arg Leu Val Lys His Trp Tyr Gln Gln Tyr Val Lys Ala Arg
    210                 215                 220

Ser Pro Arg Ala Asn Leu Pro Pro Leu Tyr Ala Leu Glu Leu Leu Thr
225                 230                 235                 240

Ile Tyr Ala Trp Glu Met Gly Thr Glu Glu Asp Glu Asn Phe Met Leu
                245                 250                 255

Asp Glu Gly Phe Thr Thr Val Met Asp Leu Leu Leu Glu Tyr Glu Val
            260                 265                 270

Ile Cys Ile Tyr Trp Thr Lys Tyr Tyr Thr Leu His Asn Ala Ile Ile
        275                 280                 285

Glu Asp Cys Val Arg Lys Gln Leu Lys Lys Glu Arg Pro Ile Ile Leu
    290                 295                 300

Asp Pro Ala Asp Pro Thr Leu Asn Val Ala Glu Gly Tyr Arg Trp Asp
305                 310                 315                 320

Ile Val Ala Gln Arg Ala Ser Gln Cys Leu Lys Gln Asp Cys Cys Tyr
                325                 330                 335

Asp Asn Arg Glu Asn Pro Ile Ser Ser Trp Asn Val Lys Arg Ala Arg
            340                 345                 350

Asp Ile His Leu Thr Val Glu Gln Arg Gly Tyr Pro Asp Phe Asn Leu
        355                 360                 365

Ile Val Asn Pro Tyr Glu Pro Ile Arg Lys Val Lys Glu Lys Ile Arg
    370                 375                 380

Arg Thr Arg Gly Tyr Ser Gly Leu Gln Arg Leu Ser Phe Gln Val Pro
385                 390                 395                 400

Gly Ser Glu Arg Gln Leu Leu Ser Ser Arg Cys Ser Leu Ala Lys Tyr
                405                 410                 415
```

```
Gly Ile Phe Ser His Thr His Ile Tyr Leu Leu Glu Thr Ile Pro Ser
            420                 425                 430

Glu Ile Gln Val Phe Val Lys Asn Pro Asp Gly Gly Ser Tyr Ala Tyr
        435                 440                 445

Ala Ile Asn Pro Asn Ser Phe Ile Leu Gly Leu Lys Gln Gln Ile Glu
    450                 455                 460

Asp Gln Gln Gly Leu Pro Lys Lys Gln Gln Gln Leu Glu Phe Gln Gly
465                 470                 475                 480

Gln Val Leu Gln Asp Trp Leu Gly Leu Gly Ile Tyr Gly Ile Gln Asp
                485                 490                 495

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

Ala Ser
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<210> 146
<211> 255
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 17; "

<220>
<221> source
<223> /note="Gene Symbol: OASL; "

<220>
<221> source
<223> /note="Gene Name:
2'-5'-oligoadenylate synthetase-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q15646; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000341125"

<400> 146

```
Met Ala Leu Met Gln Glu Leu Tyr Ser Thr Pro Ala Ser Arg Leu Asp
1               5                   10                  15
```

```
Ser Phe Val Ala Gln Trp Leu Gln Pro His Arg Glu Trp Lys Glu Glu
            20                  25                  30

Val Leu Asp Ala Val Arg Thr Val Glu Glu Phe Leu Arg Gln Glu His
        35                  40                  45

Phe Gln Gly Lys Arg Gly Leu Asp Gln Asp Val Arg Val Leu Lys Val
    50                  55                  60

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

Glu Val Glu Leu Val Ala Phe Leu Ser Cys Phe His Ser Phe Gln Glu
                85                  90                  95

Ala Ala Lys His His Lys Asp Val Leu Arg Leu Ile Trp Lys Thr Met
            100                 105                 110

Trp Gln Ser Gln Asp Leu Leu Asp Leu Gly Leu Glu Asp Leu Arg Met
        115                 120                 125

Glu Gln Arg Val Pro Asp Ala Leu Val Phe Thr Ile Gln Thr Arg Gly
    130                 135                 140

Thr Ala Glu Pro Ile Thr Val Thr Ile Val Pro Ala Tyr Arg Ala Leu
145                 150                 155                 160

Gly Pro Ser Leu Pro Asn Ser Gln Pro Pro Pro Glu Val Tyr Val Ser
                165                 170                 175

Leu Ile Lys Ala Cys Gly Gly Pro Gly Asn Phe Cys Pro Ser Phe Ser
            180                 185                 190

Glu Leu Gln Arg Asn Phe Val Lys His Arg Pro Thr Lys Leu Lys Ser
        195                 200                 205

Leu Leu Arg Leu Val Lys His Trp Tyr Gln Gln Ala His His Pro Gly
    210                 215                 220

Ser Gly Arg Pro His Pro Gln Arg Gly Arg Arg Val Gln Met Gly His
225                 230                 235                 240
```

```
Arg Cys Ser Glu Gly Leu Pro Val Pro Glu Thr Gly Leu Leu Leu
                245                 250                 255


<210> 147
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 17; "

<220>
<221> source
<223> /note="Gene Symbol: OASL; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000444127"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 147
Xaa His Thr Ser Leu Gln Ala Gly Leu Leu Arg Gly Ser Val Ala Ala
1               5                   10                  15


Ala Pro Pro Gly Val Glu Gly Arg Gly Ala Arg Arg Cys Ala Asp Arg
            20                  25                  30


Gly Gly Val Ser Glu Ala Gly Ala Phe Pro Gly Glu Ala Trp Ala Gly
        35                  40                  45


Pro Gly Cys Ala Gly Ala Glu Gly Ser Gln Gly Pro Ser Leu Pro Asn
    50                  55                  60


Ser Gln Pro Pro Pro Glu Val Tyr Val Ser Leu Ile Lys Ala Cys Gly
65                  70                  75                  80


Gly Pro Gly Asn Phe Cys Pro Ser Phe Ser Glu Leu Gln Arg Asn Phe
                85                  90                  95
```

```
Val Lys His Arg Pro Thr Lys Leu Lys Ser Leu Leu Arg Leu Val Lys
            100                 105                 110

His Trp Tyr Gln Gln Ala His His Pro Gly Ser Gly Arg Pro His Pro
        115                 120                 125

Gln Arg Gly Arg Arg Val Gln Met Gly His Arg Cys Ser Glu Gly Leu
    130                 135                 140

Pro Val Pro Glu Thr Gly Leu Leu Leu
145                 150


<210> 148
<211> 384
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 17; "

<220>
<221> source
<223> /note="Gene Symbol: OASL; "

<220>
<221> source
<223> /note="Gene Name:
      2'-5'-oligoadenylate synthetase-like; "

<220>
<221> source
<223> /note="Uniprot ID:  Q15646; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479512"

<400> 148
Met Ala Leu Met Gln Glu Leu Tyr Ser Thr Pro Ala Ser Arg Leu Asp
1               5                   10                  15

Ser Phe Val Ala Gln Trp Leu Gln Pro His Arg Glu Trp Lys Glu Glu
            20                  25                  30

Val Leu Asp Ala Val Arg Thr Val Glu Glu Phe Leu Arg Gln Glu His
        35                  40                  45

Phe Gln Gly Lys Arg Gly Leu Asp Gln Asp Val Arg Val Leu Lys Val
```

50 55 60

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

Glu Val Glu Leu Val Ala Phe Leu Ser Cys Phe His Ser Phe Gln Glu
85 90 95

Ala Ala Lys His His Lys Asp Val Leu Arg Leu Ile Trp Lys Thr Met
100 105 110

Trp Gln Ser Gln Asp Leu Leu Asp Leu Gly Leu Glu Asp Leu Arg Met
115 120 125

Glu Gln Arg Val Pro Asp Ala Leu Val Phe Thr Ile Gln Thr Arg Gly
130 135 140

Thr Ala Glu Pro Ile Thr Val Thr Ile Val Pro Ala Tyr Arg Ala Leu
145 150 155 160

Gly Pro Ser Leu Pro Asn Ser Gln Pro Pro Pro Glu Val Tyr Val Ser
165 170 175

Leu Ile Lys Ala Cys Gly Gly Pro Gly Asn Phe Cys Pro Ser Phe Ser
180 185 190

Glu Leu Gln Arg Asn Phe Val Lys His Arg Pro Thr Lys Leu Lys Ser
195 200 205

Leu Leu Arg Leu Val Lys His Trp Tyr Gln Gln Arg Ala Arg Asp Ile
210 215 220

His Leu Thr Val Glu Gln Arg Gly Tyr Pro Asp Phe Asn Leu Ile Val
225 230 235 240

Asn Pro Tyr Glu Pro Ile Arg Lys Val Lys Glu Lys Ile Arg Arg Thr
245 250 255

Arg Gly Tyr Ser Gly Leu Gln Arg Leu Ser Phe Gln Val Pro Gly Ser
260 265 270

Glu Arg Gln Leu Leu Ser Ser Arg Cys Ser Leu Ala Lys Tyr Gly Ile
275 280 285

```
Phe Ser His Thr His Ile Tyr Leu Leu Glu Thr Ile Pro Ser Glu Ile
    290                 295                 300

Gln Val Phe Val Lys Asn Pro Asp Gly Gly Ser Tyr Ala Tyr Ala Ile
305                 310                 315                 320

Asn Pro Asn Ser Phe Ile Leu Gly Leu Lys Gln Gln Ile Glu Asp Gln
                325                 330                 335

Gln Gly Leu Pro Lys Lys Gln Gln Gln Leu Glu Phe Gln Gly Gln Val
            340                 345                 350

Leu Gln Asp Trp Leu Gly Leu Gly Ile Tyr Gly Ile Gln Asp Ser Asp
        355                 360                 365

Thr Leu Ile Leu Ser Lys Lys Lys Gly Glu Ala Leu Phe Pro Ala Ser
    370                 375                 380


<210> 149
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 18; "

<220>
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<223> /note="Gene Symbol: ADO; "

<220>
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<223> /note="Gene Name:
      2-aminoethanethiol (cysteamine)
      dioxygenase; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96SZ5; "

<220>
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<223> /note="ENSP ID: ENSP00000362888"

<400> 149
Met Pro Arg Asp Asn Met Ala Ser Leu Ile Gln Arg Ile Ala Arg Gln
1               5                   10                  15
```

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

Arg Asp Ala Ala Ser Gly Pro Glu Ala Pro Met Gln Pro Gly Phe Pro
        35                  40                  45

Glu Asn Leu Ser Lys Leu Lys Ser Leu Leu Thr Gln Leu Arg Ala Glu
    50                  55                  60

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

Asn Leu Pro Pro Val Thr Tyr Met His Ile Tyr Glu Thr Asp Gly Phe
                85                  90                  95

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

Asp His Pro Gly Met His Gly Met Leu Lys Val Leu Tyr Gly Thr Val
        115                 120                 125

Arg Ile Ser Cys Met Asp Lys Leu Asp Ala Gly Gly Gly Gln Arg Pro
    130                 135                 140

Arg Ala Leu Pro Pro Glu Gln Gln Phe Glu Pro Pro Leu Gln Pro Arg
145                 150                 155                 160

Glu Arg Glu Ala Val Arg Pro Gly Val Leu Arg Ser Arg Ala Glu Tyr
                165                 170                 175

Thr Glu Ala Ser Gly Pro Cys Ile Leu Thr Pro His Arg Asp Asn Leu
            180                 185                 190

His Gln Ile Asp Ala Val Glu Gly Pro Ala Ala Phe Leu Asp Ile Leu
        195                 200                 205

Ala Pro Pro Tyr Asp Pro Asp Asp Gly Arg Asp Cys His Tyr Tyr Arg
    210                 215                 220

Val Leu Glu Pro Val Arg Pro Lys Glu Ala Ser Ser Ser Ala Cys Asp
225                 230                 235                 240
```

```
Leu Pro Arg Glu Val Trp Leu Leu Glu Thr Pro Gln Ala Asp Asp Phe
                245                 250                 255


Trp Cys Glu Gly Glu Pro Tyr Pro Gly Pro Lys Val Phe Pro
            260                 265                 270


<210> 150
<211> 174
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<213> Homo sapiens

<220>
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<223> /note="Payload ID: 19; "

<220>
<221> source
<223> /note="Gene Symbol: DNPH1; "

<220>
<221> source
<223> /note="Gene Name:
      2'-deoxynucleoside 5'-phosphate N-hydrolase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  O43598; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000230431"

<400> 150
Met Ala Ala Ala Met Val Pro Gly Arg Ser Glu Ser Trp Glu Arg Gly
1               5                   10                  15


Glu Pro Gly Arg Pro Ala Leu Tyr Phe Cys Gly Ser Ile Arg Gly Gly
            20                  25                  30


Arg Glu Asp Arg Thr Leu Tyr Glu Arg Ile Val Ser Arg Leu Arg Arg
        35                  40                  45


Phe Gly Thr Val Leu Thr Glu His Val Ala Ala Ala Glu Leu Gly Ala
    50                  55                  60


Arg Gly Glu Glu Ala Ala Gly Gly Asp Arg Leu Ile His Glu Gln Asp
65                  70                  75                  80


Leu Glu Trp Leu Gln Gln Ala Asp Val Val Val Ala Glu Val Thr Gln
                85                  90                  95
```

```
Pro Ser Leu Gly Val Gly Tyr Glu Leu Gly Arg Ala Val Ala Phe Asn
            100                 105                 110

Lys Arg Ile Leu Cys Leu Phe Arg Pro Gln Ser Gly Arg Val Leu Ser
        115                 120                 125

Ala Met Ile Arg Gly Ala Ala Asp Gly Ser Arg Phe Gln Val Trp Asp
    130                 135                 140

Tyr Glu Glu Gly Glu Val Glu Ala Leu Leu Asp Arg Tyr Phe Glu Ala
145                 150                 155                 160

Asp Pro Pro Gly Gln Val Ala Ala Ser Pro Asp Pro Thr Thr
                165                 170


<210> 151
<211> 148
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 19; "

<220>
<221> source
<223> /note="Gene Symbol: DNPH1; "

<220>
<221> source
<223> /note="Gene Name:
      2'-deoxynucleoside 5'-phosphate N-hydrolase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  O43598; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377556"

<400> 151
Met Ala Ala Ala Met Val Pro Gly Arg Ser Glu Ser Trp Glu Arg Gly
1               5                   10                  15

Glu Pro Gly Arg Pro Ala Leu Tyr Phe Cys Gly Ser Ile Arg Gly Gly
            20                  25                  30
```

```
Arg Glu Asp Arg Thr Leu Tyr Glu Arg Ile Val Ser Arg Leu Arg Arg
        35                  40                  45

Phe Gly Thr Val Leu Thr Glu His Val Ala Ala Ala Glu Leu Gly Ala
    50                  55                  60

Arg Gly Glu Glu Ala Ala Gly Gly Asp Arg Leu Ile His Glu Gln Asp
65                  70                  75                  80

Leu Glu Trp Leu Gln Gln Ala Asp Val Val Val Ala Glu Val Thr Gln
                85                  90                  95

Pro Ser Leu Gly Val Gly Tyr Glu Leu Gly Arg Ala Val Ala Phe Asn
            100                 105                 110

Lys Arg Ile Leu Cys Leu Phe Arg Pro Gln Ser Gly Arg Gly Glu His
        115                 120                 125

Pro Lys Pro Pro Ser Trp Leu Ser Met Asp Pro Ala Leu Ser Ser Phe
    130                 135                 140

Pro Gly Gly Leu
145
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<210> 152
<211> 243
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 19; "

<220>
<221> source
<223> /note="Gene Symbol: DNPH1; "

<220>
<221> source
<223> /note="Gene Name:
2'-deoxynucleoside 5'-phosphate N-hydrolase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422440"

<400> 152

```
Ala Ala Ala Met Val Pro Gly Arg Ser Glu Ser Trp Glu Arg Gly Glu
1               5                   10                  15
```

```
Pro Gly Arg Pro Ala Leu Tyr Phe Cys Gly Ser Ile Arg Gly Gly Arg
            20                  25                  30

Glu Asp Arg Thr Leu Tyr Glu Arg Ile Val Ser Arg Leu Arg Arg Phe
        35                  40                  45

Gly Thr Val Leu Thr Glu His Val Ala Ala Ala Glu Leu Gly Ala Arg
    50                  55                  60

Gly Glu Ala Leu Gly Pro Arg Asp Ala Gly Thr Arg Ala Arg Thr Trp
65                  70                  75                  80

Leu Gly Trp Gln Gly Pro Gly Leu Ser Ala Pro Pro Thr Pro Gly Ser
                85                  90                  95

Cys Ala Pro Gly Ala Arg Ser Pro Pro Ser Tyr Pro Gly Ala Pro Ser
            100                 105                 110

Ser Ala Pro Ala Arg Glu Gly Asn Gly Pro Gly Leu Gly Leu Arg Gly
        115                 120                 125

Ser Gln Gln Ala Cys Gly Trp Glu Glu Ala Ala Gly Gly Asp Arg Leu
    130                 135                 140

Ile His Glu Gln Asp Leu Glu Trp Leu Gln Gln Ala Asp Val Val Val
145                 150                 155                 160

Ala Glu Val Thr Gln Pro Ser Leu Gly Val Gly Tyr Glu Leu Gly Arg
                165                 170                 175

Ala Val Ala Phe Asn Lys Arg Ile Leu Cys Leu Phe Arg Pro Gln Ser
            180                 185                 190

Gly Arg Val Leu Ser Ala Met Ile Arg Gly Ala Ala Asp Gly Ser Arg
        195                 200                 205

Phe Gln Val Trp Asp Tyr Glu Glu Gly Glu Val Glu Ala Leu Leu Asp
    210                 215                 220

Arg Tyr Phe Glu Ala Asp Pro Pro Gly Gln Val Ala Ala Ser Pro Asp
225                 230                 235                 240
```

Pro Thr Thr

<210> 153
<211> 578
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UJ83; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000323811"

<400> 153
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1   5   10   15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
            20   25   30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
        35   40   45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
    50   55   60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys
65   70   75   80

Leu Val Val Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala
                85   90   95

Asn Ala Asn Met Asn Cys Trp Pro Leu Leu Val Ile Gly Gly Ser Ser

```
            100                 105                 110

Glu Arg Asn Gln Glu Thr Met Gly Ala Phe Gln Glu Phe Pro Gln Val
        115                 120                 125

Glu Ala Cys Arg Leu Tyr Thr Lys Phe Ser Ala Arg Pro Ser Ser Ile
    130                 135                 140

Glu Ala Ile Pro Phe Val Ile Glu Lys Ala Val Arg Ser Ser Ile Tyr
145                 150                 155                 160

Gly Arg Pro Gly Ala Cys Tyr Val Asp Ile Pro Ala Asp Phe Val Asn
                165                 170                 175

Leu Gln Val Asn Val Asn Ser Ile Lys Tyr Met Glu Arg Cys Met Ser
            180                 185                 190

Pro Pro Ile Ser Met Ala Glu Thr Ser Ala Val Cys Thr Ala Ala Ser
        195                 200                 205

Val Ile Arg Asn Ala Lys Gln Pro Leu Leu Ile Ile Gly Lys Gly Ala
    210                 215                 220

Ala Tyr Ala His Ala Glu Glu Ser Ile Lys Lys Leu Val Glu Gln Tyr
225                 230                 235                 240

Lys Leu Pro Phe Leu Pro Thr Pro Met Gly Lys Gly Val Val Pro Asp
                245                 250                 255

Asn His Pro Tyr Cys Val Gly Ala Ala Arg Ser Arg Ala Leu Gln Phe
            260                 265                 270

Ala Asp Val Ile Val Leu Phe Gly Ala Arg Leu Asn Trp Ile Leu His
        275                 280                 285

Phe Gly Leu Pro Pro Arg Tyr Gln Pro Asp Val Lys Phe Ile Gln Val
    290                 295                 300

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

Leu Leu Gly Asn Ile His Ala Val Thr Lys Gln Leu Leu Glu Glu Leu
                325                 330                 335
```

```
Asp Lys Thr Pro Trp Gln Tyr Pro Pro Glu Ser Lys Trp Trp Lys Thr
            340                 345                 350

Leu Arg Glu Lys Met Lys Ser Asn Glu Ala Ala Ser Lys Glu Leu Ala
        355                 360                 365

Ser Lys Lys Ser Leu Pro Met Asn Tyr Tyr Thr Val Phe Tyr His Val
    370                 375                 380

Gln Glu Gln Leu Pro Arg Asp Cys Phe Val Val Ser Glu Gly Ala Asn
385                 390                 395                 400

Thr Met Asp Ile Gly Arg Thr Val Leu Gln Asn Tyr Leu Pro Arg His
                405                 410                 415

Arg Leu Asp Ala Gly Thr Phe Gly Thr Met Gly Val Gly Leu Gly Phe
            420                 425                 430

Ala Ile Ala Ala Ala Val Val Ala Lys Asp Arg Ser Pro Gly Gln Trp
        435                 440                 445

Ile Ile Cys Val Glu Gly Asp Ser Ala Phe Gly Phe Ser Gly Met Glu
    450                 455                 460

Val Glu Thr Ile Cys Arg Tyr Asn Leu Pro Ile Ile Leu Leu Val Val
465                 470                 475                 480

Asn Asn Asn Gly Ile Tyr Gln Gly Phe Asp Thr Asp Thr Trp Lys Glu
                485                 490                 495

Met Leu Lys Phe Gln Asp Ala Thr Ala Val Val Pro Pro Met Cys Leu
            500                 505                 510

Leu Pro Asn Ser His Tyr Glu Gln Val Met Thr Ala Phe Gly Gly Lys
        515                 520                 525

Gly Tyr Phe Val Gln Thr Pro Glu Glu Leu Gln Lys Ser Leu Arg Gln
    530                 535                 540

Ser Leu Ala Asp Thr Thr Lys Pro Ser Leu Ile Asn Ile Met Ile Glu
545                 550                 555                 560
```

Pro Gln Ala Thr Arg Lys Ala Gln Asp Phe His Trp Leu Thr Arg Ser
565 570 575

Asn Met

<210> 154
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373289"

<400> 154
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1 5 10 15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
20 25 30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
35 40 45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
50 55 60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys
65 70 75 80

Leu Val Val Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala
85 90 95

Asn Ala Asn Met Asn Cys Trp Leu Lys Leu Val Asp Tyr Ile Pro Ser

```
            100                 105                 110

Ser Leu Pro Ala Gln Ala Ala
        115


<210> 155
<211> 551
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
      2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UJ83; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000390699"

<400> 155
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1               5                  10                  15


Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
            20                  25                  30


Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
        35                  40                  45


Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
    50                  55                  60


Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Leu Leu Val
65                  70                  75                  80


Ile Gly Gly Ser Ser Glu Arg Asn Gln Glu Thr Met Gly Ala Phe Gln
                85                  90                  95
```

```
Glu Phe Pro Gln Val Glu Ala Cys Arg Leu Tyr Thr Lys Phe Ser Ala
            100                 105                 110

Arg Pro Ser Ser Ile Glu Ala Ile Pro Phe Val Ile Glu Lys Ala Val
        115                 120                 125

Arg Ser Ser Ile Tyr Gly Arg Pro Gly Ala Cys Tyr Val Asp Ile Pro
    130                 135                 140

Ala Asp Phe Val Asn Leu Gln Val Asn Val Asn Ser Ile Lys Tyr Met
145                 150                 155                 160

Glu Arg Cys Met Ser Pro Pro Ile Ser Met Ala Glu Thr Ser Ala Val
                165                 170                 175

Cys Thr Ala Ala Ser Val Ile Arg Asn Ala Lys Gln Pro Leu Leu Ile
            180                 185                 190

Ile Gly Lys Gly Ala Ala Tyr Ala His Ala Glu Glu Ser Ile Lys Lys
        195                 200                 205

Leu Val Glu Gln Tyr Lys Leu Pro Phe Leu Pro Thr Pro Met Gly Lys
    210                 215                 220

Gly Val Val Pro Asp Asn His Pro Tyr Cys Val Gly Ala Ala Arg Ser
225                 230                 235                 240

Arg Ala Leu Gln Phe Ala Asp Val Ile Val Leu Phe Gly Ala Arg Leu
                245                 250                 255

Asn Trp Ile Leu His Phe Gly Leu Pro Pro Arg Tyr Gln Pro Asp Val
            260                 265                 270

Lys Phe Ile Gln Val Asp Ile Cys Ala Glu Glu Leu Gly Asn Asn Val
        275                 280                 285

Lys Pro Ala Val Thr Leu Leu Gly Asn Ile His Ala Val Thr Lys Gln
    290                 295                 300

Leu Leu Glu Glu Leu Asp Lys Thr Pro Trp Gln Tyr Pro Pro Glu Ser
305                 310                 315                 320
```

```
Lys Trp Trp Lys Thr Leu Arg Glu Lys Met Lys Ser Asn Glu Ala Ala
                325                 330                 335

Ser Lys Glu Leu Ala Ser Lys Lys Ser Leu Pro Met Asn Tyr Tyr Thr
            340                 345                 350

Val Phe Tyr His Val Gln Glu Gln Leu Pro Arg Asp Cys Phe Val Val
        355                 360                 365

Ser Glu Gly Ala Asn Thr Met Asp Ile Gly Arg Thr Val Leu Gln Asn
    370                 375                 380

Tyr Leu Pro Arg His Arg Leu Asp Ala Gly Thr Phe Gly Thr Met Gly
385                 390                 395                 400

Val Gly Leu Gly Phe Ala Ile Ala Ala Ala Val Val Ala Lys Asp Arg
                405                 410                 415

Ser Pro Gly Gln Trp Ile Ile Cys Val Glu Gly Asp Ser Ala Phe Gly
            420                 425                 430

Phe Ser Gly Met Glu Val Glu Thr Ile Cys Arg Tyr Asn Leu Pro Ile
        435                 440                 445

Ile Leu Leu Val Val Asn Asn Asn Gly Ile Tyr Gln Gly Phe Asp Thr
    450                 455                 460

Asp Thr Trp Lys Glu Met Leu Lys Phe Gln Asp Ala Thr Ala Val Val
465                 470                 475                 480

Pro Pro Met Cys Leu Leu Pro Asn Ser His Tyr Glu Gln Val Met Thr
                485                 490                 495

Ala Phe Gly Gly Lys Gly Tyr Phe Val Gln Thr Pro Glu Glu Leu Gln
            500                 505                 510

Lys Ser Leu Arg Gln Ser Leu Ala Asp Thr Thr Lys Pro Ser Leu Ile
        515                 520                 525

Asn Ile Met Ile Glu Pro Gln Ala Thr Arg Lys Ala Gln Asp Phe His
    530                 535                 540

Trp Leu Thr Arg Ser Asn Met
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545 550

<210> 156
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391393"

<400> 156
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1 5 10 15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
20 25 30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
35 40 45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
50 55 60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Leu Leu Val
65 70 75 80

Ile Gly Gly Ser Ser Glu Arg Asn Gln Glu Thr Met Gly Ala Phe Gln
85 90 95

Glu Phe Pro Gln Val Glu Ala Cys Arg Leu Tyr Thr Lys Phe Ser Ala
100 105 110

Arg Pro Ser Ser Ile Glu Ala Ile Pro Phe Val Ile Glu Lys Ala Val
115 120 125

```
Arg Ser Ser Ile Tyr Gly Arg Pro Gly Ala Cys Tyr Val Asp Ile Pro
    130                 135                 140

Ala Asp Phe Val Asn Leu Gln Val Asn Val Asn Ser Ile Lys Tyr Met
145                 150                 155                 160

Glu Arg Cys Met Ser Pro Pro Ile Ser Met Ala Glu Thr Ser Ala Val
                165                 170                 175

Cys Thr Ala Ala Ser Val Ile Arg Asn Ala Lys Gln Pro Leu Leu Ile
            180                 185                 190

Ile Gly Lys Gly Ala Ala Tyr Ala His Ala Glu Glu Ser Ile Lys Lys
        195                 200                 205

Leu Val Glu Gln Tyr Lys Leu Pro Phe Leu Pro Thr Pro Met Gly Lys
    210                 215                 220

Gly Val Val Pro Asp Asn His Pro Tyr Cys Val Gly Ala Ala Arg Ser
225                 230                 235                 240

Arg Cys Val Ala
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<210> 157
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392796"

<400> 157
```
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
```

```
1               5                   10                  15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
            20                  25                  30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
        35                  40                  45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
    50                  55                  60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys
65                  70                  75                  80

Leu Val Val Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala
                85                  90                  95

Asn Ala Asn Met Asn Cys Trp Pro Leu Leu Val Ile Gly Gly Ser Ser
            100                 105                 110

Glu Arg Asn Gln Glu Thr Met Gly Ala Phe Gln Glu Phe Pro Gln Val
        115                 120                 125

His Gly Thr Leu His Val Thr Ser Tyr
    130                 135


<210> 158
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
      2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000395278"
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<400> 158
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1 5 10 15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
20 25 30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
35 40 45

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

Ile Cys Ala Glu Glu Leu Gly Asn Asn Val Lys Pro Ala Val Thr Leu
65 70 75 80

Leu Gly Asn Ile His Ala Val Thr Lys Gln Leu Leu Glu Glu Leu Asp
85 90 95

Lys Thr Pro Trp Gln Tyr Pro Pro Glu Ser Lys Trp Trp Lys Thr Leu
100 105 110

Arg Glu Lys Met Lys Ser Asn Glu Ala Ala Ser Lys Glu Leu Ala Ser
115 120 125

Lys Lys Ser Leu Pro Met Asn Tyr Tyr Thr Val Phe Tyr His Val Gln
130 135 140

Glu Gln Leu Pro Arg Asp Cys Phe Val Val Ser Glu Gly Ala Asn Thr
145 150 155 160

Met Asp Ile Gly Arg Thr Val Leu Gln Asn Tyr Leu Pro Arg His Arg
165 170 175

Leu Asp Ala Gly Thr Phe Gly Thr Met Gly Val Gly Leu Gly Phe Ala
180 185 190

Ile Ala Ala Ala Val Val Ala Lys Asp Arg Ser Pro Gly Gln Trp Ile
195 200 205

Ile Cys Val Glu Gly Asp Ser Ala Phe Gly Phe Ser Gly Met Glu Val
210 215 220

```
Glu Thr Ile Cys Arg Tyr Asn Leu Pro Ile Ile Leu Leu Val Val Asn
225                 230                 235                 240

Asn Asn Gly Ile Tyr Gln Gly Phe Asp Thr Asp Thr Trp Lys Glu Met
                245                 250                 255

Leu Lys Phe Gln Asp Ala Thr Ala Val Val Pro Pro Met Cys Leu Leu
            260                 265                 270

Pro Asn Ser His Tyr Glu Gln Val Met Thr Ala Phe Gly Gly Lys Gly
        275                 280                 285

Tyr Phe Val Gln Thr Pro Glu Glu Leu Gln Lys Ser Leu Arg Gln Ser
    290                 295                 300

Leu Ala Asp Thr Thr Lys Pro Ser Leu Ile Asn Ile Met Ile Glu Pro
305                 310                 315                 320

Gln Ala Thr Arg Lys Ala Gln Asp Phe His Trp Leu Thr Arg Ser Asn
                325                 330                 335

Met
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<210> 159
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000395352"

<400> 159

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Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1               5                   10                  15
```

```
Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
            20                  25                  30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
        35                  40                  45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Val Glu
    50                  55                  60

Ala Cys Arg Leu Tyr Thr Lys Phe Ser Ala Arg Pro Ser Ser Ile Glu
65                  70                  75                  80

Ala Ile Pro Phe Val Ile Glu Lys Ala Val Arg Ser Ser Ile Tyr Gly
                85                  90                  95

Arg Pro Gly Ala Cys Tyr Val Asp Ile Pro Ala Asp Phe Val Asn Leu
            100                 105                 110

Gln Val Asn Val Asn Ser Ile Lys Tyr Met Glu Arg Cys Met Ser Pro
        115                 120                 125

Pro Ile Ser Met Ala Glu Thr Ser Ala Val Cys Thr Ala Ala Ser Val
    130                 135                 140

Ile Arg Asn Ala Lys Gln Pro Leu Leu Ile Ile Gly Lys
145                 150                 155
```

<210> 160
<211> 496
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>

<221> source
<223> /note="Uniprot ID: Q9UJ83; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403656"

<400> 160
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1   5   10   15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
            20   25   30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
        35   40   45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
    50   55   60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys
65   70   75   80

Leu Val Val Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala
                85   90   95

Asn Ala Asn Met Asn Cys Trp Tyr Met Glu Arg Cys Met Ser Pro Pro
            100   105   110

Ile Ser Met Ala Glu Thr Ser Ala Val Cys Thr Ala Ala Ser Val Ile
        115   120   125

Arg Asn Ala Lys Gln Pro Leu Leu Ile Ile Gly Lys Gly Ala Ala Tyr
    130   135   140

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

Pro Phe Leu Pro Thr Pro Met Gly Lys Gly Val Val Pro Asp Asn His
                165   170   175

Pro Tyr Cys Val Gly Ala Ala Arg Ser Arg Ala Leu Gln Phe Ala Asp
            180   185   190

Val Ile Val Leu Phe Gly Ala Arg Leu Asn Trp Ile Leu His Phe Gly

```
        195                 200                 205

Leu Pro Pro Arg Tyr Gln Pro Asp Val Lys Phe Ile Gln Val Asp Ile
    210                 215                 220

Cys Ala Glu Glu Leu Gly Asn Asn Val Lys Pro Ala Val Thr Leu Leu
225                 230                 235                 240

Gly Asn Ile His Ala Val Thr Lys Gln Leu Leu Glu Glu Leu Asp Lys
                245                 250                 255

Thr Pro Trp Gln Tyr Pro Pro Glu Ser Lys Trp Trp Lys Thr Leu Arg
            260                 265                 270

Glu Lys Met Lys Ser Asn Glu Ala Ala Ser Lys Glu Leu Ala Ser Lys
        275                 280                 285

Lys Ser Leu Pro Met Asn Tyr Tyr Thr Val Phe Tyr His Val Gln Glu
    290                 295                 300

Gln Leu Pro Arg Asp Cys Phe Val Val Ser Glu Gly Ala Asn Thr Met
305                 310                 315                 320

Asp Ile Gly Arg Thr Val Leu Gln Asn Tyr Leu Pro Arg His Arg Leu
                325                 330                 335

Asp Ala Gly Thr Phe Gly Thr Met Gly Val Gly Leu Gly Phe Ala Ile
            340                 345                 350

Ala Ala Ala Val Val Ala Lys Asp Arg Ser Pro Gly Gln Trp Ile Ile
        355                 360                 365

Cys Val Glu Gly Asp Ser Ala Phe Gly Phe Ser Gly Met Glu Val Glu
    370                 375                 380

Thr Ile Cys Arg Tyr Asn Leu Pro Ile Ile Leu Leu Val Val Asn Asn
385                 390                 395                 400

Asn Gly Ile Tyr Gln Gly Phe Asp Thr Asp Thr Trp Lys Glu Met Leu
                405                 410                 415

Lys Phe Gln Asp Ala Thr Ala Val Val Pro Pro Met Cys Leu Leu Pro
            420                 425                 430
```

```
Asn Ser His Tyr Glu Gln Val Met Thr Ala Phe Gly Gly Lys Gly Tyr
        435                 440                 445

Phe Val Gln Thr Pro Glu Glu Leu Gln Lys Ser Leu Arg Gln Ser Leu
    450                 455                 460

Ala Asp Thr Thr Lys Pro Ser Leu Ile Asn Ile Met Ile Glu Pro Gln
465                 470                 475                 480

Ala Thr Arg Lys Ala Gln Asp Phe His Trp Leu Thr Arg Ser Asn Met
                485                 490                 495


<210> 161
<211> 518
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
<221> source
<223> /note="Gene Name:
      2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UJ83; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404883"

<400> 161
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1               5                   10                  15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
            20                  25                  30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
        35                  40                  45
```

```
Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
    50                  55                  60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys
65                  70                  75                  80

Leu Val Val Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala
                85                  90                  95

Asn Ala Asn Met Asn Cys Trp Pro Leu Leu Val Ile Gly Gly Ser Ser
            100                 105                 110

Glu Arg Asn Gln Glu Thr Met Gly Ala Phe Gln Glu Phe Pro Gln Ala
        115                 120                 125

Val Arg Ser Ser Ile Tyr Gly Arg Pro Gly Ala Cys Tyr Val Asp Ile
    130                 135                 140

Pro Ala Asp Phe Val Asn Leu Gln Val Asn Val Asn Ser Ile Lys Tyr
145                 150                 155                 160

Met Glu Arg Cys Met Ser Pro Pro Ile Ser Met Ala Glu Thr Ser Ala
                165                 170                 175

Val Cys Thr Ala Ala Ser Val Ile Arg Asn Ala Lys Gln Pro Leu Leu
            180                 185                 190

Ile Ile Gly Lys Gly Ala Ala Tyr Ala His Ala Glu Glu Ser Ile Lys
        195                 200                 205

Lys Leu Val Glu Gln Tyr Lys Leu Pro Phe Leu Pro Thr Pro Met Gly
    210                 215                 220

Lys Gly Val Val Pro Asp Asn His Pro Tyr Cys Val Gly Ala Ala Arg
225                 230                 235                 240

Ser Arg Ala Leu Gln Phe Ala Asp Val Ile Val Leu Phe Gly Ala Arg
                245                 250                 255

Leu Asn Trp Ile Leu His Phe Gly Leu Pro Pro Arg Tyr Gln Pro Asp
            260                 265                 270

Val Lys Phe Ile Gln Val Asp Ile Cys Ala Glu Glu Leu Gly Asn Asn
```

```
        275                 280                 285

Val Lys Pro Ala Val Thr Leu Leu Gly Asn Ile His Ala Val Thr Lys
    290                 295                 300

Gln Glu Leu Ala Ser Lys Lys Ser Leu Pro Met Asn Tyr Tyr Thr Val
305                 310                 315                 320

Phe Tyr His Val Gln Glu Gln Leu Pro Arg Asp Cys Phe Val Val Ser
                325                 330                 335

Glu Gly Ala Asn Thr Met Asp Ile Gly Arg Thr Val Leu Gln Asn Tyr
            340                 345                 350

Leu Pro Arg His Arg Leu Asp Ala Gly Thr Phe Gly Thr Met Gly Val
        355                 360                 365

Gly Leu Gly Phe Ala Ile Ala Ala Ala Val Val Ala Lys Asp Arg Ser
    370                 375                 380

Pro Gly Gln Trp Ile Ile Cys Val Glu Gly Asp Ser Ala Phe Gly Phe
385                 390                 395                 400

Ser Gly Met Glu Val Glu Thr Ile Cys Arg Tyr Asn Leu Pro Ile Ile
                405                 410                 415

Leu Leu Val Val Asn Asn Asn Gly Ile Tyr Gln Gly Phe Asp Thr Asp
            420                 425                 430

Thr Trp Lys Glu Met Leu Lys Phe Gln Asp Ala Thr Ala Val Val Pro
        435                 440                 445

Pro Met Cys Leu Leu Pro Asn Ser His Tyr Glu Gln Val Met Thr Ala
    450                 455                 460

Phe Gly Gly Lys Gly Tyr Phe Val Gln Thr Pro Glu Glu Leu Gln Lys
465                 470                 475                 480

Ser Leu Arg Gln Ser Leu Ala Asp Thr Thr Lys Pro Ser Leu Ile Asn
                485                 490                 495

Ile Met Ile Glu Pro Gln Ala Thr Arg Lys Ala Gln Asp Phe His Trp
            500                 505                 510
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Leu Thr Arg Ser Asn Met
515

<210> 162
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 20; "

<220>
<221> source
<223> /note="Gene Symbol: HACL1; "

<220>
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<223> /note="Gene Name:
2-hydroxyacyl-CoA lyase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486684"

<400> 162
Met Pro Asp Ser Asn Phe Ala Glu Arg Ser Glu Glu Gln Val Ser Gly
1 5 10 15

Ala Lys Val Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile
20 25 30

Phe Gly Ile Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln
35 40 45

Gln Leu Gly Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys
50 55 60

Tyr Ala Ala Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys
65 70 75 80

Leu Val Val Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala
85 90 95

Asn Ala Asn Met Asn Cys Trp Leu Lys Leu Val Asp Tyr Ile Pro Ser
100 105 110

Ser Leu Pro Ala Gln Ala Ala
        115

<210> 163
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 21; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD1; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000337196"

<400> 163
Met Asp Met Asp Pro Phe Leu His Cys Val Ile Pro Asn Phe Ile Gln
1   5   10   15

Ser Gln Asp Phe Leu Glu Gly Leu Gln Lys Glu Leu Met Asn Leu Asp
            20   25   30

Phe His Glu Asn Leu Met Ile
        35

<210> 164
<211> 46
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 21; "

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase

domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455149"

<400> 164
Met Asp Met Asp Pro Phe Leu His Cys Val Ile Pro Asn Phe Ile Gln
1 5 10 15

Ser Gln Asp Phe Leu Glu Gly Leu Gln Lys Glu Leu Met Asn Leu Asp
            20 25 30

Phe His Glu Lys Tyr Asn Asp Leu Tyr Lys Phe Gln Gln Ser
        35 40 45

<210> 165
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 21; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD1; "

<220>
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<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase
domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456016"

<400> 165
Met Asn Gly Lys Arg Pro Ala Glu Pro Gly Pro Ala Arg Val Gly Lys
1 5 10 15

Lys Gly Lys Lys Glu Val Met Ala Glu Phe Ser Asp Ala Val Thr Glu
            20 25 30

Glu Thr Leu Lys Lys Gln Val Ala Glu Ala Trp Ser Arg Arg Thr Pro
        35 40 45

Phe Ser His Glu Val Ile Val Met Asp Met Asp Pro Phe Leu His Cys
    50 55 60

```
Val Ile Pro Asn Phe Ile Gln Ser Gln Asp Phe Leu Glu Gly Leu Gln
65                  70                  75                  80


Lys Glu Leu Met Asn Leu Asp Phe His Glu Lys Tyr Asn Asp Leu Tyr
                85                  90                  95


Lys Phe Gln Gln Glu Ile Pro Phe Phe Ser Leu Phe Ser
            100                 105


<210> 166
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 21; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD1; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456111"

<400> 166
Met Asn Gly Lys Arg Pro Ala Glu Pro Gly Pro Ala Arg Val Gly Lys
1               5                   10                  15


Lys Gly Lys Lys Glu Val Met Ala Glu Phe Ser Asp Ala Val Thr Glu
            20                  25                  30


Glu Thr Leu Lys Lys Gln Val Ala Glu Ala Trp Ser Arg Arg Thr Pro
        35                  40                  45


Phe Lys Val Ile Val Met Asp Met Asp Pro Phe Leu His Cys Val Ile
    50                  55                  60


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

```
Leu Met Asn Leu Asp Phe His Glu Lys Tyr Asn Asp Leu Tyr Lys Phe
                85                  90                  95

Gln Gln Ser Asp Asp Leu Lys Lys Arg Arg Glu Pro His Ile Ser Thr
            100                 105                 110

Leu Arg Lys Ile Leu Phe Glu Asp Phe Arg Ser Trp Leu Ser Asp Ile
        115                 120                 125

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

Glu Phe Thr Asp Ala Leu Leu Cys His Asp Asp Glu Leu Glu Gly Arg
145                 150                 155                 160

Arg Ile Ala Phe
```

<210> 167
<211> 542
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 21; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD1; "

<220>
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<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase
domain containing 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N543; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457258"

<400> 167

```
Met Asn Gly Lys Arg Pro Ala Glu Pro Gly Pro Ala Arg Val Gly Lys
1               5                   10                  15
```

```
Lys Gly Lys Lys Glu Val Met Ala Glu Phe Ser Asp Ala Val Thr Glu
            20                  25                  30

Glu Thr Leu Lys Lys Gln Val Ala Glu Ala Trp Ser Arg Arg Thr Pro
        35                  40                  45

Phe Ser His Glu Val Ile Val Met Asp Met Asp Pro Phe Leu His Cys
    50                  55                  60

Val Ile Pro Asn Phe Ile Gln Ser Gln Asp Phe Leu Glu Gly Leu Gln
65                  70                  75                  80

Lys Glu Leu Met Asn Leu Asp Phe His Glu Lys Tyr Asn Asp Leu Tyr
                85                  90                  95

Lys Phe Gln Gln Ser Asp Asp Leu Lys Lys Arg Arg Glu Pro His Ile
            100                 105                 110

Ser Thr Leu Arg Lys Ile Leu Phe Glu Asp Phe Arg Ser Trp Leu Ser
        115                 120                 125

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

Lys Tyr Glu Phe Thr Asp Ala Leu Leu Cys His Asp Asp Glu Leu Glu
145                 150                 155                 160

Gly Arg Arg Ile Ala Phe Ile Leu Tyr Leu Val Pro Pro Trp Asp Arg
                165                 170                 175

Ser Met Gly Gly Thr Leu Asp Leu Tyr Ser Ile Asp Glu His Phe Gln
            180                 185                 190

Pro Lys Gln Ile Val Lys Ser Leu Ile Pro Ser Trp Asn Lys Leu Val
        195                 200                 205

Phe Phe Glu Val Ser Pro Val Ser Phe His Gln Val Ser Glu Val Leu
    210                 215                 220

Ser Glu Glu Lys Ser Arg Leu Ser Ile Ser Gly Trp Phe His Gly Pro
225                 230                 235                 240

Ser Leu Thr Arg Pro Pro Asn Tyr Phe Glu Pro Pro Ile Pro Arg Ser
```

```
                245                 250                 255

Pro His Ile Pro Gln Asp His Glu Ile Leu Tyr Asp Trp Ile Asn Pro
            260                 265                 270

Thr Tyr Leu Asp Met Asp Tyr Gln Val Gln Ile Gln Glu Glu Phe Glu
        275                 280                 285

Glu Ser Ser Glu Ile Leu Leu Lys Glu Phe Leu Lys Pro Glu Lys Phe
    290                 295                 300

Thr Lys Val Cys Glu Ala Leu Glu His Gly His Val Glu Trp Ser Ser
305                 310                 315                 320

Arg Gly Pro Pro Asn Lys Arg Phe Tyr Glu Lys Ala Glu Glu Ser Lys
                325                 330                 335

Leu Pro Glu Ile Leu Lys Glu Cys Met Lys Leu Phe Arg Ser Glu Ala
            340                 345                 350

Leu Phe Leu Leu Leu Ser Asn Phe Thr Gly Leu Lys Leu His Phe Leu
        355                 360                 365

Ala Pro Ser Glu Glu Asp Glu Met Asn Asp Lys Lys Glu Ala Glu Thr
    370                 375                 380

Thr Asp Ile Thr Glu Glu Gly Thr Ser His Ser Pro Pro Glu Pro Glu
385                 390                 395                 400

Asn Asn Gln Met Ala Ile Ser Asn Asn Ser Gln Gln Ser Asn Glu Gln
                405                 410                 415

Thr Asp Pro Glu Pro Glu Glu Asn Glu Thr Lys Lys Glu Ser Ser Val
            420                 425                 430

Pro Met Cys Gln Gly Glu Leu Arg His Trp Lys Thr Gly His Tyr Thr
        435                 440                 445

Leu Ile His Asp His Ser Lys Ala Glu Phe Ala Leu Asp Leu Ile Leu
    450                 455                 460

Tyr Cys Gly Cys Glu Gly Trp Glu Pro Glu Tyr Gly Gly Phe Thr Ser
465                 470                 475                 480
```

```
Tyr Ile Ala Lys Gly Glu Asp Glu Glu Leu Leu Thr Val Asn Pro Glu
                485                 490                 495

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

Val Lys His Ile Asn His Arg Ser Leu Glu Gln Lys Lys Thr Phe Pro
        515                 520                 525

Asn Arg Thr Gly Phe Trp Asp Phe Ser Phe Ile Tyr Tyr Glu
    530                 535                 540


<210> 168
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 21; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD1; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457553"

<400> 168
Met Asp Met Asp Pro Phe Leu His Cys Val Ile Pro Asn Phe Ile Gln
1               5                   10                  15

Ser Gln Asp Phe Leu Glu Gly Leu Gln Lys Glu Leu Met Asn Leu Asp
            20                  25                  30

Phe His Glu Lys Tyr Asn Asp Leu Tyr Lys Phe Gln Gln Ser Asp Asp
        35                  40                  45

Leu Lys Lys Arg Arg Glu Pro His Ile Ser Thr Leu Arg Lys Ile Leu
    50                  55                  60
```

```
Phe Glu Asp Phe Arg Ser Trp Leu Ser Asp Ile Ser Lys Ile Asp Leu
65                  70                  75                  80

Glu Ser Thr Ile Asp Met Ser Cys Ala Lys Tyr Glu Phe Thr Asp Ala
                85                  90                  95

Leu Leu Cys His Asp Asp Glu Leu Glu Gly Arg Arg Ile Ala Phe Ile
            100                 105                 110

Leu Tyr Leu Val Pro Pro Trp Asp Arg Ser Met Gly Gly Thr Leu Asp
        115                 120                 125

Leu Tyr Ser Ile Asp Glu His Phe Gln Pro Lys Gln Ile Val Lys Ser
    130                 135                 140

Leu Ile Pro Ser Trp Asn Lys Leu Val Phe Phe Glu Val Ser Pro Val
145                 150                 155                 160

Ser Phe His Gln Val Ser Glu Val Leu Ser Glu Glu Lys Ser Arg
                165                 170                 175


<210> 169
<211> 499
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 21; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD1; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457746"

<400> 169
Met Asn Gly Lys Arg Pro Ala Glu Pro Gly Pro Ala Arg Val Gly Lys
1               5                   10                  15
```

```
Lys Gly Lys Lys Glu Val Met Ala Glu Phe Ser Asp Ala Val Thr Glu
            20                  25                  30

Glu Thr Leu Lys Lys Gln Val Ala Glu Ala Trp Ser Arg Arg Thr Pro
        35                  40                  45

Phe Ser His Glu Val Ile Val Met Asp Met Asp Pro Phe Leu His Cys
    50                  55                  60

Val Ile Pro Asn Phe Ile Gln Ser Gln Asp Phe Leu Glu Gly Leu Gln
65                  70                  75                  80

Lys Glu Leu Met Asn Leu Asp Phe His Glu Lys Tyr Asn Asp Leu Tyr
                85                  90                  95

Lys Phe Gln Gln Ser Asp Asp Leu Lys Lys Arg Arg Glu Pro His Ile
            100                 105                 110

Ser Thr Leu Arg Lys Ile Leu Phe Glu Asp Phe Arg Ser Trp Leu Ser
        115                 120                 125

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

Lys Tyr Glu Phe Thr Asp Ala Leu Leu Cys His Asp Asp Glu Leu Glu
145                 150                 155                 160

Gly Arg Arg Ile Ala Phe Ile Leu Tyr Leu Val Pro Pro Trp Asp Arg
                165                 170                 175

Ser Met Gly Gly Thr Leu Asp Leu Tyr Ser Ile Asp Glu His Phe Gln
            180                 185                 190

Pro Lys Gln Ile Val Lys Ser Leu Ile Pro Ser Trp Asn Lys Leu Val
        195                 200                 205

Phe Phe Glu Val Ser Pro Val Ser Phe His Gln His Glu Ile Leu Tyr
    210                 215                 220

Asp Trp Ile Asn Pro Thr Tyr Leu Asp Met Asp Tyr Gln Val Gln Ile
225                 230                 235                 240

Gln Glu Glu Phe Glu Glu Ser Ser Glu Ile Leu Leu Lys Glu Phe Leu
```

```
                245                 250                 255

Lys Pro Glu Lys Phe Thr Lys Val Cys Glu Ala Leu Glu His Gly His
            260                 265                 270

Val Glu Trp Ser Ser Arg Gly Pro Pro Asn Lys Arg Phe Tyr Glu Lys
        275                 280                 285

Ala Glu Glu Ser Lys Leu Pro Glu Ile Leu Lys Glu Cys Met Lys Leu
    290                 295                 300

Phe Arg Ser Glu Ala Leu Phe Leu Leu Leu Ser Asn Phe Thr Gly Leu
305                 310                 315                 320

Lys Leu His Phe Leu Ala Pro Ser Glu Glu Asp Glu Met Asn Asp Lys
                325                 330                 335

Lys Glu Ala Glu Thr Thr Asp Ile Thr Glu Glu Gly Thr Ser His Ser
            340                 345                 350

Pro Pro Glu Pro Glu Asn Asn Gln Met Ala Ile Ser Asn Asn Ser Gln
        355                 360                 365

Gln Ser Asn Glu Gln Thr Asp Pro Glu Pro Glu Glu Asn Glu Thr Lys
    370                 375                 380

Lys Glu Ser Ser Val Pro Met Cys Gln Gly Glu Leu Arg His Trp Lys
385                 390                 395                 400

Thr Gly His Tyr Thr Leu Ile His Asp His Ser Lys Ala Glu Phe Ala
                405                 410                 415

Leu Asp Leu Ile Leu Tyr Cys Gly Cys Glu Gly Trp Glu Pro Glu Tyr
            420                 425                 430

Gly Gly Phe Thr Ser Tyr Ile Ala Lys Gly Glu Asp Glu Glu Leu Leu
        435                 440                 445

Thr Val Asn Pro Glu Ser Asn Ser Leu Ala Leu Val Tyr Arg Asp Arg
    450                 455                 460

Glu Thr Leu Lys Phe Val Lys His Ile Asn His Arg Ser Leu Glu Gln
465                 470                 475                 480
```

Lys Lys Thr Phe Pro Asn Arg Thr Gly Phe Trp Asp Phe Ser Phe Ile
485 490 495

Tyr Tyr Glu

<210> 170
<211> 350
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000228922"

<400> 170
Met Ala Thr Val Gly Ala Pro Arg His Phe Cys Arg Cys Ala Cys Phe
1 5 10 15

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

Arg Gly Glu Gln Gln Leu Arg Arg Asp Tyr Gly Pro Ile Leu Arg Ser
35 40 45

Arg Gly Cys Val Ser Ala Lys Asp Phe Gln Gln Leu Leu Ala Glu Leu
50 55 60

Glu Gln Glu Val Glu Arg Arg Gln Arg Leu Gly Gln Glu Ser Ala Ala
65 70 75 80

```
Arg Lys Ala Leu Ile Ala Ser Ser Tyr His Pro Ala Arg Pro Glu Val
                85                  90                  95

Tyr Asp Ser Leu Gln Asp Ala Ala Leu Ala Pro Glu Phe Leu Ala Val
            100                 105                 110

Thr Glu Tyr Ser Val Ser Pro Asp Ala Asp Leu Lys Gly Leu Leu Gln
        115                 120                 125

Arg Leu Glu Thr Val Ser Glu Glu Lys Arg Ile Tyr Arg Val Pro Val
    130                 135                 140

Phe Thr Ala Pro Phe Cys Gln Ala Leu Leu Glu Glu Leu Glu His Phe
145                 150                 155                 160

Glu Gln Ser Asp Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr
                165                 170                 175

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

Leu Arg Glu Arg Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp
        195                 200                 205

Cys Gly Gly Gly Arg Leu Asp Ser His Arg Ala Phe Val Val Lys Tyr
    210                 215                 220

Ala Pro Gly Gln Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu
225                 230                 235                 240

Leu Thr Leu Asn Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu
                245                 250                 255

Tyr Phe Gly Gly Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu
            260                 265                 270

Glu Val Glu His Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln
        275                 280                 285

Leu His Gly Ala Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val
    290                 295                 300
```

```
Val Trp Leu Arg Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys
305                 310                 315                 320


Cys Arg Glu Pro Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe
                325                 330                 335


Thr Arg Glu Glu Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            340                 345                 350


<210> 171
<211> 290
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase domain
      containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000380544"

<400> 171
Met Val Glu Leu Glu Gln Glu Val Glu Arg Arg Gln Arg Leu Gly Gln
1               5                   10                  15


Glu Ser Ala Ala Arg Lys Ala Leu Ile Ala Ser Ser Tyr His Pro Ala
            20                  25                  30


Arg Pro Glu Val Tyr Asp Ser Leu Gln Asp Ala Ala Leu Ala Pro Glu
        35                  40                  45


Phe Leu Ala Val Thr Glu Tyr Ser Val Ser Pro Asp Ala Asp Leu Lys
    50                  55                  60


Gly Leu Leu Gln Arg Leu Glu Thr Val Ser Glu Glu Lys Arg Ile Tyr
```

65 70 75 80

Arg Val Pro Val Phe Thr Ala Pro Phe Cys Gln Ala Leu Leu Glu Glu
85 90 95

Leu Glu His Phe Glu Gln Ser Asp Met Pro Lys Gly Arg Pro Asn Thr
100 105 110

Met Asn Asn Tyr Gly Val Leu Leu His Glu Leu Gly Leu Asp Glu Pro
115 120 125

Leu Met Thr Pro Leu Arg Glu Arg Phe Leu Gln Pro Leu Met Ala Leu
130 135 140

Leu Tyr Pro Asp Cys Gly Gly Gly Arg Leu Asp Ser His Arg Ala Phe
145 150 155 160

Val Val Lys Tyr Ala Pro Gly Gln Asp Leu Glu Leu Gly Cys His Tyr
165 170 175

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

Gly Gly Ala Leu Tyr Phe Gly Gly Leu Phe Gln Ala Pro Thr Ala Leu
195 200 205

Thr Glu Pro Leu Glu Val Glu His Val Val Gly Gln Gly Val Leu His
210 215 220

Arg Gly Gly Gln Leu His Gly Ala Arg Pro Leu Gly Thr Gly Glu Arg
225 230 235 240

Trp Asn Leu Val Val Trp Leu Arg Ala Ser Ala Val Arg Asn Ser Leu
245 250 255

Cys Pro Met Cys Cys Arg Glu Pro Asp Leu Val Asp Asp Glu Gly Phe
260 265 270

Gly Asp Gly Phe Thr Arg Glu Glu Pro Ala Thr Val Asp Val Cys Ala
275 280 285

Leu Thr
290

<210> 172
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
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<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394175"

<400> 172
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1   5   10   15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20   25   30

Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35   40   45

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

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65   70   75   80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85   90   95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
            100   105   110

```
Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160

Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe Thr Arg Glu Glu
                165                 170                 175

Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            180                 185


<210> 173
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
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<220>
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<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase domain
      containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438003"

<400> 173
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1               5                   10                  15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20                  25                  30

Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35                  40                  45
```

```
Arg Leu Asp Ser His Arg Ala Phe Val Val Lys Tyr Ala Pro Gly Gln
    50                  55                  60

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65                  70                  75                  80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85                  90                  95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
            100                 105                 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160
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<210> 174
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
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<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
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<223> /note="Uniprot ID: Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438192"

<400> 174
```
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
```

```
1               5                   10                  15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20                  25                  30

Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35                  40                  45

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

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65                  70                  75                  80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85                  90                  95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
            100                 105                 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160

Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe Thr Arg Glu Glu
                165                 170                 175

Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            180                 185


<210> 175
<211> 186
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 22; "

<220>
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<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
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<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438327"

<400> 175

```
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1               5                   10                  15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20                  25                  30

Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35                  40                  45

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

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65                  70                  75                  80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85                  90                  95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
            100                 105                 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160
```

```
Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe Thr Arg Glu Glu
                165                 170                 175


Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            180                 185


<210> 176
<211> 129
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase domain
      containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439667"

<400> 176
Met Ala Thr Val Gly Ala Pro Arg His Phe Cys Arg Cys Ala Cys Phe
1               5                   10                  15


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


Arg Gly Glu Gln Gln Leu Arg Arg Asp Tyr Gly Pro Ile Leu Arg Ser
        35                  40                  45


Arg Gly Cys Val Ser Ala Lys Asp Phe Gln Gln Leu Leu Ala Glu Trp
    50                  55                  60


Pro Gln Glu Asp Gly Arg Pro His Leu Val Thr Thr Leu Cys His Pro
65                  70                  75                  80
```

```
Ser Leu Ser Arg Arg Trp Ser Gly Gly Ser Gly Trp Gly Arg Ser Gln
                85                  90                  95

Gln Leu Gly Lys Pro Ser Ser Arg Val Pro Thr Thr Arg His Gly Leu
            100                 105                 110

Arg Ser Thr Thr His Cys Arg Met Gln Leu Trp Pro Pro Ser Ser Trp
        115                 120                 125

Pro
```

<210> 177
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442083"

<400> 177

```
Met Ala Thr Val Gly Ala Pro Arg His Phe Cys Arg Cys Ala Cys Phe
1               5                  10                  15

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

Arg Gly Glu Gln Gln Leu Arg Arg Asp Tyr Gly Pro Ile Leu Arg Ser
        35                  40                  45

Arg Gly Cys Val Ser Ala Lys Asp Phe Gln Gln Leu Leu Ala Glu Ala
    50                  55                  60

Ala Ala Arg Ala Ala Ala Pro Leu Pro Pro Pro Pro Ser Pro Gly Val
```

65 70 75 80

Ser Gly Gly Lys Leu Pro Arg Arg Val Leu Ser Asn Leu Trp Asn Thr
85 90 95

Gly Leu Gly His Asp Cys Leu Leu Ser Leu Cys Gly Pro Arg Trp Leu
100 105 110

Ser Phe Phe Ile Cys Thr Val Ala Ser Gly Gly Trp Glu Ala Pro Pro
115 120 125

Gly Asn Asn Pro Val Pro Pro Gln Leu Glu Gln Glu Val Glu Arg Arg
130 135 140

Gln Arg Leu Gly Gln Glu Ser Ala Ala Arg Lys Ala Leu Ile Ala Ser
145 150 155 160

Ser Tyr His Pro Ala Arg Pro Glu Val Tyr Asp Ser Leu Gln Asp Ala
165 170 175

Ala Leu Ala Pro Glu Phe Leu Ala Val Thr Glu Tyr Ser Val Ser Pro
180 185 190

Asp Ala Asp Leu Lys Gly Leu Leu Gln Arg Leu Glu Thr Val Ser
195 200 205

<210> 178
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442476"

<400> 178
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1 5 10 15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
20 25 30

Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
35 40 45

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

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65 70 75 80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
85 90 95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
100 105 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
115 120 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
130 135 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145 150 155 160

<210> 179
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source

<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase domain
containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442817"

<400> 179

```
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1               5                  10                  15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20                  25                  30

Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35                  40                  45

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

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65                  70                  75                  80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85                  90                  95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
            100                 105                 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160

Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe Thr Arg Glu Glu
                165                 170                 175
```

```
Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            180                 185


<210> 180
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase domain
      containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000444436"

<400> 180
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1               5                  10                  15


His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20                  25                  30


Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35                  40                  45


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


Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65                  70                  75                  80


Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85                  90                  95


Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
```

```
            100                 105                 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160

Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe Thr Arg Glu Glu
                165                 170                 175

Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            180                 185


<210> 181
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 22; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD2; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase domain
      containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6N063; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000444608"

<400> 181
Met Pro Lys Gly Arg Pro Asn Thr Met Asn Asn Tyr Gly Val Leu Leu
1               5                   10                  15

His Glu Leu Gly Leu Asp Glu Pro Leu Met Thr Pro Leu Arg Glu Arg
            20                  25                  30
```

```
Phe Leu Gln Pro Leu Met Ala Leu Leu Tyr Pro Asp Cys Gly Gly Gly
        35                  40                  45

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

Asp Leu Glu Leu Gly Cys His Tyr Asp Asn Ala Glu Leu Thr Leu Asn
65                  70                  75                  80

Val Ala Leu Gly Lys Val Phe Thr Gly Gly Ala Leu Tyr Phe Gly Gly
                85                  90                  95

Leu Phe Gln Ala Pro Thr Ala Leu Thr Glu Pro Leu Glu Val Glu His
            100                 105                 110

Val Val Gly Gln Gly Val Leu His Arg Gly Gly Gln Leu His Gly Ala
        115                 120                 125

Arg Pro Leu Gly Thr Gly Glu Arg Trp Asn Leu Val Val Trp Leu Arg
    130                 135                 140

Ala Ser Ala Val Arg Asn Ser Leu Cys Pro Met Cys Cys Arg Glu Pro
145                 150                 155                 160

Asp Leu Val Asp Asp Glu Gly Phe Gly Asp Gly Phe Thr Arg Glu Glu
                165                 170                 175

Pro Ala Thr Val Asp Val Cys Ala Leu Thr
            180                 185


<210> 182
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 23; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
<221> source
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<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase
domain containing 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q6PK18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000320116"

<400> 182

```
Met Ala Pro Gln Arg Arg Ala Ala Thr Lys Ala Pro Glu Gly Asn Gly
1               5                  10                  15

Ala Ala Glu Arg Arg Asn Arg Ser Ser Thr Lys Lys Asp Arg Ala Pro
            20                  25                  30

Arg Glu Val Gln Arg Leu Trp Gln Arg Pro Trp Leu Arg Thr Ala Gly
        35                  40                  45

Leu Gly Ala Gly Phe Val Leu Thr Ala Leu Leu Leu Trp Ser Ser Leu
    50                  55                  60

Gly Ala Asp Asp Gly Val Ala Glu Val Leu Ala Arg Arg Gly Glu Val
65                  70                  75                  80

Val Ala Gly Arg Phe Ile Glu Val Pro Cys Ser Glu Asp Tyr Asp Ser
                85                  90                  95

His Arg Arg Phe Glu Gly Cys Thr Pro Arg Lys Cys Gly Arg Gly Val
            100                 105                 110

Thr Asp Val Val Ile Thr Arg Glu Glu Ala Glu Arg Ile Arg Ser Val
        115                 120                 125

Ala Glu Lys Gly Leu Ser Leu Gly Gly Ser Asp Gly Gly Ala Ser Ile
    130                 135                 140

Leu Asp Leu His Ser Gly Ala Leu Ser Val Gly Lys His Phe Val Asn
145                 150                 155                 160

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

```
Asp Phe Arg Leu Tyr Arg Glu Val Arg Gln Lys Val Gln Leu Thr Ile
            180                 185                 190

Ala Glu Ala Phe Gly Ile Ser Ala Ser Ser Leu His Leu Thr Lys Pro
        195                 200                 205

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

Glu Tyr Trp His Ala His Val Asp Lys Val Thr Tyr Gly Ser Phe Asp
225                 230                 235                 240

Tyr Thr Ser Leu Leu Tyr Leu Ser Asn Tyr Leu Glu Asp Phe Gly Gly
                245                 250                 255

Gly Arg Phe Met Phe Met Glu Glu Gly Ala Asn Lys Thr Val Glu Pro
            260                 265                 270

Arg Ala Gly Arg Val Ser Phe Phe Thr Ser Gly Ser Glu Asn Leu His
        275                 280                 285

Arg Val Glu Lys Val His Trp Gly Thr Arg Tyr Ala Ile Thr Ile Ala
    290                 295                 300

Phe Ser Cys Asn Pro Asp His Gly Ile Glu Asp Pro Ala Phe Pro
305                 310                 315


<210> 183
<211> 331
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 23; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 3; "

<220>
<221> source
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<223> /note="Uniprot ID: Q6PK18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000330075"

<400> 183
Met Ala Pro Gln Arg Arg Ala Ala Thr Lys Ala Pro Glu Gly Asn Gly
1   5   10   15

Ala Ala Glu Arg Arg Asn Arg Ser Ser Thr Lys Lys Asp Arg Ala Pro
            20   25   30

Arg Glu Val Gln Arg Leu Trp Gln Arg Pro Trp Leu Arg Thr Ala Gly
        35   40   45

Leu Gly Ala Gly Phe Val Leu Thr Ala Leu Leu Leu Trp Ser Ser Leu
    50   55   60

Gly Ala Asp Asp Gly Val Ala Glu Val Leu Ala Arg Arg Gly Glu Val
65   70   75   80

Val Ala Gly Arg Phe Ile Glu Val Pro Cys Ser Glu Asp Tyr Asp Ser
                85   90   95

His Arg Arg Phe Glu Gly Cys Thr Pro Arg Lys Cys Gly Arg Gly Val
            100   105   110

Thr Asp Val Val Ile Thr Arg Glu Glu Ala Glu Arg Ile Arg Ser Val
        115   120   125

Ala Glu Lys Gly Leu Ser Leu Gly Gly Ser Asp Gly Gly Ala Ser Ile
    130   135   140

Leu Asp Leu His Ser Gly Ala Leu Ser Val Gly Lys His Phe Val Asn
145   150   155   160

Leu Tyr Arg Tyr Phe Gly Asp Lys Ile Gln Asn Ile Phe Ser Glu Glu
                165   170   175

Asp Phe Arg Leu Tyr Arg Glu Val Arg Gln Lys Val Gln Leu Thr Ile
            180   185   190

Ala Glu Ala Phe Gly Ile Ser Ala Ser Ser Leu His Leu Thr Lys Pro
        195   200   205

```
Thr Phe Phe Ser Arg Ile Asn Ser Thr Glu Ala Arg Thr Ala His Asp
    210                 215                 220

Glu Tyr Trp His Ala His Val Asp Lys Val Thr Tyr Gly Ser Phe Asp
225                 230                 235                 240

Tyr Thr Ser Leu Leu Tyr Leu Ser Asn Tyr Leu Glu Asp Phe Gly Gly
                245                 250                 255

Gly Arg Phe Met Phe Met Glu Glu Gly Ala Asn Lys Thr Val Glu Pro
            260                 265                 270

Arg Ala Gly Cys Phe Cys Phe Arg Met Met Ser Cys Gly Phe Gln Glu
        275                 280                 285

Val Asn Gly Pro Arg Ala Ser Glu Ala Ala Gly Ala Lys Ala Gly Val
    290                 295                 300

Arg Cys Pro Pro Gly Thr His His Pro Pro Glu Arg Gly Glu Thr His
305                 310                 315                 320

Ala Ile Leu Glu Ala Glu Ser Ile Ala Tyr Cys
                325                 330


<210> 184
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 23; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463566"
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<400> 184
Met Ala Pro Gln Arg Arg Ala Ala Thr Lys Ala Pro Glu Gly Asn Gly
1   5   10   15

Ala Ala Glu Arg Arg Asn Arg Ser Ser Thr Lys Lys Asp Arg Ala Pro
            20   25   30

Arg Glu Val Gln Arg Leu Trp Gln Arg Pro Trp Leu Arg Thr Ala Gly
        35   40   45

Leu Gly Ala Gly Phe Val Leu Thr Ala Leu Leu Leu Trp Ser Ser Leu
    50   55   60

Gly Ala Asp Asp Gly Val Ala Glu Val Leu Ala Arg Arg Gly Glu Val
65   70   75   80

Val Ala Gly Arg Phe Ile Glu Val Pro Cys Ser Glu Asp Tyr Asp Ser
                85   90   95

His Arg Arg Leu His Ser Pro Lys Val Arg Gln Arg Cys His Arg Cys
            100   105   110

Arg His His Gln Gly Gly Ser Gly Ala Asp Ser Gln Arg Ser
        115   120   125

<210> 185
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 23; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000464195"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 185
Xaa Ser Leu Gly Ala Asp Asp Gly Val Ala Glu Val Leu Ala Arg Arg
1 5 10 15

Gly Glu Val Val Ala Gly Arg Phe Ile Glu Val Pro Cys Ser Glu Asp
20 25 30

Tyr Asp Ser His Arg Arg Leu His Ser Pro Lys Val Arg Gln Arg Cys
35 40 45

His Arg Cys Arg His His Gln Gly Gly Ser Gly Ala Asp Ser Gln Ala
50 55 60

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

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

Glu Glu Asp Phe Arg Leu Tyr Arg Glu Val Arg Gln Lys Val Gln Leu
100 105 110

Thr Ile Ala Glu Ala Phe Gly Ile Ser Ala Ser Ser Leu His Leu Thr
115 120 125

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

His Asp Glu Tyr Trp His Ala His Val Asp Lys Val Thr Tyr Gly Ser
145 150 155 160

Phe Asp Tyr Thr Ser Leu Leu Tyr Leu Ser Asn Tyr Leu Glu Asp Phe
165 170 175

Gly Gly Gly Arg Phe Met Phe Met Glu Glu Gly Ala Asn Lys Thr Val
180 185 190

Glu Pro Arg Ala Gly Arg Val Ser Phe Phe Thr Ser Gly Ser Glu Asn
195 200 205

```
Leu His Arg Val Glu Lys Val His Trp Gly Thr Arg Tyr Ala Ile Thr
    210                 215                 220

Ile Ala Phe Ser Cys Asn Pro Asp His Gly Ile Glu Asp Pro Ala Phe
225                 230                 235                 240

Pro
```

<210> 186
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 23; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
<221> source
<223> /note="Gene Name:
2-oxoglutarate and iron-dependent oxygenase
domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466117"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 186

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Xaa Asp Glu Tyr Trp His Ala His Val Asp Lys Val Thr Tyr Gly Ser
1               5                   10                  15

Phe Asp Tyr Thr Ser Leu Leu Tyr Leu Ser Asn Tyr Leu Glu Asp Phe
            20                  25                  30

Gly Gly Gly Arg Phe Met Phe Met Glu Glu Gly Ala Asn Lys Thr Val
        35                  40                  45

Glu Pro Arg Ala Gly Glu Gly Phe Gly Arg Pro Ala Ser Ala Ser Arg
    50                  55                  60
```

```
Ser Pro Ala Cys Leu Pro Ser Pro Gln Lys Ser Gln Ser Gln Gln Phe
65                  70                  75                  80


Cys Gly Lys Met Lys Asn Ser Gln Ser Thr Arg Gln Ala Phe Ser
                85                  90                  95


<210> 187
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 23; "

<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
<221> source
<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466184"

<400> 187
Met Phe Met Glu Glu Gly Ala Asn Lys Thr Val Glu Pro Arg Ala
1               5                   10                  15


<210> 188
<211> 219
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: OGFOD3; "

<220>
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<223> /note="Gene Name:
      2-oxoglutarate and iron-dependent oxygenase
      domain containing 3; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000467074"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 188
Xaa Val Asn Leu Tyr Arg Tyr Phe Gly Asp Lys Ile Gln Asn Ile Phe
1 5 10 15

Ser Glu Glu Asp Phe Arg Leu Tyr Arg Glu Val Arg Gln Lys Val Gln
20 25 30

Leu Thr Ile Ala Glu Ala Phe Gly Ile Ser Ala Ser Ser Leu His Leu
35 40 45

Thr Lys Pro Thr Phe Phe Ser Arg Ile Asn Ser Thr Glu Ala Arg Thr
50 55 60

Ala His Asp Glu Tyr Trp His Ala His Val Asp Lys Val Thr Tyr Gly
65 70 75 80

Ser Phe Asp Tyr Thr Ser Leu Leu Tyr Leu Ser Asn Tyr Leu Glu Asp
85 90 95

Phe Gly Gly Gly Arg Phe Met Phe Met Glu Glu Gly Ala Asn Lys Thr
100 105 110

Val Glu Pro Arg Ala Val Val Leu Ser His Leu Cys Ile Arg Gly Arg
115 120 125

Val Trp Thr Ser Ser Leu Cys Lys Gln Glu Pro Ser Leu Ser Ala Leu
130 135 140

Thr Pro Glu Val Pro Val Thr Ala Val Leu Trp Glu Asn Glu Lys Leu
145 150 155 160

Thr Glu His Lys Thr Gly Val Phe Leu Arg Ser Gln Ala Ala Glu Ala
165 170 175

Ser Trp Asp Ser Lys Leu His Asn Phe Leu Ala Tyr Phe Asp Leu Ser
180 185 190

```
His Phe Lys His Asp Lys Tyr Leu Ser Gln Thr Phe Cys Ile Thr Ile
        195                 200                 205


Phe Phe Gln Ile Ile Lys Thr Thr Cys Leu Leu
    210                 215


<210> 189
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
      2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TE99; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000286353"

<400> 189
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala Leu
1               5                   10                  15


Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile Pro Val
            20                  25                  30


Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met
        35                  40                  45


Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala
    50                  55                  60


Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly
65                  70                  75                  80
```

```
His Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile Arg
                85                  90                  95

His Gly Asp Arg Tyr Pro Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro
            100                 105                 110

Glu Ile Asp Cys Thr Leu Val Ala Asn Arg Lys Pro Tyr His Pro Lys
        115                 120                 125

Leu Glu Ala Phe Ile Ser His Met Ser Lys Gly Ser Gly Ala Ser Phe
    130                 135                 140

Glu Ser Pro Leu Asn Ser Leu Pro Leu Tyr Pro Asn His Pro Leu Cys
145                 150                 155                 160

Glu Met Gly Glu Leu Thr Gln Thr Gly Val Val Gln His Leu Gln Asn
                165                 170                 175

Gly Gln Leu Leu Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro
            180                 185                 190

Asn Asp Trp Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser
        195                 200                 205

Arg Thr Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp
    210                 215                 220

Phe Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
225                 230                 235                 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu Lys
                245                 250                 255

Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln Leu Glu
            260                 265                 270

Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro Thr Lys Gln
        275                 280                 285

Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys His Phe Cys His
    290                 295                 300

Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys Val Asp Met Glu His
```

```
305                 310                 315                 320

Phe Lys Val Ile Lys Thr His Gln Ile Glu Asp Glu Arg Glu Arg Arg
                325                 330                 335

Glu Lys Lys Leu Tyr Phe Gly Tyr Ser Leu Leu Gly Ala His Pro Ile
            340                 345                 350

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

Glu Glu Leu Phe Ala Leu Tyr Ser Ala His Asp Val Thr Leu Ser Pro
    370                 375                 380

Val Leu Ser Ala Leu Gly Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala
385                 390                 395                 400

Ala Arg Leu Ile Phe Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu
                405                 410                 415

His Ser Val Arg Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr
            420                 425                 430

Ser Phe Cys Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro
        435                 440                 445

Leu Glu Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu
    450                 455                 460

Gly Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe
465                 470                 475                 480


<210> 190
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
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<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TE99; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376733"

<400> 190

```
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Ala Leu Ala Ala Leu
1               5                  10                  15

Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile Pro Val
            20                  25                  30

Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met
        35                  40                  45

Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala
    50                  55                  60

Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly
65                  70                  75                  80

His Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile Arg
                85                  90                  95

His Gly Asp Arg Tyr Pro Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro
            100                 105                 110

Glu Ile Asp Cys Thr Leu Val Ala Asn Arg Lys Pro Tyr His Pro Lys
        115                 120                 125

Leu Glu Ala Phe Ile Ser His Met Ser Lys Gly Ser Gly Ala Ser Phe
    130                 135                 140

Glu Ser Pro Leu Asn Ser Leu Pro Leu Tyr Pro Asn His Pro Leu Cys
145                 150                 155                 160

Glu Met Gly Glu Leu Thr Gln Thr Gly Val Val Gln His Leu Gln Asn
                165                 170                 175
```

```
Gly Gln Leu Leu Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro
            180                 185                 190

Asn Asp Trp Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser
        195                 200                 205

Arg Thr Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp
    210                 215                 220

Phe Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
225                 230                 235                 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu Lys
                245                 250                 255

Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln Leu Glu
            260                 265                 270

Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro Thr Lys Gln
        275                 280                 285

Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys His Phe Cys His
    290                 295                 300

Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys Val Asp Met Glu His
305                 310                 315                 320

Phe Lys Val Ile Lys Thr His Gln Ile Glu Asp Glu Arg Glu Arg Arg
                325                 330                 335

Glu Lys Lys Leu Tyr Phe Gly Tyr Ser Leu Leu Gly Ala His Pro Ile
            340                 345                 350

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

Glu Glu Leu Phe Ala Leu Tyr Ser Ala His Asp Val Thr Leu Ser Pro
    370                 375                 380

Val Leu Ser Ala Leu Gly Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala
385                 390                 395                 400

Ala Arg Leu Ile Phe Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu
```

405 410 415

His Ser Val Arg Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr
420 425 430

Ser Phe Cys Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro
435 440 445

Leu Glu Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu
450 455 460

Gly Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe
465 470 475 480

<210> 191
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421271"

<400> 191
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile Pro Val
20 25 30

Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met
35 40 45

Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala
50 55 60

```
Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly
65                  70                  75                  80

His Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile Arg
                85                  90                  95

His Gly Asp Arg Tyr Pro Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro
            100                 105                 110

Glu Ile Asp Cys Thr Leu Val Ala Asn Arg Lys Pro Tyr His Pro Lys
        115                 120                 125

Leu Glu Ala Phe Ile Ser His Met Ser Lys Gly Ser Gly Ala Ser Phe
    130                 135                 140

Glu
145
```

<210> 192
<211> 442
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422558"

<400> 192

```
Met Ser Ser Lys Ser Arg Lys Arg Ile Met Pro Asp Pro Val Thr Glu
1               5                   10                  15

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

Pro Ser Val Ala Glu Arg Ser Met Glu Gly His Ala Pro His His Phe
```

```
        35                  40                  45

Lys Leu Val Ser Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro
    50                  55                  60

Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu
65                  70                  75                  80

Val Ala Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser
                85                  90                  95

His Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
            100                 105                 110

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu Thr
        115                 120                 125

Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu Arg Asp
    130                 135                 140

Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp Ser Ala Asp
145                 150                 155                 160

Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr Leu Gln Ser Gly
                165                 170                 175

Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe Asp Trp Lys Lys Ile
            180                 185                 190

Tyr Phe Arg His Gln Pro Ser Ala Leu Phe Cys Ser Gly Ser Cys Tyr
        195                 200                 205

Cys Pro Val Arg Asn Gln Tyr Leu Glu Lys Glu Gln Arg Arg Gln Tyr
    210                 215                 220

Leu Leu Arg Leu Lys Asn Ser Gln Leu Glu Lys Thr Tyr Gly Glu Met
225                 230                 235                 240

Ala Lys Ile Val Asp Val Pro Thr Lys Gln Leu Arg Ala Ala Asn Pro
                245                 250                 255

Ile Asp Ser Met Leu Cys His Phe Cys His Asn Val Ser Phe Pro Cys
            260                 265                 270
```

```
Thr Arg Asn Gly Cys Val Asp Met Glu His Phe Lys Val Ile Lys Thr
        275                 280                 285

His Gln Ile Glu Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe
    290                 295                 300

Gly Tyr Ser Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly
305                 310                 315                 320

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

Tyr Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly
            340                 345                 350

Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe Glu
        355                 360                 365

Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg Ile Leu
    370                 375                 380

Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys Gln Asp His
385                 390                 395                 400

His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu Asn Leu Val Arg
                405                 410                 415

Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly Gly Ser Gly Thr Asn
            420                 425                 430

Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe
        435                 440


<210> 193
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
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<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422901"

<400> 193

```
Met Arg Tyr Phe Ile Lys Ser Met Glu His Ser Val Cys Pro Ser Ser
1               5                   10                  15

Ala Val His Leu Ile Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser
            20                  25                  30

Lys Ser Arg Lys Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val
        35                  40                  45

Thr Asp Pro Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val
    50                  55                  60

Ala Glu Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val
65                  70                  75                  80

Ser Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
                85                  90                  95

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala Asn
            100                 105                 110

Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His Met Ser
        115                 120                 125

Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser Leu Pro Leu
    130                 135                 140

Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu Thr Gln Thr Gly
145                 150                 155                 160

Val Val Gln His Leu Gln Asn Gly Gln Leu Leu Arg Asp Ile Tyr Leu
                165                 170                 175

Lys Lys His Lys Leu Leu Pro Asn Asp Trp Ser Ala Asp Gln Leu Tyr
```

```
            180                 185                 190

Leu Glu Thr Thr Gly Lys Ser Arg Thr Leu Gln Ser Gly Leu Ala Leu
        195                 200                 205

Leu Tyr Gly Phe Leu Pro Asp Phe Asp Trp Lys Lys Ile Tyr Phe Arg
    210                 215                 220

His Gln Pro Ser Ala Leu Phe Cys Ser Gly Ser Cys Tyr Cys Pro Val
225                 230                 235                 240

Arg Asn Gln Tyr Leu Glu Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg
                245                 250                 255

Leu Lys Asn Ser Gln Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile
            260                 265                 270

Val Asp Val Pro Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser
        275                 280                 285

Met Leu Cys His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn
    290                 295                 300

Gly Cys Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile
305                 310                 315                 320

Glu Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser
                325                 330                 335

Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met Gln
            340                 345                 350

Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr Ser Ala
        355                 360                 365

His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly Leu Ser Glu
    370                 375                 380

Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe Glu Leu Trp Gln
385                 390                 395                 400

Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg Ile Leu Tyr Asn Gly
                405                 410                 415
```

```
Val Asp Val Thr Phe His Thr Ser Phe Cys Gln Asp His His Lys Arg
            420                 425                 430

Ser Pro Lys Pro Met Cys Pro Leu Glu Asn Leu Val Arg Phe Val Lys
        435                 440                 445

Arg Asp Met Phe Val Ala Leu Gly Gly Ser Gly Thr Asn Tyr Tyr Asp
    450                 455                 460

Ala Cys His Arg Glu Gly Phe
465                 470


<210> 194
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
      2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423702"

<400> 194
Met Ser Ser Lys Ser Arg Lys Arg Ile Met Pro Asp Pro Val Thr Glu
1               5                   10                  15

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

Pro Ser Val Ala Glu Arg Ser Met Glu Gly His Ala Pro His His Phe
        35                  40                  45

Lys Leu Val Ser Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro
    50                  55                  60
```

```
Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu
65                  70                  75                  80


Val Ala Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser
                85                  90                  95


His Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
            100                 105                 110


Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu Thr
        115                 120                 125


Gln Thr
    130


<210> 195
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
      2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425264"

<400> 195
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala Leu
1               5                   10                  15


Leu Ala Phe Val Ser Leu Ser Leu Gln Phe
            20                  25


<210> 196
<211> 26
<212> PRT
<213> Homo sapiens

<220>
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<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426348"

<400> 196
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Ala Phe Val Ser Leu Ser Leu Gln Phe
20 25

<210> 197
<211> 463
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426877"

<400> 197
Met Asp Val Leu Thr Ala Leu Leu Leu Val His Leu Ile Pro Val Ser
1 5 10 15

Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met Pro
20 25 30

Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala Leu

```
        35                  40                  45

Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly His
    50                  55                  60

Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile Arg His
65                  70                  75                  80

Gly Asp Arg Tyr Pro Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro Glu
                85                  90                  95

Ile Asp Cys Thr Leu Val Ala Asn Arg Lys Pro Tyr His Pro Lys Leu
            100                 105                 110

Glu Ala Phe Ile Ser His Met Ser Lys Gly Ser Gly Ala Ser Phe Glu
        115                 120                 125

Ser Pro Leu Asn Ser Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu
    130                 135                 140

Met Gly Glu Leu Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly
145                 150                 155                 160

Gln Leu Leu Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn
                165                 170                 175

Asp Trp Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg
            180                 185                 190

Thr Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe
        195                 200                 205

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe Cys
    210                 215                 220

Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu Lys Glu
225                 230                 235                 240

Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln Leu Glu Lys
                245                 250                 255

Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro Thr Lys Gln Leu
            260                 265                 270
```

```
Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys His Phe Cys His Asn
        275                 280                 285

Val Ser Phe Pro Cys Thr Arg Asn Gly Cys Val Asp Met Glu His Phe
    290                 295                 300

Lys Val Ile Lys Thr His Gln Ile Glu Asp Glu Arg Glu Arg Arg Glu
305                 310                 315                 320

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

Asn Gln Thr Ile Gly Arg Met Gln Arg Ala Thr Glu Gly Arg Lys Glu
            340                 345                 350

Glu Leu Phe Ala Leu Tyr Ser Ala His Asp Val Thr Leu Ser Pro Val
        355                 360                 365

Leu Ser Ala Leu Gly Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala
    370                 375                 380

Arg Leu Ile Phe Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His
385                 390                 395                 400

Ser Val Arg Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser
                405                 410                 415

Phe Cys Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu
            420                 425                 430

Glu Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly
        435                 440                 445

Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe
    450                 455                 460
```

<210> 198
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 24; "

<220>
<221> source
<223> /note="Gene Symbol: PXYLP1; "

<220>
<221> source
<223> /note="Gene Name:
2-phosphoxylose phosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426956"

<400> 198
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile Pro Val
20 25 30

Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met
35 40 45

Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala
50 55 60

Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly
65 70 75 80

His Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile
85 90 95

<210> 199
<211> 308
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 25; "

<220>
<221> source
<223> /note="Gene Symbol: BPNT1; "

<220>
<221> source
<223> /note="Gene Name:
3'(2'), 5'-bisphosphate nucleotidase 1; "

<220>
<221> source
<223> /note="Uniprot ID: O95861; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000318852"

<400> 199
Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1   5   10   15

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
            20   25   30

Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
        35   40   45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
    50   55   60

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

Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
                85   90   95

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

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly
        115   120   125

Leu Leu Asp Asn Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys
    130   135   140

Ala Ile Ala Gly Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly
145   150   155   160

Pro Asp Ala Val Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly
                165   170   175

Ala Phe Gly Phe Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile
            180   185   190

```
Thr Thr Thr Arg Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala
        195                 200                 205

Ala Met Asn Pro Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys
    210                 215                 220

Ile Ile Gln Leu Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser
225                 230                 235                 240

Pro Gly Cys Lys Lys Trp Asp Thr Cys Ala Pro Glu Val Ile Leu His
                245                 250                 255

Ala Val Gly Gly Lys Leu Thr Asp Ile His Gly Asn Val Leu Gln Tyr
            260                 265                 270

His Lys Asp Val Lys His Met Asn Ser Ala Gly Val Leu Ala Thr Leu
        275                 280                 285

Arg Asn Tyr Asp Tyr Tyr Ala Ser Arg Val Pro Glu Ser Ile Lys Asn
    290                 295                 300

Ala Leu Val Pro
305
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<210> 200
<211> 291
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: BPNT1; "

<220>
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<223> /note="Gene Name:
3'(2'), 5'-bisphosphate nucleotidase 1; "

<220>
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<223> /note="ENSP ID: ENSP00000346862"

<400> 200
Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr

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1               5                   10                  15

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
            20                  25                  30

Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
        35                  40                  45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
    50                  55                  60

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

Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
                85                  90                  95

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

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly
        115                 120                 125

Leu Leu Asp Asn Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys
    130                 135                 140

Ala Ile Ala Gly Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Asn Asn
145                 150                 155                 160

Glu Lys Gln Gln Leu Arg Glu His Arg Asn Glu Ala Lys Ala Gly Pro
                165                 170                 175

Asp Ala Val Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly Ala
            180                 185                 190

Phe Gly Phe Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile Thr
        195                 200                 205

Thr Thr Arg Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala Ala
    210                 215                 220

Met Asn Pro Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys Ile
225                 230                 235                 240
```

```
Ile Gln Leu Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser Pro
                245                 250                 255


Gly Cys Lys Lys Trp Asp Thr Cys Ala Pro Glu Val Ile Leu His Ala
            260                 265                 270


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


Lys Asp Val
    290


<210> 201
<211> 272
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O95861; "

<220>
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<400> 201
Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1               5                   10                  15


Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
            20                  25                  30


Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
        35                  40                  45
```

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
50 55 60

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Leu Val Val Trp Val
65 70 75 80

Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly Leu Leu Asp Asn
85 90 95

Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys Ala Ile Ala Gly
100 105 110

Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly Pro Asp Ala Val
115 120 125

Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly Ala Phe Gly Phe
130 135 140

Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile Thr Thr Thr Arg
145 150 155 160

Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala Ala Met Asn Pro
165 170 175

Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys Ile Ile Gln Leu
180 185 190

Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser Pro Gly Cys Lys
195 200 205

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

Lys Leu Thr Asp Ile His Gly Asn Val Leu Gln Tyr His Lys Asp Val
225 230 235 240

Lys His Met Asn Ser Ala Gly Val Leu Ala Thr Leu Arg Asn Tyr Asp
245 250 255

Tyr Tyr Ala Ser Arg Val Pro Glu Ser Ile Lys Asn Ala Leu Val Pro
260 265 270

<210> 202

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

<220>
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3'(2'), 5'-bisphosphate nucleotidase 1; "

<220>
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<223> /note="Uniprot ID: O95861; "

<220>
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<223> /note="ENSP ID: ENSP00000444398"

<400> 202

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

```
Glu Val Pro Ala Gly Lys His Ile Ile Thr Thr Thr Arg Ser His Ser
    130                 135                 140

Asn Lys Leu Val Thr Asp Cys Val Ala Ala Met Asn Pro Asp Ala Val
145                 150                 155                 160

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

Lys Ala Ser Ala Tyr Val Phe Ala Ser Pro Gly Cys Lys Lys Trp Asp
            180                 185                 190

Thr Cys Ala Pro Glu Val Ile Leu His Ala Val Gly Gly Lys Leu Thr
        195                 200                 205

Asp Ile His Gly Asn Val Leu Gln Tyr His Lys Asp Val Lys His Met
    210                 215                 220

Asn Ser Ala Gly Val Leu Ala Thr Leu Arg Asn Tyr Asp Tyr Tyr Ala
225                 230                 235                 240

Ser Arg Val Pro Glu Ser Ile Lys Asn Ala Leu Val Pro
                245                 250


<210> 203
<211> 308
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O95861; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000446828"

<400> 203

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Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1               5                  10                  15

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
            20                  25                  30

Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
        35                  40                  45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
    50                  55                  60

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

Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
                85                  90                  95

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

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly
        115                 120                 125

Leu Leu Asp Asn Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys
    130                 135                 140

Ala Ile Ala Gly Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly
145                 150                 155                 160

Pro Asp Ala Val Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly
                165                 170                 175

Ala Phe Gly Phe Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile
            180                 185                 190

Thr Thr Thr Arg Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala
        195                 200                 205

Ala Met Asn Pro Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys
    210                 215                 220
```

```
Ile Ile Gln Leu Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser
225                 230                 235                 240


Pro Gly Cys Lys Lys Trp Asp Thr Cys Ala Pro Glu Val Ile Leu His
                245                 250                 255


Ala Val Gly Gly Lys Leu Thr Asp Ile His Gly Asn Val Leu Gln Tyr
            260                 265                 270


His Lys Asp Val Lys His Met Asn Ser Ala Gly Val Leu Ala Thr Leu
        275                 280                 285


Arg Asn Tyr Asp Tyr Tyr Ala Ser Arg Val Pro Glu Ser Ile Lys Asn
    290                 295                 300


Ala Leu Val Pro
305


<210> 204
<211> 136
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 25; "

<220>
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<223> /note="Gene Symbol: BPNT1; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000446850"

<400> 204
Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1               5                   10                  15


Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
            20                  25                  30
```

```
Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
        35                  40                  45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
    50                  55                  60

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Leu Val Val Trp Val
65                  70                  75                  80

Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly Leu Leu Asp Asn
                85                  90                  95

Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys Ala Ile Ala Gly
            100                 105                 110

Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly Pro Asp Ala Val
        115                 120                 125

Leu Gly Arg Thr Ile Trp Gly Val
    130                 135


<210> 205
<211> 170
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 25; "

<220>
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<223> /note="Gene Symbol: BPNT1; "

<220>
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<223> /note="Gene Name:
      3'(2'), 5'-bisphosphate nucleotidase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446953"

<400> 205
Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1               5                   10                  15

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
            20                  25                  30
```

```
Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
        35                  40                  45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
    50                  55                  60

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Leu Val Val Trp Val
65                  70                  75                  80

Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly Leu Leu Asp Asn
                85                  90                  95

Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys Ala Ile Ala Gly
            100                 105                 110

Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly Pro Asp Ala Val
        115                 120                 125

Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly Ala Phe Gly Phe
    130                 135                 140

Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile Thr Thr Thr Arg
145                 150                 155                 160

Ser His Ser Asn Lys Leu Val Thr Asp Cys
                165                 170
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<210> 206
<211> 116
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: BPNT1; "

<220>
<221> source
<223> /note="Gene Name:
3'(2'), 5'-bisphosphate nucleotidase 1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000448740"

<400> 206
Met Ser Ile Cys Ser Ser Leu Ala Arg Lys Phe Pro Lys Leu Thr Ile
1   5   10   15

Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val Asp Gln Glu Leu Ile
            20   25   30

Glu Asp Ser Gln Trp Glu Glu Ile Leu Lys Gln Pro Cys Pro Ser Gln
        35   40   45

Tyr Ser Ala Ile Lys Glu Glu Asp Leu Val Val Trp Val Asp Pro Leu
    50   55   60

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

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

Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly Pro Asp Ala Val Leu Gly Arg
            100   105   110

Thr Ile Trp Gly
        115

<210> 207
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 25; "

<220>
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<223> /note="Gene Symbol: BPNT1; "

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000449883"

<400> 207
Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
1 5 10 15

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
20 25 30

Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
35 40 45

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
50 55 60

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

Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
85 90 95

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

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly
115 120 125

Leu Leu
130

<210> 208
<211> 888
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<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 26; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCR; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>

<221> source
<223> /note="Uniprot ID: P04035; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000287936"

<400> 208
Met Leu Ser Arg Leu Phe Arg Met His Gly Leu Phe Val Ala Ser His
1   5   10   15

Pro Trp Glu Val Ile Val Gly Thr Val Thr Leu Thr Ile Cys Met Met
            20   25   30

Ser Met Asn Met Phe Thr Gly Asn Asn Lys Ile Cys Gly Trp Asn Tyr
        35   40   45

Glu Cys Pro Lys Phe Glu Glu Asp Val Leu Ser Ser Asp Ile Ile Ile
    50   55   60

Leu Thr Ile Thr Arg Cys Ile Ala Ile Leu Tyr Ile Tyr Phe Gln Phe
65   70   75   80

Gln Asn Leu Arg Gln Leu Gly Ser Lys Tyr Ile Leu Gly Ile Ala Gly
                85   90   95

Leu Phe Thr Ile Phe Ser Ser Phe Val Phe Ser Thr Val Val Ile His
            100   105   110

Phe Leu Asp Lys Glu Leu Thr Gly Leu Asn Glu Ala Leu Pro Phe Phe
        115   120   125

Leu Leu Leu Ile Asp Leu Ser Arg Ala Ser Thr Leu Ala Lys Phe Ala
    130   135   140

Leu Ser Ser Asn Ser Gln Asp Glu Val Arg Glu Asn Ile Ala Arg Gly
145   150   155   160

Met Ala Ile Leu Gly Pro Thr Phe Thr Leu Asp Ala Leu Val Glu Cys
                165   170   175

Leu Val Ile Gly Val Gly Thr Met Ser Gly Val Arg Gln Leu Glu Ile
            180   185   190

Met Cys Cys Phe Gly Cys Met Ser Val Leu Ala Asn Tyr Phe Val Phe

```
        195                 200                 205

Met Thr Phe Phe Pro Ala Cys Val Ser Leu Val Leu Glu Leu Ser Arg
    210                 215                 220

Glu Ser Arg Glu Gly Arg Pro Ile Trp Gln Leu Ser His Phe Ala Arg
225                 230                 235                 240

Val Leu Glu Glu Glu Glu Asn Lys Pro Asn Pro Val Thr Gln Arg Val
                245                 250                 255

Lys Met Ile Met Ser Leu Gly Leu Val Leu Val His Ala His Ser Arg
            260                 265                 270

Trp Ile Ala Asp Pro Ser Pro Gln Asn Ser Thr Ala Asp Thr Ser Lys
        275                 280                 285

Val Ser Leu Gly Leu Asp Glu Asn Val Ser Lys Arg Ile Glu Pro Ser
    290                 295                 300

Val Ser Leu Trp Gln Phe Tyr Leu Ser Lys Met Ile Ser Met Asp Ile
305                 310                 315                 320

Glu Gln Val Ile Thr Leu Ser Leu Ala Leu Leu Leu Ala Val Lys Tyr
                325                 330                 335

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

Pro Ile Thr Ser Pro Val Val Thr Gln Lys Lys Val Pro Asp Asn Cys
        355                 360                 365

Cys Arg Arg Glu Pro Met Leu Val Arg Asn Asn Gln Lys Cys Asp Ser
    370                 375                 380

Val Glu Glu Glu Thr Gly Ile Asn Arg Glu Arg Lys Val Glu Val Ile
385                 390                 395                 400

Lys Pro Leu Val Ala Glu Thr Asp Thr Pro Asn Arg Ala Thr Phe Val
                405                 410                 415

Val Gly Asn Ser Ser Leu Leu Asp Thr Ser Ser Val Leu Val Thr Gln
            420                 425                 430
```

```
Glu Pro Glu Ile Glu Leu Pro Arg Glu Pro Arg Pro Asn Glu Glu Cys
        435                 440                 445

Leu Gln Ile Leu Gly Asn Ala Glu Lys Gly Ala Lys Phe Leu Ser Asp
    450                 455                 460

Ala Glu Ile Ile Gln Leu Val Asn Ala Lys His Ile Pro Ala Tyr Lys
465                 470                 475                 480

Leu Glu Thr Leu Met Glu Thr His Glu Arg Gly Val Ser Ile Arg Arg
                485                 490                 495

Gln Leu Leu Ser Lys Lys Leu Ser Glu Pro Ser Ser Leu Gln Tyr Leu
            500                 505                 510

Pro Tyr Arg Asp Tyr Asn Tyr Ser Leu Val Met Gly Ala Cys Cys Glu
        515                 520                 525

Asn Val Ile Gly Tyr Met Pro Ile Pro Val Gly Val Ala Gly Pro Leu
    530                 535                 540

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

Cys Leu Val Ala Ser Thr Asn Arg Gly Cys Arg Ala Ile Gly Leu Gly
                565                 570                 575

Gly Gly Ala Ser Ser Arg Val Leu Ala Asp Gly Met Thr Arg Gly Pro
            580                 585                 590

Val Val Arg Leu Pro Arg Ala Cys Asp Ser Ala Glu Val Lys Ala Trp
        595                 600                 605

Leu Glu Thr Ser Glu Gly Phe Ala Val Ile Lys Glu Ala Phe Asp Ser
    610                 615                 620

Thr Ser Arg Phe Ala Arg Leu Gln Lys Leu His Thr Ser Ile Ala Gly
625                 630                 635                 640

Arg Asn Leu Tyr Ile Arg Phe Gln Ser Arg Ser Gly Asp Ala Met Gly
                645                 650                 655
```

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

Glu Tyr Phe Pro Glu Met Gln Ile Leu Ala Val Ser Gly Asn Tyr Cys
        675                 680                 685

Thr Asp Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys
    690                 695                 700

Ser Val Val Cys Glu Ala Val Ile Pro Ala Lys Val Val Arg Glu Val
705                 710                 715                 720

Leu Lys Thr Thr Thr Glu Ala Met Ile Glu Val Asn Ile Asn Lys Asn
                725                 730                 735

Leu Val Gly Ser Ala Met Ala Gly Ser Ile Gly Gly Tyr Asn Ala His
            740                 745                 750

Ala Ala Asn Ile Val Thr Ala Ile Tyr Ile Ala Cys Gly Gln Asp Ala
        755                 760                 765

Ala Gln Asn Val Gly Ser Ser Asn Cys Ile Thr Leu Met Glu Ala Ser
    770                 775                 780

Gly Pro Thr Asn Glu Asp Leu Tyr Ile Ser Cys Thr Met Pro Ser Ile
785                 790                 795                 800

Glu Ile Gly Thr Val Gly Gly Gly Thr Asn Leu Leu Pro Gln Gln Ala
                805                 810                 815

Cys Leu Gln Met Leu Gly Val Gln Gly Ala Cys Lys Asp Asn Pro Gly
            820                 825                 830

Glu Asn Ala Arg Gln Leu Ala Arg Ile Val Cys Gly Thr Val Met Ala
        835                 840                 845

Gly Glu Leu Ser Leu Met Ala Ala Leu Ala Ala Gly His Leu Val Lys
    850                 855                 860

Ser His Met Ile His Asn Arg Ser Lys Ile Asn Leu Gln Asp Leu Gln
865                 870                 875                 880
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Gly Ala Cys Thr Lys Lys Thr Ala
885

<210> 209
<211> 835
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 26; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCR; "

<220>
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<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>
<221> source
<223> /note="Uniprot ID: P04035; "

<220>
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<223> /note="ENSP ID: ENSP00000340816"

<400> 209
Met Leu Ser Arg Leu Phe Arg Met His Gly Leu Phe Val Ala Ser His
1 5 10 15

Pro Trp Glu Val Ile Val Gly Thr Val Thr Leu Thr Ile Cys Met Met
20 25 30

Ser Met Asn Met Phe Thr Gly Asn Asn Lys Ile Cys Gly Trp Asn Tyr
35 40 45

Glu Cys Pro Lys Phe Glu Glu Asp Val Leu Ser Ser Asp Ile Ile Ile
50 55 60

Leu Thr Ile Thr Arg Cys Ile Ala Ile Leu Tyr Ile Tyr Phe Gln Phe
65 70 75 80

Gln Asn Leu Arg Gln Leu Gly Ser Lys Tyr Ile Leu Gly Ile Ala Gly
85 90 95

Leu Phe Thr Ile Phe Ser Ser Phe Val Phe Ser Thr Val Val Ile His
100 105 110

```
Phe Leu Asp Lys Glu Leu Thr Gly Leu Asn Glu Ala Leu Pro Phe Phe
        115                 120                 125

Leu Leu Leu Ile Asp Leu Ser Arg Ala Ser Thr Leu Ala Lys Phe Ala
    130                 135                 140

Leu Ser Ser Asn Ser Gln Asp Glu Val Arg Glu Asn Ile Ala Arg Gly
145                 150                 155                 160

Met Ala Ile Leu Gly Pro Thr Phe Thr Leu Asp Ala Leu Val Glu Cys
                165                 170                 175

Leu Val Ile Gly Val Gly Thr Met Ser Gly Val Arg Gln Leu Glu Ile
            180                 185                 190

Met Cys Cys Phe Gly Cys Met Ser Val Leu Ala Asn Tyr Phe Val Phe
        195                 200                 205

Met Thr Phe Phe Pro Ala Cys Val Ser Leu Val Leu Glu Leu Ser Arg
    210                 215                 220

Glu Ser Arg Glu Gly Arg Pro Ile Trp Gln Leu Ser His Phe Ala Arg
225                 230                 235                 240

Val Leu Glu Glu Glu Glu Asn Lys Pro Asn Pro Val Thr Gln Arg Val
                245                 250                 255

Lys Met Ile Met Ser Leu Gly Leu Val Leu Val His Ala His Ser Arg
            260                 265                 270

Trp Ile Ala Asp Pro Ser Pro Gln Asn Ser Thr Ala Asp Thr Ser Lys
        275                 280                 285

Val Ser Leu Gly Leu Asp Glu Asn Val Ser Lys Arg Ile Glu Pro Ser
    290                 295                 300

Val Ser Leu Trp Gln Phe Tyr Leu Ser Lys Met Ile Ser Met Asp Ile
305                 310                 315                 320

Glu Gln Val Ile Thr Leu Ser Leu Ala Leu Leu Leu Ala Val Lys Tyr
                325                 330                 335
```

```
Ile Phe Phe Glu Gln Thr Glu Thr Glu Ser Thr Leu Ser Leu Lys Asn
            340                 345                 350

Pro Ile Thr Ser Pro Val Val Thr Gln Lys Lys Val Pro Asp Asn Cys
        355                 360                 365

Cys Arg Arg Glu Pro Met Leu Val Arg Asn Asn Gln Lys Cys Asp Ser
    370                 375                 380

Val Glu Glu Glu Thr Gly Ile Asn Arg Glu Arg Lys Val Glu Val Ile
385                 390                 395                 400

Lys Pro Leu Val Ala Glu Thr Asp Thr Pro Asn Arg Ala Thr Phe Val
                405                 410                 415

Val Gly Asn Ser Ser Leu Leu Asp Thr Ser Ser Val Leu Val Thr Gln
            420                 425                 430

Glu Pro Glu Ile Glu Leu Pro Arg Glu Pro Arg Pro Asn Glu Glu Cys
        435                 440                 445

Leu Gln Ile Leu Gly Asn Ala Glu Lys Gly Ala Lys Phe Leu Ser Asp
    450                 455                 460

Ala Glu Ile Ile Gln Leu Val Asn Ala Lys His Ile Pro Ala Tyr Lys
465                 470                 475                 480

Leu Glu Thr Leu Met Glu Thr His Glu Arg Gly Val Ser Ile Arg Arg
                485                 490                 495

Gln Leu Leu Ser Lys Lys Leu Ser Glu Pro Ser Ser Leu Gln Tyr Leu
            500                 505                 510

Pro Tyr Arg Asp Tyr Asn Tyr Ser Leu Leu Gly Gly Gly Ala Ser Ser
        515                 520                 525

Arg Val Leu Ala Asp Gly Met Thr Arg Gly Pro Val Val Arg Leu Pro
    530                 535                 540

Arg Ala Cys Asp Ser Ala Glu Val Lys Ala Trp Leu Glu Thr Ser Glu
545                 550                 555                 560
```

Gly Phe Ala Val Ile Lys Glu Ala Phe Asp Ser Thr Ser Arg Phe Ala
565 570 575

Arg Leu Gln Lys Leu His Thr Ser Ile Ala Gly Arg Asn Leu Tyr Ile
580 585 590

Arg Phe Gln Ser Arg Ser Gly Asp Ala Met Gly Met Asn Met Ile Ser
595 600 605

Lys Gly Thr Glu Lys Ala Leu Ser Lys Leu His Glu Tyr Phe Pro Glu
610 615 620

Met Gln Ile Leu Ala Val Ser Gly Asn Tyr Cys Thr Asp Lys Lys Pro
625 630 635 640

Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu
645 650 655

Ala Val Ile Pro Ala Lys Val Val Arg Glu Val Leu Lys Thr Thr Thr
660 665 670

Glu Ala Met Ile Glu Val Asn Ile Asn Lys Asn Leu Val Gly Ser Ala
675 680 685

Met Ala Gly Ser Ile Gly Gly Tyr Asn Ala His Ala Ala Asn Ile Val
690 695 700

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

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

Asp Leu Tyr Ile Ser Cys Thr Met Pro Ser Ile Glu Ile Gly Thr Val
740 745 750

Gly Gly Gly Thr Asn Leu Leu Pro Gln Gln Ala Cys Leu Gln Met Leu
755 760 765

Gly Val Gln Gly Ala Cys Lys Asp Asn Pro Gly Glu Asn Ala Arg Gln
770 775 780

Leu Ala Arg Ile Val Cys Gly Thr Val Met Ala Gly Glu Leu Ser Leu

785 790 795 800

Met Ala Ala Leu Ala Ala Gly His Leu Val Lys Ser His Met Ile His
805 810 815

Asn Arg Ser Lys Ile Asn Leu Gln Asp Leu Gln Gly Ala Cys Thr Lys
820 825 830

Lys Thr Ala
835

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

<220>
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<223> /note="Payload ID: 26; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCR; "

<220>
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<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000409100"

<400> 210
Met Leu Ser Arg Leu Phe Arg Met His Gly Leu Phe Val Ala Ser His
1 5 10 15

Pro Trp

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

<220>
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<223> /note="Payload ID: 26; "

<220>
<221> source

<223> /note="Gene Symbol: HMGCR; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420871"

<400> 211
Tyr Phe Pro Glu Met Gln Ile Leu Ala Val Ser Gly Asn Tyr Cys Thr
1 5 10 15

Asp Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser
20 25 30

Val Val Cys Glu Ala Val Ile Pro Ala Lys Val Val Arg Glu Met Leu
35 40 45

Gly Val Gln Gly Ala Cys Lys Asp Asn Pro Gly Glu Asn Ala Arg Gln
50 55 60

Leu Ala Arg Ile Val Cys Gly Thr Val Met Ala Gly Glu Leu Ser Leu
65 70 75 80

Met Ala Ala Leu Ala Ala Gly His Leu Val Lys Ser His Met Ile His
85 90 95

Asn Arg Ser Lys Ile Asn Leu Gln Asp Leu Gln Gly Ala Cys Thr Lys
100 105 110

Lys Thr Ala
115

<210> 212
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 26; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCR; "

<220>
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<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421378"

<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 212
Xaa His Glu Tyr Phe Pro Glu Met Gln Ile Leu Ala Val Ser Gly Asn
1 5 10 15

Tyr Cys Thr Asp Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg
20 25 30

Gly Lys Ser Val Val Cys Glu Ala Val Ile Pro Ala Lys Val Val Arg
35 40 45

Glu Val Leu Lys Thr Thr Thr Glu Ala Met Ile Glu Val Asn Ile Asn
50 55 60

Lys Asn Leu Val Gly Ser Ala Met Ala Gly Ser Ile Gly Gly Tyr Asn
65 70 75 80

Ala His Ala Ala Asn Ile Val Thr Ala Ile Tyr Ile Ala Cys Gly Gln
85 90 95

Met Leu Gly Val Gln Gly Ala Cys Lys Asp Asn Pro Gly Glu Asn Ala
100 105 110

Arg Gln Leu Ala Arg Ile Val Cys Gly Thr Val Met Ala Gly Glu Leu
115 120 125

Ser Leu Met Ala Ala Leu Ala Ala Gly His Leu Val Lys Ser His Met
130 135 140

Ile His Asn Arg Ser Lys Ile Asn Leu Gln Asp Leu Gln Gly Ala Cys
145 150 155 160

Thr Lys Lys Thr Ala

165

<210> 213
<211> 888
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 26; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCR; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>
<221> source
<223> /note="Uniprot ID: P04035; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426745"

<400> 213
Met Leu Ser Arg Leu Phe Arg Met His Gly Leu Phe Val Ala Ser His
1   5   10   15

Pro Trp Glu Val Ile Val Gly Thr Val Thr Leu Thr Ile Cys Met Met
            20   25   30

Ser Met Asn Met Phe Thr Gly Asn Asn Lys Ile Cys Gly Trp Asn Tyr
        35   40   45

Glu Cys Pro Lys Phe Glu Glu Asp Val Leu Ser Ser Asp Ile Ile Ile
    50   55   60

Leu Thr Ile Thr Arg Cys Ile Ala Ile Leu Tyr Ile Tyr Phe Gln Phe
65   70   75   80

Gln Asn Leu Arg Gln Leu Gly Ser Lys Tyr Ile Leu Gly Ile Ala Gly
                85   90   95

Leu Phe Thr Ile Phe Ser Ser Phe Val Phe Ser Thr Val Val Ile His
            100   105   110

```
Phe Leu Asp Lys Glu Leu Thr Gly Leu Asn Glu Ala Leu Pro Phe Phe
        115                 120                 125

Leu Leu Leu Ile Asp Leu Ser Arg Ala Ser Thr Leu Ala Lys Phe Ala
    130                 135                 140

Leu Ser Ser Asn Ser Gln Asp Glu Val Arg Glu Asn Ile Ala Arg Gly
145                 150                 155                 160

Met Ala Ile Leu Gly Pro Thr Phe Thr Leu Asp Ala Leu Val Glu Cys
                165                 170                 175

Leu Val Ile Gly Val Gly Thr Met Ser Gly Val Arg Gln Leu Glu Ile
            180                 185                 190

Met Cys Cys Phe Gly Cys Met Ser Val Leu Ala Asn Tyr Phe Val Phe
        195                 200                 205

Met Thr Phe Phe Pro Ala Cys Val Ser Leu Val Leu Glu Leu Ser Arg
    210                 215                 220

Glu Ser Arg Glu Gly Arg Pro Ile Trp Gln Leu Ser His Phe Ala Arg
225                 230                 235                 240

Val Leu Glu Glu Glu Glu Asn Lys Pro Asn Pro Val Thr Gln Arg Val
                245                 250                 255

Lys Met Ile Met Ser Leu Gly Leu Val Leu Val His Ala His Ser Arg
            260                 265                 270

Trp Ile Ala Asp Pro Ser Pro Gln Asn Ser Thr Ala Asp Thr Ser Lys
        275                 280                 285

Val Ser Leu Gly Leu Asp Glu Asn Val Ser Lys Arg Ile Glu Pro Ser
    290                 295                 300

Val Ser Leu Trp Gln Phe Tyr Leu Ser Lys Met Ile Ser Met Asp Ile
305                 310                 315                 320

Glu Gln Val Ile Thr Leu Ser Leu Ala Leu Leu Leu Ala Val Lys Tyr
                325                 330                 335
```

```
Ile Phe Phe Glu Gln Thr Glu Thr Glu Ser Thr Leu Ser Leu Lys Asn
            340                 345                 350

Pro Ile Thr Ser Pro Val Val Thr Gln Lys Lys Val Pro Asp Asn Cys
        355                 360                 365

Cys Arg Arg Glu Pro Met Leu Val Arg Asn Asn Gln Lys Cys Asp Ser
    370                 375                 380

Val Glu Glu Glu Thr Gly Ile Asn Arg Glu Arg Lys Val Glu Val Ile
385                 390                 395                 400

Lys Pro Leu Val Ala Glu Thr Asp Thr Pro Asn Arg Ala Thr Phe Val
                405                 410                 415

Val Gly Asn Ser Ser Leu Leu Asp Thr Ser Ser Val Leu Val Thr Gln
            420                 425                 430

Glu Pro Glu Ile Glu Leu Pro Arg Glu Pro Arg Pro Asn Glu Glu Cys
        435                 440                 445

Leu Gln Ile Leu Gly Asn Ala Glu Lys Gly Ala Lys Phe Leu Ser Asp
    450                 455                 460

Ala Glu Ile Ile Gln Leu Val Asn Ala Lys His Ile Pro Ala Tyr Lys
465                 470                 475                 480

Leu Glu Thr Leu Met Glu Thr His Glu Arg Gly Val Ser Ile Arg Arg
                485                 490                 495

Gln Leu Leu Ser Lys Lys Leu Ser Glu Pro Ser Ser Leu Gln Tyr Leu
            500                 505                 510

Pro Tyr Arg Asp Tyr Asn Tyr Ser Leu Val Met Gly Ala Cys Cys Glu
        515                 520                 525

Asn Val Ile Gly Tyr Met Pro Ile Pro Val Gly Val Ala Gly Pro Leu
    530                 535                 540

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

Cys Leu Val Ala Ser Thr Asn Arg Gly Cys Arg Ala Ile Gly Leu Gly
```

565 570 575

Gly Gly Ala Ser Ser Arg Val Leu Ala Asp Gly Met Thr Arg Gly Pro
580 585 590

Val Val Arg Leu Pro Arg Ala Cys Asp Ser Ala Glu Val Lys Ala Trp
595 600 605

Leu Glu Thr Ser Glu Gly Phe Ala Val Ile Lys Glu Ala Phe Asp Ser
610 615 620

Thr Ser Arg Phe Ala Arg Leu Gln Lys Leu His Thr Ser Ile Ala Gly
625 630 635 640

Arg Asn Leu Tyr Ile Arg Phe Gln Ser Arg Ser Gly Asp Ala Met Gly
645 650 655

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

Glu Tyr Phe Pro Glu Met Gln Ile Leu Ala Val Ser Gly Asn Tyr Cys
675 680 685

Thr Asp Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys
690 695 700

Ser Val Val Cys Glu Ala Val Ile Pro Ala Lys Val Val Arg Glu Val
705 710 715 720

Leu Lys Thr Thr Thr Glu Ala Met Ile Glu Val Asn Ile Asn Lys Asn
725 730 735

Leu Val Gly Ser Ala Met Ala Gly Ser Ile Gly Gly Tyr Asn Ala His
740 745 750

Ala Ala Asn Ile Val Thr Ala Ile Tyr Ile Ala Cys Gly Gln Asp Ala
755 760 765

Ala Gln Asn Val Gly Ser Ser Asn Cys Ile Thr Leu Met Glu Ala Ser
770 775 780

Gly Pro Thr Asn Glu Asp Leu Tyr Ile Ser Cys Thr Met Pro Ser Ile
785 790 795 800

```
Glu Ile Gly Thr Val Gly Gly Gly Thr Asn Leu Leu Pro Gln Gln Ala
                805                 810                 815

Cys Leu Gln Met Leu Gly Val Gln Gly Ala Cys Lys Asp Asn Pro Gly
            820                 825                 830

Glu Asn Ala Arg Gln Leu Ala Arg Ile Val Cys Gly Thr Val Met Ala
        835                 840                 845

Gly Glu Leu Ser Leu Met Ala Ala Leu Ala Ala Gly His Leu Val Lys
    850                 855                 860

Ser His Met Ile His Asn Arg Ser Lys Ile Asn Leu Gln Asp Leu Gln
865                 870                 875                 880

Gly Ala Cys Thr Lys Lys Thr Ala
                885


<210> 214
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 26; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCR; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxy-3-methylglutaryl-CoA reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427340"

<400> 214
Met Leu Ser Arg Leu Phe Arg Met His Gly Leu Phe Val Ala Ser His
1               5                   10                  15

Pro Trp Glu Val Ile Val Gly Thr Val Thr Leu Thr Ile Cys Met Met
            20                  25                  30
```

```
Ser Met Asn Met Phe Thr Gly Asn Asn Lys Ile Cys Gly Trp Asn Tyr
        35                  40                  45

Glu Cys Pro Lys Phe Glu Glu Asp Val Leu Ser Ser Asp Ile Ile Ile
    50                  55                  60

Leu Thr Ile Thr Arg Cys Ile Ala Ile Leu Tyr Ile Tyr Phe Gln Phe
65                  70                  75                  80

Gln Asn Leu Arg Gln Leu Gly Ser Lys Tyr Ile Leu Gly Ile Ala Gly
                85                  90                  95

Leu Phe Thr Ile Phe Ser Ser Phe Val Phe Ser Thr Val Val Ile
            100                 105                 110


<210> 215
<211> 520
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 27; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCS1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble); "

<220>
<221> source
<223> /note="Uniprot ID:  Q01581; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000322706"

<400> 215
Met Pro Gly Ser Leu Pro Leu Asn Ala Glu Ala Cys Trp Pro Lys Asp
1               5                   10                  15

Val Gly Ile Val Ala Leu Glu Ile Tyr Phe Pro Ser Gln Tyr Val Asp
            20                  25                  30

Gln Ala Glu Leu Glu Lys Tyr Asp Gly Val Asp Ala Gly Lys Tyr Thr
        35                  40                  45
```

```
Ile Gly Leu Gly Gln Ala Lys Met Gly Phe Cys Thr Asp Arg Glu Asp
    50                  55                  60

Ile Asn Ser Leu Cys Met Thr Val Val Gln Asn Leu Met Glu Arg Asn
65                  70                  75                  80

Asn Leu Ser Tyr Asp Cys Ile Gly Arg Leu Glu Val Gly Thr Glu Thr
                85                  90                  95

Ile Ile Asp Lys Ser Lys Ser Val Lys Thr Asn Leu Met Gln Leu Phe
            100                 105                 110

Glu Glu Ser Gly Asn Thr Asp Ile Glu Gly Ile Asp Thr Thr Asn Ala
        115                 120                 125

Cys Tyr Gly Gly Thr Ala Ala Val Phe Asn Ala Val Asn Trp Ile Glu
    130                 135                 140

Ser Ser Ser Trp Asp Gly Arg Tyr Ala Leu Val Val Ala Gly Asp Ile
145                 150                 155                 160

Ala Val Tyr Ala Thr Gly Asn Ala Arg Pro Thr Gly Gly Val Gly Ala
                165                 170                 175

Val Ala Leu Leu Ile Gly Pro Asn Ala Pro Leu Ile Phe Glu Arg Gly
            180                 185                 190

Leu Arg Gly Thr His Met Gln His Ala Tyr Asp Phe Tyr Lys Pro Asp
        195                 200                 205

Met Leu Ser Glu Tyr Pro Ile Val Asp Gly Lys Leu Ser Ile Gln Cys
    210                 215                 220

Tyr Leu Ser Ala Leu Asp Arg Cys Tyr Ser Val Tyr Cys Lys Lys Ile
225                 230                 235                 240

His Ala Gln Trp Gln Lys Glu Gly Asn Asp Lys Asp Phe Thr Leu Asn
                245                 250                 255

Asp Phe Gly Phe Met Ile Phe His Ser Pro Tyr Cys Lys Leu Val Gln
            260                 265                 270
```

```
Lys Ser Leu Ala Arg Met Leu Leu Asn Asp Phe Leu Asn Asp Gln Asn
        275                 280                 285

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

Lys Leu Glu Asp Thr Tyr Phe Asp Arg Asp Val Glu Lys Ala Phe Met
305                 310                 315                 320

Lys Ala Ser Ser Glu Leu Phe Ser Gln Lys Thr Lys Ala Ser Leu Leu
                325                 330                 335

Val Ser Asn Gln Asn Gly Asn Met Tyr Thr Ser Ser Val Tyr Gly Ser
            340                 345                 350

Leu Ala Ser Val Leu Ala Gln Tyr Ser Pro Gln Gln Leu Ala Gly Lys
        355                 360                 365

Arg Ile Gly Val Phe Ser Tyr Gly Ser Gly Leu Ala Ala Thr Leu Tyr
    370                 375                 380

Ser Leu Lys Val Thr Gln Asp Ala Thr Pro Gly Ser Ala Leu Asp Lys
385                 390                 395                 400

Ile Thr Ala Ser Leu Cys Asp Leu Lys Ser Arg Leu Asp Ser Arg Thr
                405                 410                 415

Gly Val Ala Pro Asp Val Phe Ala Glu Asn Met Lys Leu Arg Glu Asp
            420                 425                 430

Thr His His Leu Val Asn Tyr Ile Pro Gln Gly Ser Ile Asp Ser Leu
        435                 440                 445

Phe Glu Gly Thr Trp Tyr Leu Val Arg Val Asp Glu Lys His Arg Arg
    450                 455                 460

Thr Tyr Ala Arg Arg Pro Thr Pro Asn Asp Asp Thr Leu Asp Glu Gly
465                 470                 475                 480

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

```
Ala Lys Lys Val Pro Arg Leu Pro Ala Thr Ala Ala Glu Pro Glu Ala
            500                 505                 510

Ala Val Ile Ser Asn Gly Glu His
        515                 520


<210> 216
<211> 520
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 27; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCS1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble); "

<220>
<221> source
<223> /note="Uniprot ID:  Q01581; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399402"

<400> 216
Met Pro Gly Ser Leu Pro Leu Asn Ala Glu Ala Cys Trp Pro Lys Asp
1               5                   10                  15

Val Gly Ile Val Ala Leu Glu Ile Tyr Phe Pro Ser Gln Tyr Val Asp
            20                  25                  30

Gln Ala Glu Leu Glu Lys Tyr Asp Gly Val Asp Ala Gly Lys Tyr Thr
        35                  40                  45

Ile Gly Leu Gly Gln Ala Lys Met Gly Phe Cys Thr Asp Arg Glu Asp
    50                  55                  60

Ile Asn Ser Leu Cys Met Thr Val Val Gln Asn Leu Met Glu Arg Asn
65                  70                  75                  80

Asn Leu Ser Tyr Asp Cys Ile Gly Arg Leu Glu Val Gly Thr Glu Thr
                85                  90                  95
```

```
Ile Ile Asp Lys Ser Lys Ser Val Lys Thr Asn Leu Met Gln Leu Phe
            100                 105                 110

Glu Glu Ser Gly Asn Thr Asp Ile Glu Gly Ile Asp Thr Thr Asn Ala
        115                 120                 125

Cys Tyr Gly Gly Thr Ala Ala Val Phe Asn Ala Val Asn Trp Ile Glu
    130                 135                 140

Ser Ser Ser Trp Asp Gly Arg Tyr Ala Leu Val Val Ala Gly Asp Ile
145                 150                 155                 160

Ala Val Tyr Ala Thr Gly Asn Ala Arg Pro Thr Gly Gly Val Gly Ala
                165                 170                 175

Val Ala Leu Leu Ile Gly Pro Asn Ala Pro Leu Ile Phe Glu Arg Gly
            180                 185                 190

Leu Arg Gly Thr His Met Gln His Ala Tyr Asp Phe Tyr Lys Pro Asp
        195                 200                 205

Met Leu Ser Glu Tyr Pro Ile Val Asp Gly Lys Leu Ser Ile Gln Cys
    210                 215                 220

Tyr Leu Ser Ala Leu Asp Arg Cys Tyr Ser Val Tyr Cys Lys Lys Ile
225                 230                 235                 240

His Ala Gln Trp Gln Lys Glu Gly Asn Asp Lys Asp Phe Thr Leu Asn
                245                 250                 255

Asp Phe Gly Phe Met Ile Phe His Ser Pro Tyr Cys Lys Leu Val Gln
            260                 265                 270

Lys Ser Leu Ala Arg Met Leu Leu Asn Asp Phe Leu Asn Asp Gln Asn
        275                 280                 285

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

Lys Leu Glu Asp Thr Tyr Phe Asp Arg Asp Val Glu Lys Ala Phe Met
305                 310                 315                 320
```

```
Lys Ala Ser Ser Glu Leu Phe Ser Gln Lys Thr Lys Ala Ser Leu Leu
                325                 330                 335

Val Ser Asn Gln Asn Gly Asn Met Tyr Thr Ser Ser Val Tyr Gly Ser
            340                 345                 350

Leu Ala Ser Val Leu Ala Gln Tyr Ser Pro Gln Gln Leu Ala Gly Lys
        355                 360                 365

Arg Ile Gly Val Phe Ser Tyr Gly Ser Gly Leu Ala Ala Thr Leu Tyr
    370                 375                 380

Ser Leu Lys Val Thr Gln Asp Ala Thr Pro Gly Ser Ala Leu Asp Lys
385                 390                 395                 400

Ile Thr Ala Ser Leu Cys Asp Leu Lys Ser Arg Leu Asp Ser Arg Thr
                405                 410                 415

Gly Val Ala Pro Asp Val Phe Ala Glu Asn Met Lys Leu Arg Glu Asp
            420                 425                 430

Thr His His Leu Val Asn Tyr Ile Pro Gln Gly Ser Ile Asp Ser Leu
        435                 440                 445

Phe Glu Gly Thr Trp Tyr Leu Val Arg Val Asp Glu Lys His Arg Arg
    450                 455                 460

Thr Tyr Ala Arg Arg Pro Thr Pro Asn Asp Asp Thr Leu Asp Glu Gly
465                 470                 475                 480

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

Ala Lys Lys Val Pro Arg Leu Pro Ala Thr Ala Ala Glu Pro Glu Ala
            500                 505                 510

Ala Val Ile Ser Asn Gly Glu His
        515                 520
```

<210> 217
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 27; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCS1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427339"

<400> 217
Met Pro Gly Ser Leu Pro Leu Asn Ala Glu Ala Cys Trp Pro Lys Asp
1 5 10 15

Val Gly Ile Val Ala Leu Glu Ile Tyr Phe Pro Ser Gln Tyr Val Asp
20 25 30

Gln Ala Glu Leu Glu Lys Tyr Asp Gly Val Asp Ala Gly Lys Tyr Thr
35 40 45

Ile Gly Leu Gly Gln Ala Lys Met Gly Phe Cys Thr Asp Arg Glu Asp
50 55 60

Ile Asn Ser Leu Cys Met Thr Val Val Gln Asn Leu Met Glu Arg Asn
65 70 75 80

Asn Leu Ser Tyr Asp Cys Ile Gly Arg Leu Glu Val Gly Thr Glu
85 90 95

<210> 218
<211> 508
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 28; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCS2; "

<220>

<221> source
<223> /note="Gene Name:
3-hydroxy-3-methylglutaryl-CoA synthase 2
(mitochondrial) beta-mannosyltransferase-like; "

<220>
<221> source
<223> /note="Uniprot ID: P54868; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358414"

<400> 218

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Met Gln Arg Leu Leu Thr Pro Val Lys Arg Ile Leu Gln Leu Thr Arg
1               5                  10                  15

Ala Val Gln Glu Thr Ser Leu Thr Pro Ala Arg Leu Leu Pro Val Ala
            20                  25                  30

His Gln Arg Phe Ser Thr Ala Ser Ala Val Pro Leu Ala Lys Thr Asp
        35                  40                  45

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

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

Ala Gly Lys Tyr Thr Val Gly Leu Gly Gln Thr Arg Met Gly Phe Cys
                85                  90                  95

Ser Val Gln Glu Asp Ile Asn Ser Leu Cys Leu Thr Val Val Gln Arg
            100                 105                 110

Leu Met Glu Arg Ile Gln Leu Pro Trp Asp Ser Val Gly Arg Leu Glu
        115                 120                 125

Val Gly Thr Glu Thr Ile Ile Asp Lys Ser Lys Ala Val Lys Thr Val
    130                 135                 140

Leu Met Glu Leu Phe Gln Asp Ser Gly Asn Thr Asp Ile Glu Gly Ile
145                 150                 155                 160

Asp Thr Thr Asn Ala Cys Tyr Gly Gly Thr Ala Ser Leu Phe Asn Ala
                165                 170                 175
```

```
Ala Asn Trp Met Glu Ser Ser Ser Trp Asp Gly Arg Tyr Ala Met Val
            180                 185                 190

Val Cys Gly Asp Ile Ala Val Tyr Pro Ser Gly Asn Ala Arg Pro Thr
        195                 200                 205

Gly Gly Ala Gly Ala Val Ala Met Leu Ile Gly Pro Lys Ala Pro Leu
    210                 215                 220

Ala Leu Glu Arg Gly Leu Arg Gly Thr His Met Glu Asn Val Tyr Asp
225                 230                 235                 240

Phe Tyr Lys Pro Asn Leu Ala Ser Glu Tyr Pro Ile Val Asp Gly Lys
                245                 250                 255

Leu Ser Ile Gln Cys Tyr Leu Arg Ala Leu Asp Arg Cys Tyr Thr Ser
            260                 265                 270

Tyr Arg Lys Lys Ile Gln Asn Gln Trp Lys Gln Ala Gly Ser Asp Arg
        275                 280                 285

Pro Phe Thr Leu Asp Asp Leu Gln Tyr Met Ile Phe His Thr Pro Phe
    290                 295                 300

Cys Lys Met Val Gln Lys Ser Leu Ala Arg Leu Met Phe Asn Asp Phe
305                 310                 315                 320

Leu Ser Ala Ser Ser Asp Thr Gln Thr Ser Leu Tyr Lys Gly Leu Glu
                325                 330                 335

Ala Phe Gly Gly Leu Lys Leu Glu Asp Thr Tyr Thr Asn Lys Asp Leu
            340                 345                 350

Asp Lys Ala Leu Leu Lys Ala Ser Gln Asp Met Phe Asp Lys Lys Thr
        355                 360                 365

Lys Ala Ser Leu Tyr Leu Ser Thr His Asn Gly Asn Met Tyr Thr Ser
    370                 375                 380

Ser Leu Tyr Gly Cys Leu Ala Ser Leu Leu Ser His His Ser Ala Gln
385                 390                 395                 400
```

```
Glu Leu Ala Gly Ser Arg Ile Gly Ala Phe Ser Tyr Gly Ser Gly Leu
                405                 410                 415

Ala Ala Ser Phe Phe Ser Phe Arg Val Ser Gln Asp Ala Ala Pro Gly
            420                 425                 430

Ser Pro Leu Asp Lys Leu Val Ser Ser Thr Ser Asp Leu Pro Lys Arg
        435                 440                 445

Leu Ala Ser Arg Lys Cys Val Ser Pro Glu Glu Phe Thr Glu Ile Met
    450                 455                 460

Asn Gln Arg Glu Gln Phe Tyr His Lys Val Asn Phe Ser Pro Pro Gly
465                 470                 475                 480

Asp Thr Asn Ser Leu Phe Pro Gly Thr Trp Tyr Leu Glu Arg Val Asp
                485                 490                 495

Glu Gln His Arg Arg Lys Tyr Ala Arg Arg Pro Val
            500                 505


<210> 219
<211> 466
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 28; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCS2; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxy-3-methylglutaryl-CoA synthase 2
      (mitochondrial); "

<220>
<221> source
<223> /note="Uniprot ID:  P54868; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439495"

<400> 219
Met Gln Arg Leu Leu Thr Pro Val Lys Arg Ile Leu Gln Leu Thr Arg
```

```
1               5                   10                  15

Ala Val Gln Glu Thr Ser Leu Thr Pro Ala Arg Leu Leu Pro Val Ala
            20                  25                  30

His Gln Arg Phe Ser Thr Ala Ser Ala Val Pro Leu Ala Lys Thr Asp
        35                  40                  45

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

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

Ala Gly Lys Tyr Thr Val Gly Leu Gly Gln Thr Arg Met Gly Phe Cys
                85                  90                  95

Ser Val Gln Glu Asp Ile Asn Ser Leu Cys Leu Thr Val Val Gln Arg
            100                 105                 110

Leu Met Glu Arg Ile Gln Leu Pro Trp Asp Ser Val Gly Arg Leu Glu
        115                 120                 125

Val Gly Thr Glu Thr Ile Ile Asp Lys Ser Lys Ala Val Lys Thr Val
    130                 135                 140

Leu Met Glu Leu Phe Gln Asp Ser Gly Asn Thr Asp Ile Glu Gly Ile
145                 150                 155                 160

Asp Thr Thr Asn Ala Cys Tyr Gly Gly Thr Ala Ser Leu Phe Asn Ala
                165                 170                 175

Ala Asn Trp Met Glu Ser Ser Ser Trp Asp Gly Leu Arg Gly Thr His
            180                 185                 190

Met Glu Asn Val Tyr Asp Phe Tyr Lys Pro Asn Leu Ala Ser Glu Tyr
        195                 200                 205

Pro Ile Val Asp Gly Lys Leu Ser Ile Gln Cys Tyr Leu Arg Ala Leu
    210                 215                 220

Asp Arg Cys Tyr Thr Ser Tyr Arg Lys Lys Ile Gln Asn Gln Trp Lys
225                 230                 235                 240
```

```
Gln Ala Gly Ser Asp Arg Pro Phe Thr Leu Asp Asp Leu Gln Tyr Met
                245                 250                 255

Ile Phe His Thr Pro Phe Cys Lys Met Val Gln Lys Ser Leu Ala Arg
            260                 265                 270

Leu Met Phe Asn Asp Phe Leu Ser Ala Ser Ser Asp Thr Gln Thr Ser
        275                 280                 285

Leu Tyr Lys Gly Leu Glu Ala Phe Gly Gly Leu Lys Leu Glu Asp Thr
    290                 295                 300

Tyr Thr Asn Lys Asp Leu Asp Lys Ala Leu Leu Lys Ala Ser Gln Asp
305                 310                 315                 320

Met Phe Asp Lys Lys Thr Lys Ala Ser Leu Tyr Leu Ser Thr His Asn
                325                 330                 335

Gly Asn Met Tyr Thr Ser Ser Leu Tyr Gly Cys Leu Ala Ser Leu Leu
            340                 345                 350

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

Ser Tyr Gly Ser Gly Leu Ala Ala Ser Phe Phe Ser Phe Arg Val Ser
    370                 375                 380

Gln Asp Ala Ala Pro Gly Ser Pro Leu Asp Lys Leu Val Ser Ser Thr
385                 390                 395                 400

Ser Asp Leu Pro Lys Arg Leu Ala Ser Arg Lys Cys Val Ser Pro Glu
                405                 410                 415

Glu Phe Thr Glu Ile Met Asn Gln Arg Glu Gln Phe Tyr His Lys Val
            420                 425                 430

Asn Phe Ser Pro Pro Gly Asp Thr Asn Ser Leu Phe Pro Gly Thr Trp
        435                 440                 445

Tyr Leu Glu Arg Val Asp Glu Gln His Arg Arg Lys Tyr Ala Arg Arg
    450                 455                 460
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Pro Val
465

<210> 220
<211> 158
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 29; "

<220>
<221> source
<223> /note="Gene Symbol: HACD1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000322923"

<400> 220
Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala
1 5 10 15

Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr
20 25 30

Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr
35 40 45

Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Glu
50 55 60

Arg Arg Arg Leu Gly Val Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp
65 70 75 80

Ile Ala Met Thr Ala Gly Arg Arg Leu Ile Leu Ser Pro Arg Leu Glu
85 90 95

Cys Ile Gly Ala Ile Ser Ala His Cys Gln Pro Gln Pro Pro Glu Phe
100 105 110

Lys Arg Phe Ser Cys Leu Gly Leu Arg Ser Ser Trp Asp Tyr Lys Arg

```
        115                 120                 125

Gly Pro Pro Arg Pro Ile Asn Phe Cys Ile Phe Gly Arg Asp Arg Val
    130                 135                 140

Ser Pro Cys Trp Pro Gly Trp Ser Arg Thr Pro Asp Leu Lys
145                 150                 155


<210> 221
<211> 288
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 29; "

<220>
<221> source
<223> /note="Gene Symbol: HACD1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  B0YJ81; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355308"

<400> 221
Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala
1               5                   10                  15

Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr
            20                  25                  30

Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr
        35                  40                  45

Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Glu
    50                  55                  60

Arg Arg Arg Leu Gly Val Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp
65                  70                  75                  80
```

```
Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg
                85                  90                  95

Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln
            100                 105                 110

Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His
        115                 120                 125

Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln
    130                 135                 140

Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys
145                 150                 155                 160

Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr
                165                 170                 175

Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp
            180                 185                 190

His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile
        195                 200                 205

Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala
    210                 215                 220

Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn
225                 230                 235                 240

Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met
                245                 250                 255

Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg
            260                 265                 270

Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys Asp Asp
        275                 280                 285
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<210> 222
<211> 174
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 29; "

<220>
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<223> /note="Gene Symbol: HACD1; "

<220>
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<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462336"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 222
Xaa Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr Asn Gly
1 5 10 15

Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Glu Arg Arg
20 25 30

Arg Leu Gly Val Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp Ile Ala
35 40 45

Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg Phe Tyr
50 55 60

Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln Lys Thr
65 70 75 80

Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His Cys Leu
85 90 95

Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln Val Ser
100 105 110

Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys Pro Ile
115 120 125

Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr Val Thr
    130   135   140

Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp His Leu
145   150   155   160

Pro Tyr Phe Ile Lys Trp Ala Arg Trp Arg Tyr Leu Ala Val
                165   170

<210> 223
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 29; "

<220>
<221> source
<223> /note="Gene Symbol: HACD1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462868"

<400> 223
Ile Val His Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr
1   5   10   15

Gly Val Gln Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His
            20   25   30

Ser Ile Lys Pro Ile
        35

<210> 224
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 30; "

<220>

<221> source
<223> /note="Gene Symbol: HACD2; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6Y1H2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373153"

<400> 224

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

```
Pro Tyr Leu Ile Lys Trp Ala Arg Tyr Thr Leu Phe Ile Val Leu Tyr
                165                 170                 175

Pro Met Gly Val Ser Gly Glu Leu Leu Thr Ile Tyr Ala Ala Leu Pro
            180                 185                 190

Phe Val Arg Gln Ala Gly Leu Tyr Ser Ile Ser Leu Pro Asn Lys Tyr
        195                 200                 205

Asn Phe Ser Phe Asp Tyr Tyr Ala Phe Leu Ile Leu Ile Met Ile Ser
    210                 215                 220

Tyr Ile Pro Ile Phe Pro Gln Leu Tyr Phe His Met Ile His Gln Arg
225                 230                 235                 240

Arg Lys Ile Leu Ser His Thr Glu Glu His Lys Lys Phe Glu
                245                 250


<210> 225
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 30; "

<220>
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<223> /note="Gene Symbol: HACD2; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417567"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 225
Xaa Tyr Thr Leu Phe Ile Val Leu Tyr Pro Met Gly Val Ser Gly Glu
1               5                   10                  15
```

```
Leu Leu Thr Ile Tyr Ala Ala Leu Pro Phe Val Arg Gln Ala Gly Leu
            20                  25                  30

Tyr Ser Ile Ser Leu Pro Asn Lys Tyr Asn Phe Ser Phe Asp Tyr Tyr
        35                  40                  45

Ala Phe Leu Ile Leu Ile Met Ile Ser Tyr Ile Pro Ser
    50                  55                  60


<210> 226
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 30; "

<220>
<221> source
<223> /note="Gene Symbol: HACD2; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419237"

<400> 226
Met Ser Arg Val Phe Leu Ile Trp Ala Val Thr His Ser Val Lys Glu
1               5                   10                  15

Val Gln Ser Glu Asp Ser Val Leu Leu Phe Val Ile Ala Trp Thr Ile
            20                  25                  30

Thr Glu Ile Ile Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asn His
        35                  40                  45

Leu Pro Tyr Leu Ile Lys Trp Ala Arg Tyr Thr Leu Phe Ile Val Leu
    50                  55                  60

Tyr Pro Met Gly Val Ser Gly Glu Leu Leu Thr Ile Tyr Ala Ala Leu
65                  70                  75                  80

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

<210> 227
<211> 362
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 31; "

<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9P035; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000261875"

<400> 227
Met Glu Asn Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His
1   5   10   15

Arg Glu Leu Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala
            20   25   30

Ile Ser Ile Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly
        35   40   45

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

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

Thr Val Gln Lys Lys Val Ser Gln Trp Trp Glu Arg Leu Thr Lys Gln
                85   90   95

```
Glu Lys Arg Pro Leu Phe Leu Ala Pro Asp Phe Asp Arg Trp Leu Asp
            100                 105                 110

Glu Ser Asp Ala Glu Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu
        115                 120                 125

Asn Lys Leu Arg Leu Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn
    130                 135                 140

Leu Arg Lys Gly Tyr Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly
145                 150                 155                 160

Phe Ser Trp Ile Phe Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly
                165                 170                 175

Lys Glu Ser Phe Tyr Asp Thr Phe His Thr Val Ala Asp Met Met Tyr
            180                 185                 190

Phe Cys Gln Met Leu Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly
        195                 200                 205

Val Thr Thr Ser Pro Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg
    210                 215                 220

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

Lys Ala Val Val Phe Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile
                245                 250                 255

Phe Arg Tyr Ser Phe Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys
            260                 265                 270

Val Leu Thr Trp Leu Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu
        275                 280                 285

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

Asn Glu Thr Gly Arg Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile
305                 310                 315                 320

Lys Val Arg Phe Ser Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe
```

```
                325                 330                 335

Leu Gly Leu Tyr Ile Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg
            340                 345                 350

Arg Tyr Gly Gln Lys Lys Lys Lys Ile His
        355                 360


<210> 228
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 31; "

<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
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<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9P035; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392491"

<400> 228
Met Glu Asn Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His
1               5                   10                  15

Arg Glu Leu Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala
            20                  25                  30

Ile Ser Ile Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly
        35                  40                  45

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

Val Lys Pro Glu Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu Glu Ser
65                  70                  75                  80
```

```
Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr Leu Phe
                85                  90                  95

Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe Val Asn
            100                 105                 110

Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr Asp Thr
        115                 120                 125

Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu Ala Val
    130                 135                 140

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

Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe Ile Ile
                165                 170                 175

Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe Phe Val
            180                 185                 190

Phe Tyr Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe Tyr Met
        195                 200                 205

Leu Thr Cys Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu Arg Tyr
    210                 215                 220

Thr Leu Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu Ala Val
225                 230                 235                 240

Ser Val Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg Phe Ser
                245                 250                 255

Phe Thr Leu Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser Phe Phe
            260                 265                 270

Leu Gln Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile Asn Phe
        275                 280                 285

Arg His Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys Lys Lys
    290                 295                 300
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Lys Ile His
305

<210> 229
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 31; "

<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454610"

<400> 229
Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu
1 5 10 15

Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr
20 25 30

Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe
35 40 45

Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr
50 55 60

Asp Thr Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu
65 70 75 80

Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro
85 90 95

Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe
100 105 110

Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe
115 120 125

```
Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile
    130                 135


<210> 230
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 31; "

<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454873"

<400> 230
Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu
1               5                   10                  15


Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr
            20                  25                  30


Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe
        35                  40                  45


Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr
    50                  55                  60


Asp Thr Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu
65                  70                  75                  80


Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro
                85                  90                  95


Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe
            100                 105                 110
```

```
Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe
        115                 120                 125

Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe
    130                 135                 140

Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu
145                 150                 155                 160

Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu
                165                 170                 175

Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg
            180                 185                 190

Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser
        195                 200                 205

Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile
    210                 215                 220

Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys
225                 230                 235                 240

Lys Lys Lys Ile His
                245


<210> 231
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 31; "

<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455530"
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<400> 231
Met Glu Asn Gln Asn Pro Ala Ile Ser Ile Thr Glu Asn Val Leu His
1 5 10 15

Phe Lys Ala Gln Gly His Gly Ala Lys Gly Asp Asn Val Tyr Glu Phe
20 25 30

His Leu Glu Phe Leu Asp Leu Val Lys Pro Glu Pro Val Tyr Lys Leu
35 40 45

Thr Gln Arg Gln Val Asn Ile Thr Val Gln Lys Lys Val Ser Gln Trp
50 55 60

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

Asp Phe Asp Arg Trp Leu Asp Glu Ser Asp Ala Glu Met Glu Leu Arg
85 90 95

Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu Glu Ser Glu Gly
100 105 110

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

Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe Val Asn Leu Thr
130 135 140

Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr Asp Thr Phe His
145 150 155 160

Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu Ala Val Val Glu
165 170 175

Thr Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro Val Leu Pro Ser
180 185 190

Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe Ile Ile Phe Gly
195 200 205

Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe Phe Val Phe Tyr
210 215 220

```
Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe Tyr Met Leu Thr
225                 230                 235                 240

Cys Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu Arg Tyr Thr Leu
                245                 250                 255

Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu Ala Val Ser Val
            260                 265                 270

Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg Phe Ser Phe Thr
        275                 280                 285

Leu Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser Phe Phe Leu Gln
    290                 295                 300

Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile Asn Phe Arg His
305                 310                 315                 320

Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys Lys Lys Lys Ile
                325                 330                 335

His
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<210> 232
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 31; "

<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455587"

<400> 232

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Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu
```

```
1               5                   10                  15

Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr
            20                  25                  30

Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe
        35                  40                  45

Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr
    50                  55                  60

Asp Thr Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu
65                  70                  75                  80

Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro
                85                  90                  95

Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe
            100                 105                 110

Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe
        115                 120                 125

Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe
    130                 135                 140

Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu
145                 150                 155                 160

Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu
                165                 170                 175

Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg
            180                 185                 190

Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser
        195                 200                 205

Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile
    210                 215                 220

Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys
225                 230                 235                 240
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Lys Lys Lys Ile His
245

<210> 233
<211> 245
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 31; "

<220>
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<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455686"

<400> 233
Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu
1 5 10 15

Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr
20 25 30

Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe
35 40 45

Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr
50 55 60

Asp Thr Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu
65 70 75 80

Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro
85 90 95

Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe
100 105 110

```
Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe
        115                 120                 125

Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe
    130                 135                 140

Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu
145                 150                 155                 160

Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu
                165                 170                 175

Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg
            180                 185                 190

Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser
        195                 200                 205

Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile
    210                 215                 220

Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys
225                 230                 235                 240

Lys Lys Lys Ile His
                245


<210> 234
<211> 245
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000456300"
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<400> 234
Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu
1 5 10 15

Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr
20 25 30

Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe
35 40 45

Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr
50 55 60

Asp Thr Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu
65 70 75 80

Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro
85 90 95

Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe
100 105 110

Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val Val Phe
115 120 125

Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe
130 135 140

Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu
145 150 155 160

Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu
165 170 175

Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg
180 185 190

Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser
195 200 205

Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile
210 215 220

```
Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys
225                 230                 235                 240


Lys Lys Lys Ile His
                245


<210> 235
<211> 400
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: HACD3; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyacyl-CoA dehydratase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456568"

<400> 235
Met Glu Asn Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His
1               5                   10                  15


Arg Glu Leu Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Gly Leu Thr
            20                  25                  30


Leu Leu Pro Arg Leu Glu Cys Ser Ser Val Ile Ile Ala His Arg Ser
        35                  40                  45


Leu Glu Leu Leu Gly Leu Ser Ser Pro Pro Gly Ser Ala Tyr Gln Val
    50                  55                  60


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


Lys Ala Gln Gly His Gly Ala Lys Gly Asp Asn Val Tyr Glu Phe His
                85                  90                  95


Leu Glu Phe Leu Asp Leu Val Lys Pro Glu Pro Val Tyr Lys Leu Thr
```

```
            100                 105                 110

Gln Arg Gln Val Asn Ile Thr Val Gln Lys Lys Val Ser Gln Trp Trp
        115                 120                 125

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

Phe Asp Arg Trp Leu Asp Glu Ser Asp Ala Glu Met Glu Leu Arg Ala
145                 150                 155                 160

Lys Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu Glu Ser Glu Gly Ser
                165                 170                 175

Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr Leu Phe Met Tyr Asn
            180                 185                 190

Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe Val Asn Leu Thr Val
        195                 200                 205

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

Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu Ala Val Val Glu Thr
225                 230                 235                 240

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

Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe Ile Ile Phe Gly Thr
            260                 265                 270

Met Glu Glu Met Gln Asn Lys Ala Val Val Phe Phe Val Phe Tyr Leu
        275                 280                 285

Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe Tyr Met Leu Thr Cys
    290                 295                 300

Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu Arg Tyr Thr Leu Trp
305                 310                 315                 320

Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu Ala Val Ser Val Ile
                325                 330                 335
```

```
Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg Phe Ser Phe Thr Leu
            340                 345                 350

Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser Phe Phe Leu Gln Ile
        355                 360                 365

Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile Asn Phe Arg His Leu
    370                 375                 380

Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys Lys Lys Lys Ile His
385                 390                 395                 400
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<210> 236
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 32; "

<220>
<221> source
<223> /note="Gene Symbol: HACD4; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyacyl-CoA dehydratase 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q5VWC8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419503"

<400> 236

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Met Gly Pro Leu Ala Leu Pro Ala Trp Leu Gln Pro Arg Tyr Arg Lys
1               5                   10                  15

Asn Ala Tyr Leu Phe Ile Tyr Tyr Leu Ile Gln Phe Cys Gly His Ser
            20                  25                  30

Trp Ile Phe Thr Asn Met Thr Val Arg Phe Phe Ser Phe Gly Lys Asp
        35                  40                  45
```

```
Ser Met Val Asp Thr Phe Tyr Ala Ile Gly Leu Val Met Arg Leu Cys
    50                  55                  60

Gln Ser Val Ser Leu Leu Glu Leu Leu His Ile Tyr Val Gly Ile Glu
65                  70                  75                  80

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

Ile Leu Phe Val Val Ile Thr Ser Gln Glu Glu Val Gln Glu Lys Tyr
            100                 105                 110

Val Val Cys Val Leu Phe Val Phe Trp Asn Leu Leu Asp Met Val Arg
        115                 120                 125

Tyr Thr Tyr Ser Met Leu Ser Val Ile Gly Ile Ser Tyr Ala Val Leu
    130                 135                 140

Thr Trp Leu Ser Gln Thr Leu Trp Met Pro Ile Tyr Pro Leu Cys Val
145                 150                 155                 160

Leu Ala Glu Ala Phe Ala Ile Tyr Gln Ser Leu Pro Tyr Phe Glu Ser
                165                 170                 175

Phe Gly Thr Tyr Ser Thr Lys Leu Pro Phe Asp Leu Ser Ile Tyr Phe
            180                 185                 190

Pro Tyr Val Leu Lys Ile Tyr Leu Met Met Leu Phe Ile Gly Met Tyr
        195                 200                 205

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

Phe Pro Ile Lys Lys Lys Lys Met
225                 230


<210> 237
<211> 286
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 33; "
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<220>
<221> source
<223> /note="Gene Symbol: HAAO; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyanthranilate 3,4-dioxygenase; "

<220>
<221> source
<223> /note="Uniprot ID: P46952; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000294973"

<400> 237
Met Glu Arg Arg Leu Gly Val Arg Ala Trp Val Lys Glu Asn Arg Gly
1   5   10   15

Ser Phe Gln Pro Pro Val Cys Asn Lys Leu Met His Gln Glu Gln Leu
            20   25   30

Lys Val Met Phe Ile Gly Gly Pro Asn Thr Arg Lys Asp Tyr His Ile
        35   40   45

Glu Glu Gly Glu Glu Val Phe Tyr Gln Leu Glu Gly Asp Met Val Leu
    50   55   60

Arg Val Leu Glu Gln Gly Lys His Arg Asp Val Val Ile Arg Gln Gly
65   70   75   80

Glu Ile Phe Leu Leu Pro Ala Arg Val Pro His Ser Pro Gln Arg Phe
                85   90   95

Ala Asn Thr Val Gly Leu Val Val Glu Arg Arg Arg Leu Glu Thr Glu
            100   105   110

Leu Asp Gly Leu Arg Tyr Tyr Val Gly Asp Thr Met Asp Val Leu Phe
        115   120   125

Glu Lys Trp Phe Tyr Cys Lys Asp Leu Gly Thr Gln Leu Ala Pro Ile
    130   135   140

Ile Gln Glu Phe Phe Ser Ser Glu Gln Tyr Arg Thr Gly Lys Pro Ile
145   150   155   160

```
Pro Asp Gln Leu Leu Lys Glu Pro Pro Phe Pro Leu Ser Thr Arg Ser
                165                 170                 175

Ile Met Glu Pro Met Ser Leu Asp Ala Trp Leu Asp Ser His His Arg
            180                 185                 190

Glu Leu Gln Ala Gly Thr Pro Leu Ser Leu Phe Gly Asp Thr Tyr Glu
        195                 200                 205

Thr Gln Val Ile Ala Tyr Gly Gln Gly Ser Ser Glu Gly Leu Arg Gln
    210                 215                 220

Asn Val Asp Val Trp Leu Trp Gln Leu Glu Gly Ser Ser Val Val Thr
225                 230                 235                 240

Met Gly Gly Arg Arg Leu Ser Leu Ala Pro Asp Asp Ser Leu Leu Val
                245                 250                 255

Leu Ala Gly Thr Ser Tyr Ala Trp Glu Arg Thr Gln Gly Ser Val Ala
            260                 265                 270

Leu Ser Val Thr Gln Asp Pro Ala Cys Lys Lys Pro Leu Gly
        275                 280                 285


<210> 238
<211> 176
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 33; "

<220>
<221> source
<223> /note="Gene Symbol: HAAO; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyanthranilate 3,4-dioxygenase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412601"

<400> 238
Met Phe Ile Gly Gly Pro Asn Thr Arg Lys Asp Tyr His Ile Glu Glu
```

```
1               5                   10                  15

Gly Glu Glu Val Phe Tyr Gln Leu Glu Gly Asp Met Val Leu Arg Val
            20                  25                  30

Leu Glu Gln Gly Lys His Arg Asp Val Val Ile Arg Gln Gly Glu Ile
        35                  40                  45

Phe Leu Leu Pro Ala Arg Val Pro His Ser Pro Gln Arg Phe Ala Asn
    50                  55                  60

Thr Val Gly Leu Val Val Glu Arg Arg Arg Leu Glu Thr Glu Leu Asp
65                  70                  75                  80

Gly Leu Arg Tyr Tyr Val Gly Asp Thr Met Asp Val Leu Phe Glu Lys
                85                  90                  95

Trp Phe Tyr Cys Lys Asp Leu Gly Thr Gln Leu Ala Pro Ile Ile Gln
            100                 105                 110

Glu Phe Phe Ser Ser Glu Gln Tyr Arg Thr Gly Lys Pro Ile Pro Asp
        115                 120                 125

Gln Leu Leu Lys Glu Pro Pro Phe Pro Leu Ser Thr Arg Ser Ile Met
    130                 135                 140

Glu Pro Met Ser Leu Asp Ala Trp Leu Asp Ser His His Arg Glu Leu
145                 150                 155                 160

Gln Ala Gly Thr Pro Leu Ser Leu Phe Gly Asp Thr Tyr Glu Thr Gln
                165                 170                 175


<210> 239
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
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<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q02338; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000350914"

<400> 239

```
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1               5                  10                  15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
            20                  25                  30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
        35                  40                  45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
    50                  55                  60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65                  70                  75                  80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
                85                  90                  95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
            100                 105                 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
        115                 120                 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
    130                 135                 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
                165                 170                 175
```

```
Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Arg Val Val Asn
            180                 185                 190

Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr
        195                 200                 205

Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr
    210                 215                 220

Glu Met Tyr Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly Asn
225                 230                 235                 240

Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile
                245                 250                 255

Ala Lys Lys Met Trp Glu Glu Leu Pro Glu Val Val Arg Lys Asp Tyr
            260                 265                 270

Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys
        275                 280                 285

Ser Ser Gly Ser Thr Asp Thr Ser Pro Val Ile Asp Ala Val Thr His
    290                 295                 300

Ala Leu Thr Ala Thr Thr Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr
305                 310                 315                 320

Tyr Trp Trp Leu Arg Met Gln Ile Met Thr His Leu Pro Gly Ala Ile
                325                 330                 335

Ser Asp Met Ile Tyr Ile Arg
            340
```

<210> 240
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q02338; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376183"

<400> 240
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1 5 10 15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
20 25 30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
35 40 45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
50 55 60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65 70 75 80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
85 90 95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
100 105 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
115 120 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
130 135 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
165 170 175

```
Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Arg Val Val Asn
            180                 185                 190

Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr
        195                 200                 205

Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr
    210                 215                 220

Glu Met Tyr Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly Asn
225                 230                 235                 240

Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile
                245                 250                 255

Ala Lys Lys Met Trp Glu Glu Leu Pro Glu Val Val Arg Lys Asp Tyr
            260                 265                 270

Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys
        275                 280                 285

Ser Ser Gly Ser Thr Asp Thr Ser Pro Val Ile Asp Ala Val Thr His
    290                 295                 300

Ala Leu Thr Ala Thr Thr Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr
305                 310                 315                 320

Tyr Trp Trp Leu Arg Met Gln Ile Met Thr His Leu Pro Gly Ala Ile
                325                 330                 335

Ser Asp Met Ile Tyr Ile Arg
            340
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<210> 241
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q02338; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376184"

<400> 241

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

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
            20                  25                  30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
        35                  40                  45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
    50                  55                  60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65                  70                  75                  80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
                85                  90                  95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
            100                 105                 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
        115                 120                 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
    130                 135                 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
                165                 170                 175
```

```
Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Arg Val Val Asn
            180                 185                 190

Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr
        195                 200                 205

Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr
    210                 215                 220

Glu Met Tyr Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly Asn
225                 230                 235                 240

Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile
                245                 250                 255

Ala Lys Lys Met Trp Glu Glu Leu Pro Glu Val Val Arg Lys Asp Tyr
            260                 265                 270

Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys
        275                 280                 285

Ser Ser Gly Ser Thr Asp Thr Ser Pro Val Ile Asp Ala Val Thr His
    290                 295                 300

Ala Leu Thr Ala Thr Thr Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr
305                 310                 315                 320

Tyr Trp Trp Leu Arg Met Gln Ile Met Thr His Leu Pro Gly Ala Ile
                325                 330                 335

Ser Asp Met Ile Tyr Ile Arg
            340
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<210> 242
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source

<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387648"

<400> 242

```
Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu Asp Ser Leu Asn
1               5                  10                  15

Ser Asp Arg Leu Arg Thr Val Gln Leu Asn Val Cys Ser Ser Glu Glu
            20                  25                  30

Val Glu Lys Val Val Glu Ile Val Arg Ser Ser Leu Lys Asp Pro Glu
        35                  40                  45

Lys Gly Met Trp Gly Leu Val Asn Asn Ala Gly Ile Ser Thr Phe Gly
    50                  55                  60

Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln Val Ala Glu Val
65                  70                  75                  80

Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe Leu Pro Leu Ile
                85                  90                  95

Arg Arg Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly Arg
            100                 105                 110

Met Ala Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly Val
        115                 120                 125

Glu Ala Phe Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly Val
    130                 135                 140

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

Tyr Ser Pro Glu Ser Ile
                165
```

<210> 243

<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396149"

<400> 243
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1 5 10 15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
20 25 30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
35 40 45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
50 55 60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65 70 75 80

Leu Val Phe Ala Gly Cys Leu Met Lys
85

<210> 244
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source

<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405462"

<400> 244
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1 5 10 15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
20 25 30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
35 40 45

Ala Ala
50

<210> 245
<211> 129
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 34; "

<220>
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<223> /note="Gene Symbol: BDH1; "

<220>
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<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
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<223> /note="ENSP ID: ENSP00000408016"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 245

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

Thr Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met
            20                  25                  30

Thr Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Glu Trp Glu
        35                  40                  45

Arg Glu Leu Pro Pro Ala Pro Glu Pro Ala Pro Arg Val His Leu Cys
    50                  55                  60

Ser Glu Trp Lys Tyr Leu Ser Gln Gln Leu Gln Cys Pro Gln Leu Ser
65                  70                  75                  80

Arg Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly Arg Met Ala Asn
                85                  90                  95

Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly Val Glu Ala Phe
            100                 105                 110

Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly Val Lys Val Ser
        115                 120                 125

Val
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<210> 246
<211> 168
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
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<223> /note="ENSP ID: ENSP00000408685"

<400> 246
Met Ala Ser Asn Gly Ile Gln Lys Arg Arg Pro Leu Leu Leu Gly Ser
1 5 10 15

Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser Ala Ala Glu
20 25 30

Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp Ser Gly Phe
35 40 45

Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe Leu Val Phe
50 55 60

Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu
65 70 75 80

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

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

Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn Ala Gly Ile
115 120 125

Ser Thr Phe Gly Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln
130 135 140

Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe
145 150 155 160

Leu Pro Leu Ile Arg Arg Ala Lys
165

<210> 247
<211> 186
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: BDH1; "

<220>
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<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000409849"

<400> 247

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

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
            20                  25                  30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
        35                  40                  45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
    50                  55                  60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65                  70                  75                  80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
                85                  90                  95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
            100                 105                 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
        115                 120                 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
    130                 135                 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
                165                 170                 175

Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala
```

180 185

<210> 248
<211> 256
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 34; "

<220>
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<223> /note="Gene Symbol: BDH1; "

<220>
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<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000411014"

<400> 248
Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu Asp Ser Leu Asn
1 5 10 15

Ser Asp Arg Leu Arg Thr Val Gln Leu Asn Val Cys Ser Ser Glu Glu
20 25 30

Val Glu Lys Val Val Glu Ile Val Arg Ser Ser Leu Lys Asp Pro Glu
35 40 45

Lys Gly Met Trp Gly Leu Val Asn Asn Ala Gly Ile Ser Thr Phe Gly
50 55 60

Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln Val Ala Glu Val
65 70 75 80

Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe Leu Pro Leu Ile
85 90 95

Arg Arg Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly Arg
100 105 110

Met Ala Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly Val
115 120 125

```
Glu Ala Phe Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly Val
    130                 135                 140

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

Tyr Ser Pro Glu Ser Ile Gln Ala Ile Ala Lys Lys Met Trp Glu Glu
                165                 170                 175

Leu Pro Glu Val Val Arg Lys Asp Tyr Gly Lys Lys Tyr Phe Asp Glu
            180                 185                 190

Lys Ile Ala Lys Met Glu Thr Tyr Cys Ser Ser Gly Ser Thr Asp Thr
        195                 200                 205

Ser Pro Val Ile Asp Ala Val Thr His Ala Leu Thr Ala Thr Thr Pro
    210                 215                 220

Tyr Thr Arg Tyr His Pro Met Asp Tyr Tyr Trp Trp Leu Arg Met Gln
225                 230                 235                 240

Ile Met Thr His Leu Pro Gly Ala Ile Ser Asp Met Ile Tyr Ile Arg
                245                 250                 255


<210> 249
<211> 343
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
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<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 1; "

<220>
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<223> /note="Uniprot ID:  Q02338; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000482744"

<400> 249

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

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
            20                  25                  30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
        35                  40                  45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
    50                  55                  60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65                  70                  75                  80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
                85                  90                  95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
            100                 105                 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
        115                 120                 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
    130                 135                 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
                165                 170                 175

Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Arg Val Val Asn
            180                 185                 190

Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr
        195                 200                 205

Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr
    210                 215                 220
```

```
Glu Met Tyr Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly Asn
225                 230                 235                 240

Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile
                245                 250                 255

Ala Lys Lys Met Trp Glu Glu Leu Pro Glu Val Val Arg Lys Asp Tyr
            260                 265                 270

Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys
        275                 280                 285

Ser Ser Gly Ser Thr Asp Thr Ser Pro Val Ile Asp Ala Val Thr His
    290                 295                 300

Ala Leu Thr Ala Thr Thr Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr
305                 310                 315                 320

Tyr Trp Trp Leu Arg Met Gln Ile Met Thr His Leu Pro Gly Ala Ile
                325                 330                 335

Ser Asp Met Ile Tyr Ile Arg
            340


<210> 250
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
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<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 1; "

<220>
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<223> /note="Uniprot ID:  Q02338; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000484421"

<400> 250
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1 5 10 15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
20 25 30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
35 40 45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
50 55 60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65 70 75 80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
85 90 95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
100 105 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
115 120 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
130 135 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
165 170 175

Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys Gly Arg Val Val Asn
180 185 190

Ile Ser Ser Met Leu Gly Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr
195 200 205

Cys Ile Thr Lys Phe Gly Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr

```
    210                 215                 220

Glu Met Tyr Pro Leu Gly Val Lys Val Ser Val Val Glu Pro Gly Asn
225                 230                 235                 240

Phe Ile Ala Ala Thr Ser Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile
                245                 250                 255

Ala Lys Lys Met Trp Glu Glu Leu Pro Glu Val Val Arg Lys Asp Tyr
            260                 265                 270

Gly Lys Lys Tyr Phe Asp Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys
        275                 280                 285

Ser Ser Gly Ser Thr Asp Thr Ser Pro Val Ile Asp Ala Val Thr His
    290                 295                 300

Ala Leu Thr Ala Thr Thr Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr
305                 310                 315                 320

Tyr Trp Trp Leu Arg Met Gln Ile Met Thr His Leu Pro Gly Ala Ile
                325                 330                 335

Ser Asp Met Ile Tyr Ile Arg
            340


<210> 251
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
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<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485973"
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<400> 251
Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu Asp Ser Leu Asn
1 5 10 15

Ser Asp Arg Leu Arg Thr Val Gln Leu Asn Val Cys Ser Ser Glu Glu
20 25 30

Val Glu Lys Val Val Glu Ile Val Arg Ser Ser Leu Lys Asp Pro Glu
35 40 45

Lys Gly Met Trp Gly Leu Val Asn Asn Ala Gly Ile Ser Thr Phe Gly
50 55 60

Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln Val Ala Glu Val
65 70 75 80

Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe Leu Pro Leu Ile
85 90 95

Arg Arg Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly Arg
100 105 110

Met Ala Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly Val
115 120 125

Glu Ala Phe Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly Val
130 135 140

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

Tyr Ser Pro Glu Ser Ile
165

<210> 252
<211> 256
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486316"

<400> 252
Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu Asp Ser Leu Asn
1 5 10 15

Ser Asp Arg Leu Arg Thr Val Gln Leu Asn Val Cys Ser Ser Glu Glu
20 25 30

Val Glu Lys Val Val Glu Ile Val Arg Ser Ser Leu Lys Asp Pro Glu
35 40 45

Lys Gly Met Trp Gly Leu Val Asn Asn Ala Gly Ile Ser Thr Phe Gly
50 55 60

Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln Val Ala Glu Val
65 70 75 80

Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe Leu Pro Leu Ile
85 90 95

Arg Arg Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly Arg
100 105 110

Met Ala Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly Val
115 120 125

Glu Ala Phe Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly Val
130 135 140

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

Tyr Ser Pro Glu Ser Ile Gln Ala Ile Ala Lys Lys Met Trp Glu Glu
165 170 175

Leu Pro Glu Val Val Arg Lys Asp Tyr Gly Lys Lys Tyr Phe Asp Glu
180 185 190

```
Lys Ile Ala Lys Met Glu Thr Tyr Cys Ser Ser Gly Ser Thr Asp Thr
        195                 200                 205

Ser Pro Val Ile Asp Ala Val Thr His Ala Leu Thr Ala Thr Thr Pro
    210                 215                 220

Tyr Thr Arg Tyr His Pro Met Asp Tyr Tyr Trp Trp Leu Arg Met Gln
225                 230                 235                 240

Ile Met Thr His Leu Pro Gly Ala Ile Ser Asp Met Ile Tyr Ile Arg
                245                 250                 255


<210> 253
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486552"

<400> 253
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1               5                   10                  15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
            20                  25                  30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
        35                  40                  45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
    50                  55                  60
```

```
Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65                  70                  75                  80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
                85                  90                  95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
            100                 105                 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
        115                 120                 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
    130                 135                 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
                165                 170                 175

Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala
            180                 185


<210> 254
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486776"

<400> 254
Met Ala Ser Asn Gly Ile Gln Lys Arg Arg Pro Leu Leu Leu Gly Ser
1               5                   10                  15
```

```
Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser Ala Ala Glu
            20                  25                  30

Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp Ser Gly Phe
        35                  40                  45

Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe Leu Val Phe
    50                  55                  60

Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu
65                  70                  75                  80

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

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

Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn Ala Gly Ile
        115                 120                 125

Ser Thr Phe Gly Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln
    130                 135                 140

Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe
145                 150                 155                 160

Leu Pro Leu Ile Arg Arg Ala Lys
                165
```

<210> 255
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source

<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487163"

<400> 255

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

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
            20                  25                  30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
        35                  40                  45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
    50                  55                  60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65                  70                  75                  80

Leu Val Phe Ala Gly Cys Leu Met Lys Asp Lys Gly His Asp Gly Val
                85                  90                  95

Lys Glu Leu Asp Ser Leu Asn Ser Asp Arg Leu Arg Thr Val Gln Leu
            100                 105                 110

Asn Val Cys Ser Ser Glu Glu Val Glu Lys Val Val Glu Ile Val Arg
        115                 120                 125

Ser Ser Leu Lys Asp Pro Glu Lys Gly Met Trp Gly Leu Val Asn Asn
    130                 135                 140

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

Tyr Lys Gln Val Ala Glu Val Asn Leu Trp Gly Thr Val Arg Met Thr
                165                 170                 175

Lys Ser Phe Leu Pro Leu Ile Arg Arg Ala Lys
            180                 185
```

<210> 256

<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 34; "

<220>
<221> source
<223> /note="Gene Symbol: BDH1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487308"

<400> 256
Met Leu Ala Thr Arg Leu Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys
1 5 10 15

Thr Leu Ser Ala Cys Asp Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu
20 25 30

Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser
35 40 45

Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr Gly Cys Asp
50 55 60

Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser Lys Gly Phe
65 70 75 80

Leu Val Phe Ala Gly Cys Leu Met Lys
85

<210> 257
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 35; "

<220>
<221> source

<223> /note="Gene Symbol: BDH2; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BUT1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000296424"

<400> 257

```
Met Gly Arg Leu Asp Gly Lys Val Ile Ile Leu Thr Ala Ala Ala Gln
1               5                   10                  15

Gly Ile Gly Gln Ala Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys
            20                  25                  30

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

Tyr Pro Gly Ile Gln Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln
    50                  55                  60

Ile Asp Gln Phe Ala Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn
65                  70                  75                  80

Val Ala Gly Phe Val His His Gly Thr Val Leu Asp Cys Glu Glu Lys
                85                  90                  95

Asp Trp Asp Phe Ser Met Asn Leu Asn Val Arg Ser Met Tyr Leu Met
            100                 105                 110

Ile Lys Ala Phe Leu Pro Lys Met Leu Ala Gln Lys Ser Gly Asn Ile
        115                 120                 125

Ile Asn Met Ser Ser Val Ala Ser Ser Val Lys Gly Val Val Asn Arg
    130                 135                 140

Cys Val Tyr Ser Thr Thr Lys Ala Ala Val Ile Gly Leu Thr Lys Ser
145                 150                 155                 160

Val Ala Ala Asp Phe Ile Gln Gln Gly Ile Arg Cys Asn Cys Val Cys
```

```
                165                 170                 175

Pro Gly Thr Val Asp Thr Pro Ser Leu Gln Glu Arg Ile Gln Ala Arg
            180                 185                 190

Gly Asn Pro Glu Glu Ala Arg Asn Asp Phe Leu Lys Arg Gln Lys Thr
        195                 200                 205

Gly Arg Phe Ala Thr Ala Glu Glu Ile Ala Met Leu Cys Val Tyr Leu
    210                 215                 220

Ala Ser Asp Glu Ser Ala Tyr Val Thr Gly Asn Pro Val Ile Ile Asp
225                 230                 235                 240

Gly Gly Trp Ser Leu
                245


<210> 258
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 35; "

<220>
<221> source
<223> /note="Gene Symbol: BDH2; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421516"

<400> 258
Met Gly Arg Leu Asp Gly Lys Val Ile Ile Leu Thr Ala Ala Ala Gln
1               5                   10                  15

Gly Ile Gly Gln Ala Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys
            20                  25                  30

Val Ile Ala Thr Asp Ile Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys
        35                  40                  45
```

```
Tyr Pro Gly Ile Gln Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln
    50                  55                  60

Ile Asp Gln Phe Ala Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn
65                  70                  75                  80

Val Ala Gly Val Cys Leu Gly Ser Pro Gly
                85                  90


<210> 259
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 35; "

<220>
<221> source
<223> /note="Gene Symbol: BDH2; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxybutyrate dehydrogenase, type 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422891"

<400> 259
Met Gly Arg Leu Asp Gly Lys Val Ile Ile Leu Thr Ala Ala Ala Gln
1               5                   10                  15

Gly Ile Gly Gln Ala Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys
            20                  25                  30

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

Tyr Pro Gly Ile Gln Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln
    50                  55                  60

Ile Asp Gln Phe Ala Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn
65                  70                  75                  80

Val Ala Gly Phe Val His His Gly Thr Val Leu Asp Cys Glu Glu Lys
```

```
                85                  90                  95

Asp Trp Asp Phe Ser Met Asn Leu Asn Val Arg Ser Met Tyr Leu Met
            100                 105                 110

Ile Lys Ala Phe
        115
```

<210> 260
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 35; "

<220>
<221> source
<223> /note="Gene Symbol: BDH2; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424173"

<400> 260

```
Met Gly Arg Leu Asp Gly Lys Val Ile Ile Leu Thr Ala Ala Ala Gln
1               5                  10                  15

Gly Ile Gly Gln Ala Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys
            20                  25                  30

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

Tyr Pro Val Pro Leu Val Leu Phe Phe Arg Tyr Ser Asn Ser Cys Pro
    50                  55                  60
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<210> 261
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 35; "

<220>
<221> source
<223> /note="Gene Symbol: BDH2; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxybutyrate dehydrogenase, type 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427442"

<400> 261

Met	Gly	Arg	Leu	Asp	Gly	Lys	Val	Ile	Ile	Leu	Thr	Ala	Ala	Ala	Gln
1				5				10						15	

Gly	Ile	Gly	Gln	Ala	Ala	Ala	Leu	Ala	Phe	Ala	Arg	Glu	Gly	Ala	Lys
			20					25					30		

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

Tyr	Pro	Gly	Ile	Gln	Thr	Arg	Val	Leu	Asp	Val	Thr	Lys	Lys	Lys	Gln
	50					55					60				

Ile	Asp	Gln	Phe	Ala	Asn	Glu	Val	Glu	Arg	Leu	Asp	Val	Leu	Phe	Asn
65					70					75					80

Val	Ala	Gly	Phe	Val	His	His	Gly	Thr	Val	Leu	Asp	Cys	Glu	Glu	Lys
				85					90					95	

Asp	Trp	Asp	Phe	Ser	Met	Asn	Leu	Asn	Val	Arg	Ser	Met	Tyr	Leu	Met
			100					105					110		

Ile	Lys	Ala	Phe	Leu	Pro	Lys	Met	Leu	Ala	Gln	Lys	Ser	Gly	Asn	Ile
		115					120					125			

Ile	Asn	
	130	

<210> 262
<211> 336
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 36; "

<220>
<221> source
<223> /note="Gene Symbol: HIBADH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyrate dehydrogenase; "

<220>
<221> source
<223> /note="Uniprot ID: P31937; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000265395"

<400> 262
Met Ala Ala Ser Leu Arg Leu Leu Gly Ala Ala Ser Gly Leu Arg Tyr
1   5   10   15

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

Ser Arg Ser Val Ala Ser Lys Thr Pro Val Gly Phe Ile Gly Leu Gly
        35   40   45

Asn Met Gly Asn Pro Met Ala Lys Asn Leu Met Lys His Gly Tyr Pro
    50   55   60

Leu Ile Ile Tyr Asp Val Phe Pro Asp Ala Cys Lys Glu Phe Gln Asp
65   70   75   80

Ala Gly Glu Gln Val Val Ser Ser Pro Ala Asp Val Ala Glu Lys Ala
                85   90   95

Asp Arg Ile Ile Thr Met Leu Pro Thr Ser Ile Asn Ala Ile Glu Ala
            100   105   110

Tyr Ser Gly Ala Asn Gly Ile Leu Lys Lys Val Lys Lys Gly Ser Leu
        115   120   125

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

```
Lys Glu Val Glu Lys Met Gly Ala Val Phe Met Asp Ala Pro Val Ser
145                 150                 155                 160

Gly Gly Val Gly Ala Ala Arg Ser Gly Asn Leu Thr Phe Met Val Gly
                165                 170                 175

Gly Val Glu Asp Glu Phe Ala Ala Ala Gln Glu Leu Leu Gly Cys Met
            180                 185                 190

Gly Ser Asn Val Val Tyr Cys Gly Ala Val Gly Thr Gly Gln Ala Ala
        195                 200                 205

Lys Ile Cys Asn Asn Met Leu Leu Ala Ile Ser Met Ile Gly Thr Ala
    210                 215                 220

Glu Ala Met Asn Leu Gly Ile Arg Leu Gly Leu Asp Pro Lys Leu Leu
225                 230                 235                 240

Ala Lys Ile Leu Asn Met Ser Ser Gly Arg Cys Trp Ser Ser Asp Thr
                245                 250                 255

Tyr Asn Pro Val Pro Gly Val Met Asp Gly Val Pro Ser Ala Asn Asn
            260                 265                 270

Tyr Gln Gly Gly Phe Gly Thr Thr Leu Met Ala Lys Asp Leu Gly Leu
        275                 280                 285

Ala Gln Asp Ser Ala Thr Ser Thr Lys Ser Pro Ile Leu Leu Gly Ser
    290                 295                 300

Leu Ala His Gln Ile Tyr Arg Met Met Cys Ala Lys Gly Tyr Ser Lys
305                 310                 315                 320

Lys Asp Phe Ser Ser Val Phe Gln Phe Leu Arg Glu Glu Glu Thr Phe
                325                 330                 335


<210> 263
<211> 206
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 36; "
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<220>
<221> source
<223> /note="Gene Symbol: HIBADH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyrate dehydrogenase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000390205"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 263
Xaa Glu Leu Pro His Thr Leu Lys Leu Pro Gly Leu Pro Leu Phe Pro
1 5 10 15

Asn Lys Phe Leu Ile Ser Leu Val Leu Leu Ile Leu Val Ser Ser Pro
20 25 30

Ala Asp Val Ala Glu Lys Ala Asp Arg Ile Ile Thr Met Leu Pro Thr
35 40 45

Ser Ile Asn Ala Ile Glu Ala Tyr Ser Gly Ala Asn Gly Ile Leu Lys
50 55 60

Lys Val Lys Lys Gly Ser Leu Leu Ile Asp Ser Ser Thr Ile Asp Pro
65 70 75 80

Ala Val Ser Lys Glu Leu Ala Lys Glu Val Glu Lys Met Gly Ala Val
85 90 95

Phe Met Asp Ala Pro Val Ser Gly Gly Val Gly Ala Ala Arg Ser Gly
100 105 110

Asn Leu Thr Phe Met Val Gly Gly Val Glu Asp Glu Phe Ala Ala Ala
115 120 125

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

```
Val Gly Thr Gly Gln Ala Ala Lys Ile Cys Asn Asn Met Leu Leu Ala
145                 150                 155                 160

Ile Ser Met Ile Gly Thr Ala Glu Ala Met Asn Leu Gly Ile Arg Leu
                165                 170                 175

Gly Leu Asp Pro Lys Leu Leu Ala Lys Ile Leu Asn Met Ser Ser Gly
            180                 185                 190

Arg Cys Trp Ser Ser Asp Thr Tyr Asn Pro Val Pro Gly Val
        195                 200                 205
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<210> 264
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 36; "

<220>
<221> source
<223> /note="Gene Symbol: HIBADH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyrate dehydrogenase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393365"

<400> 264

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Met Ala Ala Ser Leu Arg Leu Leu Gly Ala Ala Ser Gly Leu Arg Tyr
1               5                   10                  15

Trp Ser Arg Arg Leu Arg Pro Ala Ala Gly Ser Phe Ala Ala Gly Ser
            20                  25                  30

Ile Phe Pro Ser Arg Cys Cys
        35
```

<210> 265
<211> 386
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="Uniprot ID: Q6NVY1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000352706"

<400> 265

```
Met Gly Gln Arg Glu Met Trp Arg Leu Met Ser Arg Phe Asn Ala Phe
1               5                  10                  15

Lys Arg Thr Asn Thr Ile Leu His His Leu Arg Met Ser Lys His Thr
            20                  25                  30

Asp Ala Ala Glu Glu Val Leu Leu Glu Lys Lys Gly Cys Thr Gly Val
        35                  40                  45

Ile Thr Leu Asn Arg Pro Lys Phe Leu Asn Ala Leu Thr Leu Asn Met
    50                  55                  60

Ile Arg Gln Ile Tyr Pro Gln Leu Lys Lys Trp Glu Gln Asp Pro Glu
65                  70                  75                  80

Thr Phe Leu Ile Ile Ile Lys Gly Ala Gly Gly Lys Ala Phe Cys Ala
                85                  90                  95

Gly Gly Asp Ile Arg Val Ile Ser Glu Ala Glu Lys Ala Lys Gln Lys
            100                 105                 110

Ile Ala Pro Val Phe Phe Arg Glu Glu Tyr Met Leu Asn Asn Ala Val
        115                 120                 125

Gly Ser Cys Gln Lys Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met
    130                 135                 140
```

```
Gly Gly Gly Val Gly Leu Ser Val His Gly Gln Phe Arg Val Ala Thr
145                 150                 155                 160

Glu Lys Cys Leu Phe Ala Met Pro Glu Thr Ala Ile Gly Leu Phe Pro
                165                 170                 175

Asp Val Gly Gly Gly Tyr Phe Leu Pro Arg Leu Gln Gly Lys Leu Gly
            180                 185                 190

Tyr Phe Leu Ala Leu Thr Gly Phe Arg Leu Lys Gly Arg Asp Val Tyr
        195                 200                 205

Arg Ala Gly Ile Ala Thr His Phe Val Asp Ser Glu Lys Leu Ala Met
    210                 215                 220

Leu Glu Glu Asp Leu Leu Ala Leu Lys Ser Pro Ser Lys Glu Asn Ile
225                 230                 235                 240

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

Lys Ser Phe Ile Leu Glu Glu His Met Asp Lys Ile Asn Ser Cys Phe
            260                 265                 270

Ser Ala Asn Thr Val Glu Glu Ile Ile Glu Asn Leu Gln Gln Asp Gly
        275                 280                 285

Ser Ser Phe Ala Leu Glu Gln Leu Lys Val Ile Asn Lys Met Ser Pro
    290                 295                 300

Thr Ser Leu Lys Ile Thr Leu Arg Gln Leu Met Glu Gly Ser Ser Lys
305                 310                 315                 320

Thr Leu Gln Glu Val Leu Thr Met Glu Tyr Arg Leu Ser Gln Ala Cys
                325                 330                 335

Met Arg Gly His Asp Phe His Glu Gly Val Arg Ala Val Leu Ile Asp
            340                 345                 350

Lys Asp Gln Ser Pro Lys Trp Lys Pro Ala Asp Leu Lys Glu Val Thr
        355                 360                 365

Glu Glu Asp Leu Asn Asn His Phe Lys Ser Leu Gly Ser Ser Asp Leu
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370 375 380

Lys Phe
385

<210> 266
<211> 338
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="Uniprot ID: Q6NVY1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376144"

<400> 266
Met Gly Gln Arg Glu Met Trp Arg Leu Met Ser Arg Phe Asn Ala Phe
1 5 10 15

Lys Arg Thr Asn Thr Ile Leu His His Leu Arg Met Ser Lys His Thr
20 25 30

Asp Ala Ala Glu Glu Val Leu Leu Glu Lys Lys Gly Cys Thr Gly Val
35 40 45

Ile Thr Leu Asn Arg Pro Lys Phe Leu Asn Ala Leu Thr Leu Asn Met
50 55 60

Ile Arg Gln Ile Tyr Pro Gln Leu Lys Lys Trp Glu Gln Asp Pro Glu
65 70 75 80

Thr Phe Leu Ile Ile Ile Lys Gly Ala Gly Gly Lys Ala Phe Cys Ala
85 90 95

```
Gly Gly Asp Ile Arg Val Ile Ser Glu Ala Glu Lys Ala Lys Gln Lys
            100                 105                 110

Ile Ala Pro Val Phe Phe Arg Glu Glu Tyr Met Leu Asn Asn Ala Val
        115                 120                 125

Gly Ser Cys Gln Lys Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met
    130                 135                 140

Gly Gly Gly Val Gly Leu Ser Val His Gly Gln Phe Arg Val Ala Thr
145                 150                 155                 160

Glu Lys Cys Leu Phe Ala Met Pro Glu Thr Ala Ile Gly Leu Phe Pro
                165                 170                 175

Asp Val Gly Gly Gly Tyr Phe Leu Pro Arg Leu Gln Gly Lys Leu Gly
            180                 185                 190

Tyr Phe Leu Ala Leu Thr Gly Phe Arg Leu Lys Gly Arg Asp Val Tyr
        195                 200                 205

Arg Ala Gly Ile Ala Thr His Phe Val Asp Ser Glu Lys Leu Ala Met
    210                 215                 220

Leu Glu Glu Asp Leu Leu Ala Leu Lys Ser Pro Ser Lys Glu Asn Ile
225                 230                 235                 240

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

Lys Ser Phe Ile Leu Glu Glu His Met Asp Lys Ile Asn Ser Cys Phe
            260                 265                 270

Ser Ala Asn Thr Val Glu Glu Ile Ile Glu Asn Leu Gln Gln Asp Gly
        275                 280                 285

Ser Ser Phe Ala Leu Glu Gln Leu Lys Val Ile Asn Lys Met Ser Pro
    290                 295                 300

Thr Ser Leu Lys Ile Thr Leu Arg Gln Leu Met Glu Gly Ser Ser Lys
305                 310                 315                 320
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Thr Leu Gln Glu Val Leu Thr Met Glu Tyr Arg Leu Ser Gln Ala Cys
325 330 335

Met Phe

<210> 267
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376145"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 267
Xaa Ile Ser Glu Ala Glu Lys Ala Lys Gln Lys Ile Ala Pro Val Phe
1 5 10 15

Phe Arg Glu Glu Tyr Met Leu Asn Asn Ala Val Gly Ser Cys Gln Lys
20 25 30

Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met Gly Gly Asp Cys Ser
35 40 45

Leu Met Trp Val Glu Val Ile Ser Cys His Asp Ser Lys Glu Asn Leu
50 55 60

Val Thr Ser Leu His
65

<210> 268
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000386274"

<400> 268
Met Leu Glu Glu Asp Leu Leu Ala Leu Lys Ser Pro Ser Lys Glu Asn
1 5 10 15

Ile Ala Ser Val Leu Glu Asn Tyr His Thr Glu Ser Lys Ile Asp Arg
20 25 30

Asp Lys Ser Phe Ile Leu Glu Glu His Met Asp Lys Ile Asn Ser Cys
35 40 45

Phe Ser Ala Asn Thr Val Glu Glu Ile Ile Glu Asn Leu Gln Gln Asp
50 55 60

Gly Ser Ser Phe Ala Leu Glu Gln Leu Lys Val Ile Asn Lys Met Ser
65 70 75 80

Pro Thr Ser Leu Lys Ile Thr Leu Arg Gln Leu Met Glu Gly Ser Ser
85 90 95

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

Cys Met Arg Gly His Asp Phe His Glu Gly Val Arg Ala Val Leu Ile
115 120 125

Asp Lys Asp Gln Ser Pro Lys Trp Lys Pro Ala Asp Leu Lys Glu Val
130 135 140

Thr Glu Glu Asp Leu Asn Asn His Phe Lys Ser Leu Gly Ser Ser Asp
145 150 155 160

Leu Lys Phe

<210> 269
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387098"

<400> 269
Met Leu Ala Met Leu Glu Glu Asp Leu Leu Ala Leu Lys Ser Pro Ser
1 5 10 15

Lys Glu Asn Ile Ala Ser Val Leu Glu Asn Tyr His Thr Glu Ser Lys
20 25 30

Ile Asp Arg Asp Lys Ser Phe Ile Leu Glu Glu His Met Asp Lys Ile
35 40 45

Asn Ser Cys Phe Ser Ala Asn Thr Val Glu Glu Ile Ile Glu Asn Leu
50 55 60

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

Lys Met Ser Pro Thr Ser Leu Lys Ile Thr Leu Arg Gln Leu Met Glu
85 90 95

Gly Ser Ser Lys Thr Leu Gln Glu Val Leu Thr Met Glu Tyr Arg Leu
100 105 110

Ser Gln Ala Cys Met Arg Gly His Asp Phe His Glu Gly Val Arg Ala
115 120 125

<210> 270
<211> 273
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387247"

<400> 270
Met Pro Gly Met Pro Gly Arg Ala Arg Pro Gly Ala Ala Ser Leu Pro
1 5 10 15

Gly Gln Gly Pro Arg Arg Pro Ala Arg Arg Gly Glu Glu Pro Ser Arg
20 25 30

Arg His Arg Leu Thr Tyr Pro Arg Arg Gly Asp Gly Ala Arg Arg Ser
35 40 45

Pro Ala Arg Ala Pro Asp Pro Arg Arg Arg Gly Ser Gly Ala Gly Thr
50 55 60

Leu Trp Phe Asn Ala Phe Lys Arg Thr Asn Thr Ile Leu His His Leu
65 70 75 80

Arg Met Ser Lys His Thr Asp Ala Ala Glu Glu Val Leu Leu Glu Lys
85 90 95

Lys Gly Cys Thr Gly Val Ile Thr Leu Asn Arg Pro Lys Phe Leu Asn
100 105 110

```
Ala Leu Thr Leu Asn Met Ile Arg Gln Ile Tyr Pro Gln Leu Lys Lys
        115                 120                 125

Trp Glu Gln Asp Pro Glu Thr Phe Leu Ile Ile Ile Lys Gly Ala Gly
    130                 135                 140

Gly Lys Ala Phe Cys Ala Gly Gly Asp Ile Arg Val Ile Ser Glu Ala
145                 150                 155                 160

Glu Lys Ala Lys Gln Lys Ile Ala Pro Val Phe Phe Arg Glu Glu Tyr
                165                 170                 175

Met Leu Asn Asn Ala Val Gly Ser Cys Gln Lys Pro Tyr Val Ala Leu
            180                 185                 190

Ile His Gly Ile Thr Met Gly Gly Gly Val Gly Leu Ser Val His Gly
        195                 200                 205

Gln Phe Arg Val Ala Thr Glu Lys Cys Leu Phe Ala Met Pro Glu Thr
    210                 215                 220

Ala Ile Gly Leu Phe Pro Asp Val Gly Gly Gly Tyr Phe Leu Pro Arg
225                 230                 235                 240

Leu Gln Gly Lys Leu Gly Tyr Phe Leu Ala Leu Thr Gly Phe Arg Leu
                245                 250                 255

Lys Gly Arg Asp Val Tyr Arg Ala Gly Ile Ala Thr His Phe Val Asp
            260                 265                 270

Ser
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<210> 271
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source

<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398060"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 271
Xaa Leu Ile Asp Lys Asp Gln Ser Pro Lys Trp Lys Pro Ala Asp Leu
1 5 10 15

Lys Glu Val Thr Glu Glu Asp Leu Asn Asn His Phe Lys Ser Leu Gly
20 25 30

Ser Ser Asp Leu Lys Phe
35

<210> 272
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399263"

<400> 272
Gln Ser Lys Ile Asp Arg Asp Lys Ser Phe Ile Leu Glu Glu His Met
1 5 10 15

```
Asp Lys Ile Asn Ser Cys Phe Ser Ala Asn Thr Val Glu Glu Ile Ile
            20                  25                  30

Glu Asn Leu Gln Gln Asp Gly Ser Ser Phe Ala Leu Glu Gln Leu Lys
        35                  40                  45

Val Ile Asn Lys Met Ser Pro Thr Ser Leu Lys Ile Thr Leu Arg Gln
    50                  55                  60

Leu Met Glu Gly Ser Ser Lys Thr Leu Gln Glu Val Leu Thr Met Glu
65                  70                  75                  80

Tyr Arg Leu Ser Gln Ala Cys Met Arg Gly His Asp Phe His Glu Gly
                85                  90                  95

Val Arg Ala Gly Lys Trp Gln Met Gly Thr Tyr His Phe Gly Glu Met
            100                 105                 110

Gly Phe Val Ser Ile Cys Cys
        115


<210> 273
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414820"

<400> 273
Asp Val Gly Gly Gly Tyr Phe Leu Pro Arg Leu Gln Gly Lys Leu Gly
1               5                   10                  15

Tyr Phe Leu Ala Leu Thr Gly Phe Arg Leu Lys Gly Arg Asp Val Tyr
            20                  25                  30
```

```
Arg Ala Gly Ile Ala Thr His Phe Val Asp Ser Glu Lys Asn Gly Asp
        35                  40                  45


Asp Thr Ile Thr
    50


<210> 274
<211> 380
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 37; "

<220>
<221> source
<223> /note="Gene Symbol: HIBCH; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxyisobutyryl-CoA hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481055"

<400> 274
Met Trp Arg Leu Met Ser Arg Phe Asn Ala Phe Lys Arg Thr Asn Thr
1               5                   10                  15


Ile Leu His His Leu Arg Met Ser Lys His Thr Asp Ala Ala Glu Glu
            20                  25                  30


Val Leu Leu Glu Lys Lys Gly Cys Thr Gly Val Ile Thr Leu Asn Arg
        35                  40                  45


Pro Lys Phe Leu Asn Ala Leu Thr Leu Asn Met Ile Arg Gln Ile Tyr
    50                  55                  60


Pro Gln Leu Lys Lys Trp Glu Gln Asp Pro Glu Thr Phe Leu Ile Ile
65                  70                  75                  80


Ile Lys Gly Ala Gly Gly Lys Ala Phe Cys Ala Gly Gly Asp Ile Arg
                85                  90                  95
```

```
Val Ile Ser Glu Ala Glu Lys Ala Lys Gln Lys Ile Ala Pro Val Phe
            100                 105                 110

Phe Arg Glu Glu Tyr Met Leu Asn Asn Ala Val Gly Ser Cys Gln Lys
        115                 120                 125

Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met Gly Gly Gly Val Gly
    130                 135                 140

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

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

Tyr Phe Leu Thr Thr Pro Arg Lys Thr Trp Leu Leu Pro Cys Ile Asn
            180                 185                 190

Gly Phe Arg Leu Lys Gly Arg Asp Val Tyr Arg Ala Gly Ile Ala Thr
        195                 200                 205

His Phe Val Asp Ser Glu Lys Leu Ala Met Leu Glu Glu Asp Leu Leu
    210                 215                 220

Ala Leu Lys Ser Pro Ser Lys Glu Asn Ile Ala Ser Val Leu Glu Asn
225                 230                 235                 240

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

Glu His Met Asp Lys Ile Asn Ser Cys Phe Ser Ala Asn Thr Val Glu
            260                 265                 270

Glu Ile Ile Glu Asn Leu Gln Gln Asp Gly Ser Ser Phe Ala Leu Glu
        275                 280                 285

Gln Leu Lys Val Ile Asn Lys Met Ser Pro Thr Ser Leu Lys Ile Thr
    290                 295                 300

Leu Arg Gln Leu Met Glu Gly Ser Ser Lys Thr Leu Gln Glu Val Leu
305                 310                 315                 320

Thr Met Glu Tyr Arg Leu Ser Gln Ala Cys Met Arg Gly His Asp Phe
```

```
                325                 330                 335

His Glu Gly Val Arg Ala Val Leu Ile Asp Lys Asp Gln Ser Pro Lys
            340                 345                 350

Trp Lys Pro Ala Asp Leu Lys Glu Val Thr Glu Glu Asp Leu Asn Asn
        355                 360                 365

His Phe Lys Ser Leu Gly Ser Ser Asp Leu Lys Phe
    370                 375                 380


<210> 275
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 38; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCL; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000235958"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 275
Xaa Lys Ala Leu Pro Arg Arg Leu Val Gly Leu Ala Ser Leu Arg Ala
1               5                   10                  15

Val Ser Thr Ser Ser Met Gly Thr Leu Pro Lys Arg Val Lys Ile Val
            20                  25                  30

Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Thr Lys Lys
        35                  40                  45

Phe Tyr Ser Met Gly Cys Tyr Glu Ile Ser Leu Gly Asp Thr Ile Gly
```

```
    50                  55                  60

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

Glu Val Pro Leu Ala Ala Leu Ala Val His Cys His Asp Thr Tyr Gly
                85                  90                  95

Gln Ala Leu Ala Asn Thr Leu Met Ala Leu Gln Met Gly Val Ser Val
            100                 105                 110

Val Asp Ser Ser Val Ala Gly Leu Gly Gly Cys Pro Tyr Ala Gln Gly
        115                 120                 125

Ala Ser Gly Asn Leu Ala Thr Glu Asp Leu Val Tyr Met Leu Glu Gly
    130                 135                 140

Leu Gly Ile His Thr Gly Val Asn Leu Gln Lys Leu Leu Glu Ala Gly
145                 150                 155                 160

Asn Phe Ile Cys Gln Ala Leu Asn Arg Lys Thr Ser Ser Lys Val Ala
                165                 170                 175

Gln Ala Thr Cys Lys Leu
            180


<210> 276
<211> 77
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 38; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCL; "

<220>
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<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase; "

<220>
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<223> /note="ENSP ID: ENSP00000363611"
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<400> 276
Met Leu Glu Ala Arg Arg Glu Trp Ser Arg Lys Val Phe Pro Trp Ser
1   5   10   15

Gly Ala Thr Gln Gln Pro Gly Thr Pro Phe His Ser Pro Ser Gln Thr
            20   25   30

Leu Arg Arg Ser Ala Gly Gln Arg Pro Ala Gly Val Pro Val Pro Ala
        35   40   45

Asp Val Leu Leu Trp Thr Ser Ser Arg Leu Cys Val Pro Pro Leu Met
    50   55   60

Cys Ser Ser Pro Cys Pro Ala Thr Cys Val Ser Ala Cys
65   70   75

<210> 277
<211> 325
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 38; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCL; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase; "

<220>
<221> source
<223> /note="Uniprot ID: P35914; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000363614"

<400> 277
Met Ala Ala Met Arg Lys Ala Leu Pro Arg Arg Leu Val Gly Leu Ala
1   5   10   15

Ser Leu Arg Ala Val Ser Thr Ser Ser Met Gly Thr Leu Pro Lys Arg
            20   25   30

Val Lys Ile Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys

```
        35                  40                  45

Asn Ile Val Ser Thr Pro Val Lys Ile Lys Leu Ile Asp Met Leu Ser
    50                  55                  60

Glu Ala Gly Leu Ser Val Ile Glu Thr Thr Ser Phe Val Ser Pro Lys
65                  70                  75                  80

Trp Val Pro Gln Met Gly Asp His Thr Glu Val Leu Lys Gly Ile Gln
                85                  90                  95

Lys Phe Pro Gly Ile Asn Tyr Pro Val Leu Thr Pro Asn Leu Lys Gly
            100                 105                 110

Phe Glu Ala Ala Val Ala Ala Gly Ala Lys Glu Val Val Ile Phe Gly
        115                 120                 125

Ala Ala Ser Glu Leu Phe Thr Lys Lys Asn Ile Asn Cys Ser Ile Glu
    130                 135                 140

Glu Ser Phe Gln Arg Phe Asp Ala Ile Leu Lys Ala Ala Gln Ser Ala
145                 150                 155                 160

Asn Ile Ser Val Arg Gly Tyr Val Ser Cys Ala Leu Gly Cys Pro Tyr
                165                 170                 175

Glu Gly Lys Ile Ser Pro Ala Lys Val Ala Glu Val Thr Lys Lys Phe
            180                 185                 190

Tyr Ser Met Gly Cys Tyr Glu Ile Ser Leu Gly Asp Thr Ile Gly Val
        195                 200                 205

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

Val Pro Leu Ala Ala Leu Ala Val His Cys His Asp Thr Tyr Gly Gln
225                 230                 235                 240

Ala Leu Ala Asn Thr Leu Met Ala Leu Gln Met Gly Val Ser Val Val
                245                 250                 255

Asp Ser Ser Val Ala Gly Leu Gly Gly Cys Pro Tyr Ala Gln Gly Ala
            260                 265                 270
```

```
Ser Gly Asn Leu Ala Thr Glu Asp Leu Val Tyr Met Leu Glu Gly Leu
        275                 280                 285

Gly Ile His Thr Gly Val Asn Leu Gln Lys Leu Leu Glu Ala Gly Asn
    290                 295                 300

Phe Ile Cys Gln Ala Leu Asn Arg Lys Thr Ser Ser Lys Val Ala Gln
305                 310                 315                 320

Ala Thr Cys Lys Leu
                325
```

<210> 278
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 38; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCL; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxymethyl-3-methylglutaryl-CoA lyase; "

<220>
<221> source
<223> /note="Uniprot ID: P35914; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389281"

<400> 278

```
Met Ala Ala Met Arg Lys Ala Leu Pro Arg Arg Leu Val Gly Leu Ala
1               5                   10                  15

Ser Leu Arg Ala Val Ser Thr Ser Ser Met Gly Thr Leu Pro Lys Arg
            20                  25                  30

Val Lys Ile Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys
        35                  40                  45
```

```
Asn Ile Val Ser Thr Pro Val Lys Ile Lys Leu Ile Asp Met Leu Ser
    50                  55                  60

Glu Ala Gly Leu Ser Val Ile Glu Thr Thr Ser Phe Val Ser Pro Lys
65                  70                  75                  80

Trp Val Pro Gln Met Gly Asp His Thr Glu Val Leu Lys Gly Ile Gln
                85                  90                  95

Lys Phe Pro Gly Ile Asn Tyr Pro Val Leu Thr Pro Asn Leu Lys Gly
            100                 105                 110

Phe Glu Ala Ala Val Thr Lys Lys Phe Tyr Ser Met Gly Cys Tyr Glu
        115                 120                 125

Ile Ser Leu Gly Asp Thr Ile Gly Val Gly Thr Pro Gly Ile Met Lys
    130                 135                 140

Asp Met Leu Ser Ala Val Met Gln Glu Val Pro Leu Ala Ala Leu Ala
145                 150                 155                 160

Val His Cys His Asp Thr Tyr Gly Gln Ala Leu Ala Asn Thr Leu Met
                165                 170                 175

Ala Leu Gln Met Gly Val Ser Val Val Asp Ser Ser Val Ala Gly Leu
            180                 185                 190

Gly Gly Cys Pro Tyr Ala Gln Gly Ala Ser Gly Asn Leu Ala Thr Glu
        195                 200                 205

Asp Leu Val Tyr Met Leu Glu Gly Leu Gly Ile His Thr Gly Val Asn
    210                 215                 220

Leu Gln Lys Leu Leu Glu Ala Gly Asn Phe Ile Cys Gln Ala Leu Asn
225                 230                 235                 240

Arg Lys Thr Ser Ser Lys Val Ala Gln Ala Thr Cys Lys Leu
                245                 250
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<210> 279
<211> 340
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 39; "

<220>
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<223> /note="Gene Symbol: HMGCLL1; "

<220>
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<223> /note="Gene Name:
3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TB92; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000274901"

<400> 279
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1   5   10   15

Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
            20   25   30

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

Lys Ile Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val
    50   55   60

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

Thr Gly Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp
                85   90   95

Val Pro Gln Met Ala Asp His Thr Glu Val Met Lys Gly Ile His Gln
            100   105   110

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

His His Ala Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala
    130   135   140

Ala Ser Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu
145 150 155 160

Ser Met Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn
165 170 175

Ile Pro Ala Arg Gly Tyr Val Ser Cys Ala Leu Gly Cys Pro Tyr Glu
180 185 190

Gly Ser Ile Thr Pro Gln Lys Val Thr Glu Val Ser Lys Arg Leu Tyr
195 200 205

Gly Met Gly Cys Tyr Glu Ile Ser Leu Gly Asp Thr Ile Gly Val Gly
210 215 220

Thr Pro Gly Ser Met Lys Arg Met Leu Glu Ser Val Met Lys Glu Ile
225 230 235 240

Pro Pro Gly Ala Leu Ala Val His Cys His Asp Thr Tyr Gly Gln Ala
245 250 255

Leu Ala Asn Ile Leu Thr Ala Leu Gln Met Gly Ile Asn Val Val Asp
260 265 270

Ser Ala Val Ser Gly Leu Gly Gly Cys Pro Tyr Ala Lys Gly Ala Ser
275 280 285

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

Leu Asn Thr Gly Val Asn Leu Tyr Lys Val Met Glu Ala Gly Asp Phe
305 310 315 320

Ile Cys Lys Ala Val Asn Lys Thr Thr Asn Ser Lys Val Ala Gln Ala
325 330 335

Ser Phe Asn Ala
340

<210> 280
<211> 308
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TB92; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000309737"

<400> 280

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

```
Ser Met Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn
    130                 135                 140

Ile Pro Ala Arg Gly Tyr Val Ser Cys Ala Leu Gly Cys Pro Tyr Glu
145                 150                 155                 160

Gly Ser Ile Thr Pro Gln Lys Val Thr Glu Val Ser Lys Arg Leu Tyr
                165                 170                 175

Gly Met Gly Cys Tyr Glu Ile Ser Leu Gly Asp Thr Ile Gly Val Gly
            180                 185                 190

Thr Pro Gly Ser Met Lys Arg Met Leu Glu Ser Val Met Lys Glu Ile
        195                 200                 205

Pro Pro Gly Ala Leu Ala Val His Cys His Asp Thr Tyr Gly Gln Ala
    210                 215                 220

Leu Ala Asn Ile Leu Thr Ala Leu Gln Met Gly Ile Asn Val Val Asp
225                 230                 235                 240

Ser Ala Val Ser Gly Leu Gly Gly Cys Pro Tyr Ala Lys Gly Ala Ser
                245                 250                 255

Gly Asn Val Ala Thr Glu Asp Leu Ile Tyr Met Leu Asn Gly Leu Gly
            260                 265                 270

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

Ile Cys Lys Ala Val Asn Lys Thr Thr Asn Ser Lys Val Ala Gln Ala
    290                 295                 300

Ser Phe Asn Ala
305
```

<210> 281
<211> 237
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359887"

<400> 281
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1 5 10 15

Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
20 25 30

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

Lys Ile Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val
50 55 60

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

Thr Gly Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp
85 90 95

Val Pro Gln Val Ser Lys Arg Leu Tyr Gly Met Gly Cys Tyr Glu Ile
100 105 110

Ser Leu Gly Asp Thr Ile Gly Val Gly Thr Pro Gly Ser Met Lys Arg
115 120 125

Met Leu Glu Ser Val Met Lys Glu Ile Pro Pro Gly Ala Leu Ala Val
130 135 140

His Cys His Asp Thr Tyr Gly Gln Ala Leu Ala Asn Ile Leu Thr Ala
145 150 155 160

Leu Gln Met Gly Ile Asn Val Val Asp Ser Ala Val Ser Gly Leu Gly
165 170 175

```
Gly Cys Pro Tyr Ala Lys Gly Ala Ser Gly Asn Val Ala Thr Glu Asp
            180                 185                 190

Leu Ile Tyr Met Leu Asn Gly Leu Gly Leu Asn Thr Gly Val Asn Leu
        195                 200                 205

Tyr Lys Val Met Glu Ala Gly Asp Phe Ile Cys Lys Ala Val Asn Lys
    210                 215                 220

Thr Thr Asn Ser Lys Val Ala Gln Ala Ser Phe Asn Ala
225                 230                 235


<210> 282
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
      1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TB92; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359889"

<400> 282
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1               5                  10                  15

Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
            20                  25                  30

Asp Pro Ala Gln Glu Leu Gln Ser Val Met Leu Met Leu His His Gly
        35                  40                  45
```

Pro Leu Arg Lys Pro
    50

<210> 283
<211> 370
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
      1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TB92; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000381654"

<400> 283
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1   5   10   15

Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
            20   25   30

Asp Pro Ala Gln Thr Ser Leu Leu Thr Asn Leu His Cys Phe Gln Pro
        35   40   45

Asp Val Ser Gly Phe Ser Val Ser Leu Ala Gly Thr Val Ala Cys Ile
    50   55   60

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

Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Ile Val
                85   90   95

```
Pro Thr Asp Ile Lys Ile Glu Phe Ile Asn Arg Leu Ser Gln Thr Gly
            100                 105                 110

Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp Val Pro
        115                 120                 125

Gln Met Ala Asp His Thr Glu Val Met Lys Gly Ile His Gln Tyr Pro
    130                 135                 140

Gly Val Arg Tyr Pro Val Leu Thr Pro Asn Leu Gln Gly Phe His His
145                 150                 155                 160

Ala Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala Ala Ser
                165                 170                 175

Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu Ser Met
            180                 185                 190

Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn Ile Pro
        195                 200                 205

Ala Arg Gly Tyr Val Ser Cys Ala Leu Gly Cys Pro Tyr Glu Gly Ser
    210                 215                 220

Ile Thr Pro Gln Lys Val Thr Glu Val Ser Lys Arg Leu Tyr Gly Met
225                 230                 235                 240

Gly Cys Tyr Glu Ile Ser Leu Gly Asp Thr Ile Gly Val Gly Thr Pro
                245                 250                 255

Gly Ser Met Lys Arg Met Leu Glu Ser Val Met Lys Glu Ile Pro Pro
            260                 265                 270

Gly Ala Leu Ala Val His Cys His Asp Thr Tyr Gly Gln Ala Leu Ala
        275                 280                 285

Asn Ile Leu Thr Ala Leu Gln Met Gly Ile Asn Val Val Asp Ser Ala
    290                 295                 300

Val Ser Gly Leu Gly Gly Cys Pro Tyr Ala Lys Gly Ala Ser Gly Asn
305                 310                 315                 320

Val Ala Thr Glu Asp Leu Ile Tyr Met Leu Asn Gly Leu Gly Leu Asn
```

325 330 335

Thr Gly Val Asn Leu Tyr Lys Val Met Glu Ala Gly Asp Phe Ile Cys
340 345 350

Lys Ala Val Asn Lys Thr Thr Asn Ser Lys Val Ala Gln Ala Ser Phe
355 360 365

Asn Ala
370

<210> 284
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412924"

<400> 284
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1 5 10 15

Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
20 25 30

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

Lys Ile Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val
50 55 60

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

```
Thr Gly Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp
                85                  90                  95

Val Pro Gln Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala
            100                 105                 110

Ala Ser Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu
        115                 120                 125

Ser Met Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn
    130                 135                 140

Ile Pro Ala Arg Gly Tyr Leu
145                 150


<210> 285
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
      1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424309"

<400> 285
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1               5                   10                  15

Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
            20                  25                  30

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

```
Lys Ile Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val
    50                  55                  60

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

Thr Gly Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp
                85                  90                  95

Val Pro Gln Met Gly Ile Asn Val Val Asp Ser Ala Val Ser Gly Leu
            100                 105                 110

Gly Gly Cys Pro Tyr Ala Lys Gly Ala Ser Gly Asn Val Ala Thr Glu
        115                 120                 125

Asp Leu Ile Tyr Met Leu Asn Gly Leu Gly Leu Asn Thr Gly Val Asn
    130                 135                 140

Leu Tyr Lys Val Met Glu Ala Gly Asp Phe Ile Cys Lys Ala Val Asn
145                 150                 155                 160

Lys Thr Thr Asn Ser Lys Val Ala Gln Ala Ser Phe Asn Ala
                165                 170


<210> 286
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 39; "

<220>
<221> source
<223> /note="Gene Symbol: HMGCLL1; "

<220>
<221> source
<223> /note="Gene Name:
      3-hydroxymethyl-3-methylglutaryl-CoA lyase-like
      1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426054"

<400> 286
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```
Met Gly Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln
1               5                   10                  15


Leu Leu Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu
            20                  25                  30


Asp Pro Ala Gln Glu Lys Glu
        35


<210> 287
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 40; "

<220>
<221> source
<223> /note="Gene Symbol: KDSR; "

<220>
<221> source
<223> /note="Gene Name:
      3-ketodihydrosphingosine reductase; "

<220>
<221> source
<223> /note="Uniprot ID:  Q06136; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000312939"

<400> 287
Met Leu Leu Leu Ala Ala Ala Phe Leu Val Ala Phe Val Leu Leu Leu
1               5                   10                  15


Tyr Met Val Ser Pro Leu Ile Ser Pro Lys Pro Leu Ala Leu Pro Gly
            20                  25                  30


Ala His Val Val Val Thr Gly Gly Ser Ser Gly Ile Gly Lys Cys Ile
        35                  40                  45


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


Asn Glu Asp Lys Leu Leu Gln Ala Lys Lys Glu Ile Glu Met His Ser
65                  70                  75                  80
```

```
Ile Asn Asp Lys Gln Val Val Leu Cys Ile Ser Val Asp Val Ser Gln
                85                  90                  95

Asp Tyr Asn Gln Val Glu Asn Val Ile Lys Gln Ala Gln Glu Lys Leu
            100                 105                 110

Gly Pro Val Asp Met Leu Val Asn Cys Ala Gly Met Ala Val Ser Gly
        115                 120                 125

Lys Phe Glu Asp Leu Glu Val Ser Thr Phe Glu Val Lys Pro Tyr Asn
    130                 135                 140

Val Tyr Ile Thr Val Ala Tyr Pro Pro Asp Thr Asp Thr Pro Gly Phe
145                 150                 155                 160

Ala Glu Glu Asn Arg Thr Lys Pro Leu Glu Thr Arg Leu Ile Ser Glu
                165                 170                 175

Thr Thr Ser Val Cys Lys Pro Glu Gln Val Ala Lys Gln Ile Val Lys
            180                 185                 190

Asp Ala Ile Gln Gly Asn Phe Asn Ser Ser Leu Gly Ser Asp Gly Tyr
        195                 200                 205

Met Leu Ser Ala Leu Thr Cys Gly Met Ala Pro Val Thr Ser Ile Thr
    210                 215                 220

Glu Gly Leu Gln Gln Val Val Thr Met Gly Leu Phe Arg Thr Ile Ala
225                 230                 235                 240

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

Gln Arg Glu Lys Ser Glu Asn Ala Asp Lys Thr Ala
            260                 265
```

<210> 288
<211> 332
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 40; "

<220>
<221> source
<223> /note="Gene Symbol: KDSR; "

<220>
<221> source
<223> /note="Gene Name:
3-ketodihydrosphingosine reductase; "

<220>
<221> source
<223> /note="Uniprot ID: Q06136; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000385083"

<400> 288

```
Met Leu Leu Leu Ala Ala Ala Phe Leu Val Ala Phe Val Leu Leu Leu
1               5                   10                  15

Tyr Met Val Ser Pro Leu Ile Ser Pro Lys Pro Leu Ala Leu Pro Gly
            20                  25                  30

Ala His Val Val Val Thr Gly Gly Ser Ser Gly Ile Gly Lys Cys Ile
        35                  40                  45

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

Asn Glu Asp Lys Leu Leu Gln Ala Lys Lys Glu Ile Glu Met His Ser
65                  70                  75                  80

Ile Asn Asp Lys Gln Val Val Leu Cys Ile Ser Val Asp Val Ser Gln
                85                  90                  95

Asp Tyr Asn Gln Val Glu Asn Val Ile Lys Gln Ala Gln Glu Lys Leu
            100                 105                 110

Gly Pro Val Asp Met Leu Val Asn Cys Ala Gly Met Ala Val Ser Gly
        115                 120                 125

Lys Phe Glu Asp Leu Glu Val Ser Thr Phe Glu Arg Leu Met Ser Ile
    130                 135                 140

Asn Tyr Leu Gly Ser Val Tyr Pro Ser Arg Ala Val Ile Thr Thr Met
```

```
145                 150                 155                 160

Lys Glu Arg Arg Val Gly Arg Ile Val Phe Val Ser Ser Gln Ala Gly
                165                 170                 175

Gln Leu Gly Leu Phe Gly Phe Thr Ala Tyr Ser Ala Ser Lys Phe Ala
            180                 185                 190

Ile Arg Gly Leu Ala Glu Ala Leu Gln Met Glu Val Lys Pro Tyr Asn
        195                 200                 205

Val Tyr Ile Thr Val Ala Tyr Pro Pro Asp Thr Asp Thr Pro Gly Phe
    210                 215                 220

Ala Glu Glu Asn Arg Thr Lys Pro Leu Glu Thr Arg Leu Ile Ser Glu
225                 230                 235                 240

Thr Thr Ser Val Cys Lys Pro Glu Gln Val Ala Lys Gln Ile Val Lys
                245                 250                 255

Asp Ala Ile Gln Gly Asn Phe Asn Ser Ser Leu Gly Ser Asp Gly Tyr
            260                 265                 270

Met Leu Ser Ala Leu Thr Cys Gly Met Ala Pro Val Thr Ser Ile Thr
        275                 280                 285

Glu Gly Leu Gln Gln Val Val Thr Met Gly Leu Phe Arg Thr Ile Ala
    290                 295                 300

Leu Phe Tyr Leu Gly Ser Phe Asp Ser Ile Val Arg Arg Cys Met Met
305                 310                 315                 320

Gln Arg Glu Lys Ser Glu Asn Ala Asp Lys Thr Ala
                325                 330


<210> 289
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 40; "

<220>
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<221> source
<223> /note="Gene Symbol: KDSR; "

<220>
<221> source
<223> /note="Gene Name:
3-ketodihydrosphingosine reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467962"

<400> 289
Met Leu Leu Leu Ala Ala Ala Phe Leu Val Ala Phe Val Leu Leu Leu
1 5 10 15

Tyr Met Val Ser Pro Leu Ile Ser Pro Lys Pro Leu Ala Leu Pro Gly
20 25 30

Ala His Val Val Val Thr Gly Gly Ser Ser Gly Ile Gly Lys Cys Ile
35 40 45

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

Asn Glu Asp Lys Leu Leu Gln Ala Lys Lys Glu Ile Glu Met His Ser
65 70 75 80

Ile Asn Asp Lys Gln Val Val Leu Cys Ile Ser Val Asp Val Ser Gln
85 90 95

Asp Tyr Asn Gln Val Glu Asn Val Ile Lys Gln Ala Gln Glu Lys Leu
100 105 110

Gly Pro Val Asp Met Leu Val Asn Cys Ala Gly Met Ala Val Ser Gly
115 120 125

Lys Phe Glu Asp Leu Glu Arg Leu Met Ser Ile Asn Tyr Leu Gly Ser
130 135 140

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

<210> 290
<211> 203
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 40; "

<220>
<221> source
<223> /note="Gene Symbol: KDSR; "

<220>
<221> source
<223> /note="Gene Name:
3-ketodihydrosphingosine reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468203"

<400> 290
Gln Asp Tyr Asn Gln Val Glu Asn Val Ile Lys Gln Ala Gln Glu Lys
1 5 10 15

Leu Gly Pro Val Asp Met Leu Val Asn Cys Ala Gly Met Ala Val Ser
20 25 30

Gly Lys Phe Glu Asp Leu Glu Val Ser Thr Phe Glu Arg Leu Met Ser
35 40 45

Ile Asn Tyr Leu Gly Ser Val Tyr Pro Ser Arg Ala Val Ile Thr Thr
50 55 60

Met Lys Glu Arg Arg Val Gly Arg Ile Val Phe Val Ser Ser Gln Ala
65 70 75 80

Gly Gln Leu Gly Leu Phe Gly Phe Thr Ala Tyr Ser Ala Ser Lys Phe
85 90 95

Ala Ile Arg Gly Leu Ala Glu Ala Leu Gln Met Glu Val Lys Pro Tyr
100 105 110

Asn Val Tyr Ile Thr Val Ala Tyr Pro Pro Asp Thr Asp Thr Pro Gly
115 120 125

Phe Ala Glu Glu Asn Arg Thr Lys Pro Leu Glu Thr Arg Leu Ile Ser
130 135 140

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

```
Lys Asp Ala Ile Val Val Thr Met Gly Leu Phe Arg Thr Ile Ala Leu
                165                 170                 175


Phe Tyr Leu Gly Ser Phe Asp Ser Ile Val Arg Arg Cys Met Met Gln
            180                 185                 190


Arg Glu Lys Ser Glu Asn Ala Asp Lys Thr Ala
        195                 200


<210> 291
<211> 520
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 41; "

<220>
<221> source
<223> /note="Gene Symbol: OXCT1; "

<220>
<221> source
<223> /note="Gene Name:
      3-oxoacid CoA transferase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P55809; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000196371"

<400> 291
Met Ala Ala Leu Lys Leu Leu Ser Ser Gly Leu Arg Leu Cys Ala Ser
1               5                   10                  15


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


Ser Thr Ser Ala His Arg His Thr Lys Phe Tyr Thr Asp Pro Val Glu
        35                  40                  45


Ala Val Lys Asp Ile Pro Asp Gly Ala Thr Val Leu Val Gly Gly Phe
    50                  55                  60
```

```
Gly Leu Cys Gly Ile Pro Glu Asn Leu Ile Asp Ala Leu Leu Lys Thr
65                  70                  75                  80

Gly Val Lys Gly Leu Thr Ala Val Ser Asn Asn Ala Gly Val Asp Asn
                85                  90                  95

Phe Gly Leu Gly Leu Leu Leu Arg Ser Lys Gln Ile Lys Arg Met Val
            100                 105                 110

Ser Ser Tyr Val Gly Glu Asn Ala Glu Phe Glu Arg Gln Tyr Leu Ser
        115                 120                 125

Gly Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Arg
    130                 135                 140

Ile Arg Ala Gly Gly Ala Gly Val Pro Ala Phe Tyr Thr Pro Thr Gly
145                 150                 155                 160

Tyr Gly Thr Leu Val Gln Glu Gly Gly Ser Pro Ile Lys Tyr Asn Lys
                165                 170                 175

Asp Gly Ser Val Ala Ile Ala Ser Lys Pro Arg Glu Val Arg Glu Phe
            180                 185                 190

Asn Gly Gln His Phe Ile Leu Glu Glu Ala Ile Thr Gly Asp Phe Ala
        195                 200                 205

Leu Val Lys Ala Trp Lys Ala Asp Arg Ala Gly Asn Val Ile Phe Arg
    210                 215                 220

Lys Ser Ala Arg Asn Phe Asn Leu Pro Met Cys Lys Ala Ala Glu Thr
225                 230                 235                 240

Thr Val Val Glu Val Glu Glu Ile Val Asp Ile Gly Ala Phe Ala Pro
                245                 250                 255

Glu Asp Ile His Ile Pro Gln Ile Tyr Val His Arg Leu Ile Lys Gly
            260                 265                 270

Glu Lys Tyr Glu Lys Arg Ile Glu Arg Leu Ser Ile Arg Lys Glu Gly
        275                 280                 285

Asp Gly Glu Ala Lys Ser Ala Lys Pro Gly Asp Asp Val Arg Glu Arg
```

```
    290                 295                 300

Ile Ile Lys Arg Ala Ala Leu Glu Phe Glu Asp Gly Met Tyr Ala Asn
305                 310                 315                 320

Leu Gly Ile Gly Ile Pro Leu Leu Ala Ser Asn Phe Ile Ser Pro Asn
                325                 330                 335

Ile Thr Val His Leu Gln Ser Glu Asn Gly Val Leu Gly Leu Gly Pro
            340                 345                 350

Tyr Pro Arg Gln His Glu Ala Asp Ala Asp Leu Ile Asn Ala Gly Lys
        355                 360                 365

Glu Thr Val Thr Ile Leu Pro Gly Ala Ser Phe Phe Ser Ser Asp Glu
    370                 375                 380

Ser Phe Ala Met Ile Arg Gly Gly His Val Asp Leu Thr Met Leu Gly
385                 390                 395                 400

Ala Met Gln Val Ser Lys Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
                405                 410                 415

Gly Lys Met Val Lys Gly Met Gly Gly Ala Met Asp Leu Val Ser Ser
            420                 425                 430

Ala Lys Thr Lys Val Val Val Thr Met Glu His Ser Ala Lys Gly Asn
        435                 440                 445

Ala His Lys Ile Met Glu Lys Cys Thr Leu Pro Leu Thr Gly Lys Gln
    450                 455                 460

Cys Val Asn Arg Ile Ile Thr Glu Lys Ala Val Phe Asp Val Asp Lys
465                 470                 475                 480

Lys Lys Gly Leu Thr Leu Ile Glu Leu Trp Glu Gly Leu Thr Val Asp
                485                 490                 495

Asp Val Gln Lys Ser Thr Gly Cys Asp Phe Ala Val Ser Pro Lys Leu
            500                 505                 510

Met Pro Met Gln Gln Ile Ala Asn
        515                 520
```

<210> 292
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 41; "

<220>
<221> source
<223> /note="Gene Symbol: OXCT1; "

<220>
<221> source
<223> /note="Gene Name:
3-oxoacid CoA transferase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P55809; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421143"

<400> 292
Met Leu Gly Ala Met Gln Val Ser Lys Tyr Gly Asp Leu Ala Asn Trp
1   5   10   15

Met Ile Pro Gly Lys Met Val Lys Gly Met Gly Gly Ala Met Asp Leu
            20   25   30

Val Ser Ser Ala Lys Thr Lys Val Val Val Thr Met Glu His Ser Ala
        35   40   45

Lys Gly Asn Ala His Lys Ile Met Glu Lys Cys Thr Leu Pro Leu Thr
    50   55   60

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

Val Asp Lys Lys Lys Gly Leu Thr Leu Ile Glu Leu Trp Glu Gly Leu
                85   90   95

Thr Val Asp Asp Val Gln Lys Ser Thr Gly Cys Asp Phe Ala Val Ser
            100   105   110

```
Pro Lys Leu Met Pro Met Gln Gln Ile Ala Asn
        115                 120


<210> 293
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 41; "

<220>
<221> source
<223> /note="Gene Symbol: OXCT1; "

<220>
<221> source
<223> /note="Gene Name:
      3-oxoacid CoA transferase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P55809; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423144"

<400> 293
Met Leu Gly Ala Met Gln Val Ser Lys Tyr Gly Asp Leu Ala Asn Trp
1               5                  10                  15


Met Ile Pro Gly Lys Met Val Lys Gly Met Gly Gly Ala Met Asp Leu
            20                  25                  30


Val Ser Ser Ala Lys Thr Lys Val Val Val Thr Met Glu His Ser Ala
        35                  40                  45


Lys Gly Asn Ala His Lys Ile Met Glu Lys Cys Thr Leu Pro Leu Thr
    50                  55                  60


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


Val Asp Lys Lys Lys Gly Leu Thr Leu Ile Glu Leu Trp Glu Gly Leu
                85                  90                  95


Thr Val Asp Asp Val Gln Lys Ser Thr Gly Cys Asp Phe Ala Val Ser
            100                 105                 110
```

Pro Lys Leu Met Pro Met Gln Gln Ile Ala Asn
115 120

<210> 294
<211> 334
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 41; "

<220>
<221> source
<223> /note="Gene Symbol: OXCT1; "

<220>
<221> source
<223> /note="Gene Name:
3-oxoacid CoA transferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425348"

<400> 294
Met Met Val Arg Glu Phe Asn Gly Gln His Phe Ile Leu Glu Glu Ala
1 5 10 15

Ile Thr Gly Asp Phe Ala Leu Val Lys Ala Trp Lys Ala Asp Arg Ala
20 25 30

Gly Asn Val Ile Phe Arg Lys Ser Ala Arg Asn Phe Asn Leu Pro Met
35 40 45

Cys Lys Ala Ala Glu Thr Thr Val Val Glu Val Glu Glu Ile Val Asp
50 55 60

Ile Gly Ala Phe Ala Pro Glu Asp Ile His Ile Pro Gln Ile Tyr Val
65 70 75 80

His Arg Leu Ile Lys Gly Glu Lys Tyr Glu Lys Arg Ile Glu Arg Leu
85 90 95

Ser Ile Arg Lys Glu Gly Asp Gly Glu Ala Lys Ser Ala Lys Pro Gly
100 105 110

```
Asp Asp Val Arg Glu Arg Ile Ile Lys Arg Ala Ala Leu Glu Phe Glu
        115                 120                 125

Asp Gly Met Tyr Ala Asn Leu Gly Ile Gly Ile Pro Leu Leu Ala Ser
    130                 135                 140

Asn Phe Ile Ser Pro Asn Ile Thr Val His Leu Gln Ser Glu Asn Gly
145                 150                 155                 160

Val Leu Gly Leu Gly Pro Tyr Pro Arg Gln His Glu Ala Asp Ala Asp
                165                 170                 175

Leu Ile Asn Ala Gly Lys Glu Thr Val Thr Ile Leu Pro Gly Ala Ser
            180                 185                 190

Phe Phe Ser Ser Asp Glu Ser Phe Ala Met Ile Arg Gly Gly His Val
        195                 200                 205

Asp Leu Thr Met Leu Gly Ala Met Gln Val Ser Lys Tyr Gly Asp Leu
    210                 215                 220

Ala Asn Trp Met Ile Pro Gly Lys Met Val Lys Gly Met Gly Gly Ala
225                 230                 235                 240

Met Asp Leu Val Ser Ser Ala Lys Thr Lys Val Val Val Thr Met Glu
                245                 250                 255

His Ser Ala Lys Gly Asn Ala His Lys Ile Met Glu Lys Cys Thr Leu
            260                 265                 270

Pro Leu Thr Gly Lys Gln Cys Val Asn Arg Ile Ile Thr Glu Lys Ala
        275                 280                 285

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

Glu Gly Leu Thr Val Asp Asp Val Gln Lys Ser Thr Gly Cys Asp Phe
305                 310                 315                 320

Ala Val Ser Pro Lys Leu Met Pro Met Gln Gln Ile Ala Asn
                325                 330
```

<210> 295

<211> 517
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 42; "

<220>
<221> source
<223> /note="Gene Symbol: OXCT2; "

<220>
<221> source
<223> /note="Gene Name:
3-oxoacid CoA transferase 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BYC2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000361914"

<400> 295
Met Ala Ala Leu Arg Leu Leu Ala Ser Val Leu Gly Arg Gly Val Pro
1   5   10   15

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

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

Met Val Lys Asp Ile Ser Asp Gly Ala Thr Val Met Ile Gly Gly Phe
    50   55   60

Gly Leu Cys Gly Ile Pro Glu Asn Leu Ile Ala Ala Leu Leu Arg Thr
65   70   75   80

Arg Val Lys Asp Leu Gln Val Val Ser Ser Asn Val Gly Val Glu Asp
                85   90   95

Phe Gly Leu Gly Leu Leu Leu Ala Ala Arg Gln Val Arg Arg Ile Val
            100   105   110

Cys Ser Tyr Val Gly Glu Asn Thr Leu Cys Glu Ser Gln Tyr Leu Ala
        115   120   125

```
Gly Glu Leu Glu Leu Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Arg
    130                 135                 140

Ile Arg Ala Gly Gly Ala Gly Val Pro Ala Phe Tyr Thr Pro Thr Gly
145                 150                 155                 160

Tyr Gly Thr Leu Val Gln Glu Gly Gly Ala Pro Ile Arg Tyr Thr Pro
                165                 170                 175

Asp Gly His Leu Ala Leu Met Ser Gln Pro Arg Glu Val Arg Glu Phe
            180                 185                 190

Asn Gly Asp His Phe Leu Leu Glu Arg Ala Ile Arg Ala Asp Phe Ala
        195                 200                 205

Leu Val Lys Gly Trp Lys Ala Asp Arg Ala Gly Asn Val Val Phe Arg
    210                 215                 220

Arg Ser Ala Arg Asn Phe Asn Val Pro Met Cys Lys Ala Ala Asp Val
225                 230                 235                 240

Thr Ala Val Glu Val Glu Glu Ile Val Glu Val Gly Ala Phe Pro Pro
                245                 250                 255

Glu Asp Ile His Val Pro Asn Ile Tyr Val Asp Arg Val Ile Lys Gly
            260                 265                 270

Gln Lys Tyr Glu Lys Arg Ile Glu Arg Leu Thr Ile Leu Lys Glu Glu
        275                 280                 285

Asp Gly Asp Ala Gly Lys Glu Glu Asp Ala Arg Thr Arg Ile Ile Arg
    290                 295                 300

Arg Ala Ala Leu Glu Phe Glu Asp Gly Met Tyr Ala Asn Leu Gly Ile
305                 310                 315                 320

Gly Ile Pro Leu Leu Ala Ser Asn Phe Ile Ser Pro Ser Met Thr Val
                325                 330                 335

His Leu His Ser Glu Asn Gly Ile Leu Gly Leu Gly Pro Phe Pro Thr
            340                 345                 350
```

```
Glu Asp Glu Val Asp Ala Asp Leu Ile Asn Ala Gly Lys Gln Thr Val
        355                 360                 365

Thr Val Leu Pro Gly Gly Cys Phe Phe Ala Ser Asp Asp Ser Phe Ala
    370                 375                 380

Met Ile Arg Gly Gly His Ile Gln Leu Thr Met Leu Gly Ala Met Gln
385                 390                 395                 400

Val Ser Lys Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Lys
                405                 410                 415

Val Lys Gly Met Gly Gly Ala Met Asp Leu Val Ser Ser Gln Lys Thr
            420                 425                 430

Arg Val Val Val Thr Met Gln His Cys Thr Lys Asp Asn Thr Pro Lys
        435                 440                 445

Ile Met Glu Lys Cys Thr Met Pro Leu Thr Gly Lys Arg Cys Val Asp
    450                 455                 460

Arg Ile Ile Thr Glu Lys Ala Val Phe Asp Val His Arg Lys Lys Glu
465                 470                 475                 480

Leu Thr Leu Arg Glu Leu Trp Glu Gly Leu Thr Val Asp Asp Ile Lys
                485                 490                 495

Lys Ser Thr Gly Cys Ala Phe Ala Val Ser Pro Asn Leu Arg Pro Met
            500                 505                 510

Gln Gln Val Ala Pro
        515


<210> 296
<211> 459
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 43; "

<220>
<221> source
<223> /note="Gene Symbol: OXSM; "
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<220>
<221> source
<223> /note="Gene Name:
3-oxoacyl-ACP synthase,
mitochondrial; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NWU1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000280701"

<400> 296
Met Ser Asn Cys Leu Gln Asn Phe Leu Lys Ile Thr Ser Thr Arg Leu
1   5   10   15

Leu Cys Ser Arg Leu Cys Gln Gln Leu Arg Ser Lys Arg Lys Phe Phe
            20   25   30

Gly Thr Val Pro Ile Ser Arg Leu His Arg Arg Val Val Ile Thr Gly
        35   40   45

Ile Gly Leu Val Thr Pro Leu Gly Val Gly Thr His Leu Val Trp Asp
    50   55   60

Arg Leu Ile Gly Gly Glu Ser Gly Ile Val Ser Leu Val Gly Glu Glu
65   70   75   80

Tyr Lys Ser Ile Pro Cys Ser Val Ala Ala Tyr Val Pro Arg Gly Ser
                85   90   95

Asp Glu Gly Gln Phe Asn Glu Gln Asn Phe Val Ser Lys Ser Asp Ile
            100   105   110

Lys Ser Met Ser Ser Pro Thr Ile Met Ala Ile Gly Ala Ala Glu Leu
        115   120   125

Ala Met Lys Asp Ser Gly Trp His Pro Gln Ser Glu Ala Asp Gln Val
    130   135   140

Ala Thr Gly Val Ala Ile Gly Met Gly Met Ile Pro Leu Glu Val Val
145   150   155   160

Ser Glu Thr Ala Leu Asn Phe Gln Thr Lys Gly Tyr Asn Lys Val Ser
                165   170   175

```
Pro Phe Phe Val Pro Lys Ile Leu Val Asn Met Ala Ala Gly Gln Val
            180                 185                 190

Ser Ile Arg Tyr Lys Leu Lys Gly Pro Asn His Ala Val Ser Thr Ala
        195                 200                 205

Cys Thr Thr Gly Ala His Ala Val Gly Asp Ser Phe Arg Phe Ile Ala
    210                 215                 220

His Gly Asp Ala Asp Val Met Val Ala Gly Gly Thr Asp Ser Cys Ile
225                 230                 235                 240

Ser Pro Leu Ser Leu Ala Gly Phe Ser Arg Ala Arg Ala Leu Ser Thr
                245                 250                 255

Asn Ser Asp Pro Lys Leu Ala Cys Arg Pro Phe His Pro Lys Arg Asp
            260                 265                 270

Gly Phe Val Met Gly Glu Gly Ala Ala Val Leu Val Leu Glu Glu Tyr
        275                 280                 285

Glu His Ala Val Gln Arg Arg Ala Arg Ile Tyr Ala Glu Val Leu Gly
    290                 295                 300

Tyr Gly Leu Ser Gly Asp Ala Gly His Ile Thr Ala Pro Asp Pro Glu
305                 310                 315                 320

Gly Glu Gly Ala Leu Arg Cys Met Ala Ala Ala Leu Lys Asp Ala Gly
                325                 330                 335

Val Gln Pro Glu Glu Ile Ser Tyr Ile Asn Ala His Ala Thr Ser Thr
            340                 345                 350

Pro Leu Gly Asp Ala Ala Glu Asn Lys Ala Ile Lys His Leu Phe Lys
        355                 360                 365

Asp His Ala Tyr Ala Leu Ala Val Ser Ser Thr Lys Gly Ala Thr Gly
    370                 375                 380

His Leu Leu Gly Ala Ala Gly Ala Val Glu Ala Ala Phe Thr Thr Leu
385                 390                 395                 400
```

```
Ala Cys Tyr Tyr Gln Lys Leu Pro Pro Thr Leu Asn Leu Asp Cys Ser
                405                 410                 415

Glu Pro Glu Phe Asp Leu Asn Tyr Val Pro Leu Lys Ala Gln Glu Trp
            420                 425                 430

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

Gly Thr Asn Ala Thr Leu Cys Ile Ala Gly Leu
    450                 455


<210> 297
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 43; "

<220>
<221> source
<223> /note="Gene Symbol: OXSM; "

<220>
<221> source
<223> /note="Gene Name:
      3-oxoacyl-ACP synthase,
      mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392334"

<400> 297
Met Ser Asn Cys Leu Gln Asn Phe Leu Lys Ile Thr Ser Thr Arg Leu
1               5                   10                  15

Leu Cys Ser Arg Leu Cys Gln Gln Leu Arg Ser Lys Arg Lys Phe Phe
            20                  25                  30

Gly Thr Val Pro Ile Ser Arg Leu His Arg Arg Val Val Ile Thr Gly
        35                  40                  45

Ile Gly Leu Val Thr Pro Leu Gly Val Gly Thr His Leu Val Trp Asp
    50                  55                  60
```

```
Arg Leu Ile Gly Gly Glu Ser Gly Ile Val Ser Leu Val Gly Glu Glu
65                  70                  75                  80

Tyr Lys Ser Ile Pro Cys Ser Val Ala Ala Tyr Val Pro Arg Gly Ser
                85                  90                  95

Asp Glu Gly Gln Phe Asn Glu Gln Asn Phe Val Ser Lys Ser Asp Ile
            100                 105                 110

Lys Ser Met Ser Ser Pro Thr Ile Met Ala Ile Gly Ala Ala Glu Leu
        115                 120                 125

Ala Met Lys Asp Ser Gly Trp His Pro Gln Ser Glu Ala Asp Gln Val
    130                 135                 140

Ala Thr Gly Val Ala Ile Gly Met Gly Met Ile Pro Leu Glu Val Val
145                 150                 155                 160

Ser Glu Thr Ala Leu Asn Phe Gln Thr Lys Gly Tyr Asn Lys Val Ser
                165                 170                 175

Pro Phe Phe Val Pro Lys Ile Leu Val Asn Met Ala Ala Gly Gln Val
            180                 185                 190

Ser Ile Arg Tyr Lys Leu Lys Gly Pro Asn His Ala Val Ser Thr Ala
        195                 200                 205

Cys Thr Thr Gly Ala His Ala Val Gly Asp Ser Phe
    210                 215                 220


<210> 298
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 43; "

<220>
<221> source
<223> /note="Gene Symbol: OXSM; "

<220>
<221> source
<223> /note="Gene Name:
      3-oxoacyl-ACP synthase,
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mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404115"

<400> 298
Met Ser Asn Cys Leu Gln Asn Phe Leu Lys Ile Thr Ser Thr Arg Leu
1   5   10   15

Leu Cys Ser Arg Leu Cys Gln Gln Leu Arg Ser Lys Arg Lys Phe Phe
            20   25   30

Gly Thr Val Pro Ile Ser Arg Leu His Arg Arg Val Val Ile Thr Gly
        35   40   45

Ile Gly Leu Val Thr Pro Leu Gly Val Gly Thr His Leu Val Trp Asp
    50   55   60

Arg Leu Ile Gly Gly Glu Ser Gly Ile Val Ser Leu Val Gly Glu Glu
65   70   75   80

Tyr Lys Ser Ile Pro Cys Ser Val Ala Ala Tyr Val Pro Arg Gly Ser
                85   90   95

Asp Glu Glu Pro Gly Leu
            100

<210> 299
<211> 231
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 43; "

<220>
<221> source
<223> /note="Gene Symbol: OXSM; "

<220>
<221> source
<223> /note="Gene Name:
3-oxoacyl-ACP synthase,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000409817"

<400> 299
Met Ser Asn Cys Leu Gln Asn Phe Leu Lys Ile Thr Ser Thr Arg Leu
1 5 10 15

Leu Cys Ser Arg Leu Cys Gln Gln Leu Arg Ser Lys Arg Lys Phe Phe
20 25 30

Gly Thr Val Pro Ile Ser Arg Leu His Arg Arg Val Val Ile Thr Gly
35 40 45

Ile Gly Leu Val Thr Pro Leu Gly Val Gly Thr His Leu Val Trp Asp
50 55 60

Arg Leu Ile Gly Gly Glu Ser Gly Ile Val Ser Leu Val Gly Glu Glu
65 70 75 80

Tyr Lys Ser Ile Pro Cys Ser Val Ala Ala Tyr Val Pro Arg Gly Ser
85 90 95

Asp Glu Gly Gln Phe Asn Glu Gln Asn Phe Val Ser Lys Ser Asp Ile
100 105 110

Lys Ser Met Ser Ser Pro Thr Ile Met Ala Ile Gly Ala Ala Glu Leu
115 120 125

Ala Met Lys Asp Ser Gly Trp His Pro Gln Ser Glu Ala Asp Gln Val
130 135 140

Ala Thr Gly Val Ala Ile Gly Met Gly Met Ile Pro Leu Glu Val Val
145 150 155 160

Ser Glu Thr Ala Leu Asn Phe Gln Thr Lys Gly Tyr Asn Lys Val Ser
165 170 175

Pro Phe Phe Val Pro Lys Ile Leu Val Asn Met Ala Ala Gly Gln Val
180 185 190

Ser Ile Arg Tyr Lys Leu Lys Gly Pro Asn His Ala Val Ser Thr Ala
195 200 205

Cys Thr Thr Gly Ala His Ala Val Gly Asp Ser Phe Arg Phe Ile Ala
210 215 220

```
His Gly Asp Ala Asp Val Met
225                 230


<210> 300
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 43; "

<220>
<221> source
<223> /note="Gene Symbol: OXSM; "

<220>
<221> source
<223> /note="Gene Name:
      3-oxoacyl-ACP synthase,
      mitochondrial; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NWU1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000411303"

<400> 300
Met Ser Asn Cys Leu Gln Asn Phe Leu Lys Ile Thr Ser Thr Arg Leu
1               5                   10                  15


Leu Cys Ser Arg Leu Cys Gln Gln Leu Arg Ser Lys Arg Lys Phe Phe
            20                  25                  30


Gly Thr Val Pro Ile Ser Arg Leu His Arg Arg Val Val Ile Thr Gly
        35                  40                  45


Ile Gly Leu Val Thr Pro Leu Gly Val Gly Thr His Leu Val Trp Asp
    50                  55                  60


Arg Leu Ile Gly Gly Glu Ser Gly Ile Val Ser Leu Val Gly Glu Glu
65                  70                  75                  80


Tyr Lys Ser Ile Pro Cys Ser Val Ala Ala Tyr Val Pro Arg Gly Ser
                85                  90                  95
```

```
Asp Glu Gly Gln Phe Asn Glu Gln Asn Phe Val Ser Lys Ser Asp Ile
            100                 105                 110

Lys Ser Met Ser Ser Pro Thr Ile Met Ala Ile Gly Ala Ala Glu Leu
        115                 120                 125

Ala Met Lys Asp Ser Gly Trp His Pro Gln Ser Glu Ala Asp Gln Val
    130                 135                 140

Ala Thr Gly Val Ala Ile Gly Met Gly Met Ile Pro Leu Glu Val Val
145                 150                 155                 160

Ser Glu Thr Ala Leu Asn Phe Gln Thr Lys Gly Tyr Asn Lys Val Ser
                165                 170                 175

Pro Phe Phe Val Pro Lys Ile Leu Val Asn Met Ala Ala Gly Gln Val
            180                 185                 190

Ser Ile Arg Tyr Lys Leu Lys Gly Pro Asn His Ala Val Ser Thr Ala
        195                 200                 205

Cys Thr Thr Gly Ala His Ala Val Gly Asp Ser Phe Arg Phe Ile Ala
    210                 215                 220

His Gly Asp Ala Gly His Ile Thr Ala Pro Asp Pro Glu Gly Glu Gly
225                 230                 235                 240

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

Glu Glu Ile Ser Tyr Ile Asn Ala His Ala Thr Ser Thr Pro Leu Gly
            260                 265                 270

Asp Ala Ala Glu Asn Lys Ala Ile Lys His Leu Phe Lys Asp His Ala
        275                 280                 285

Tyr Ala Leu Ala Val Ser Ser Thr Lys Gly Ala Thr Gly His Leu Leu
    290                 295                 300

Gly Ala Ala Gly Ala Val Glu Ala Ala Phe Thr Thr Leu Ala Cys Tyr
305                 310                 315                 320

Tyr Gln Lys Leu Pro Pro Thr Leu Asn Leu Asp Cys Ser Glu Pro Glu
```

```
                325                 330                 335

Phe Asp Leu Asn Tyr Val Pro Leu Lys Ala Gln Glu Trp Lys Thr Glu
            340                 345                 350

Lys Arg Phe Ile Gly Leu Thr Asn Ser Phe Gly Phe Gly Gly Thr Asn
        355                 360                 365

Ala Thr Leu Cys Ile Ala Gly Leu
    370                 375


<210> 301
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 43; "

<220>
<221> source
<223> /note="Gene Symbol: OXSM; "

<220>
<221> source
<223> /note="Gene Name:
      3-oxoacyl-ACP synthase,
      mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487031"

<400> 301
Met Ser Asn Cys Leu Gln Asn Phe Leu Lys Ile Thr Ser Thr Arg Leu
1               5                   10                  15

Leu Cys Ser Arg Leu Cys Gln Gln Leu Arg Ser Lys Arg Lys Phe Phe
            20                  25                  30

Gly Thr Val Pro Ile Ser Arg Leu His Arg Arg Val Val Ile Thr Gly
        35                  40                  45

Ile Gly Leu Val Thr Pro Leu Gly Val Gly Thr His Leu Val Trp Asp
    50                  55                  60

Arg Leu Ile Gly Gly Glu Ser Gly Ile Val Ser Leu Val Gly Glu Glu
65                  70                  75                  80
```

```
Tyr Lys Ser Ile Pro Cys Ser Val Ala Ala Tyr Val Pro Arg Gly Ser
                85                  90                  95


Asp Glu Glu Pro Gly Leu
            100


<210> 302
<211> 624
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 44; "

<220>
<221> source
<223> /note="Gene Symbol: PAPSS1; "

<220>
<221> source
<223> /note="Gene Name:
      3'-phosphoadenosine 5'-phosphosulfate synthase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  O43252; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000265174"

<400> 302
Met Glu Ile Pro Gly Ser Leu Cys Lys Lys Val Lys Leu Ser Asn Asn
1               5                  10                  15


Ala Gln Asn Trp Gly Met Gln Arg Ala Thr Asn Val Thr Tyr Gln Ala
            20                  25                  30


His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly Thr Arg Gly
        35                  40                  45


Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser Gly Ala Gly
    50                  55                  60


Lys Thr Thr Val Ser Met Ala Leu Glu Glu Tyr Leu Val Cys His Gly
65                  70                  75                  80
```

```
Ile Pro Cys Tyr Thr Leu Asp Gly Asp Asn Ile Arg Gln Gly Leu Asn
                85                  90                  95

Lys Asn Leu Gly Phe Ser Pro Glu Asp Arg Glu Glu Asn Val Arg Arg
            100                 105                 110

Ile Ala Glu Val Ala Lys Leu Phe Ala Asp Ala Gly Leu Val Cys Ile
        115                 120                 125

Thr Ser Phe Ile Ser Pro Tyr Thr Gln Asp Arg Asn Asn Ala Arg Gln
    130                 135                 140

Ile His Glu Gly Ala Ser Leu Pro Phe Phe Glu Val Phe Val Asp Ala
145                 150                 155                 160

Pro Leu His Val Cys Glu Gln Arg Asp Val Lys Gly Leu Tyr Lys Lys
                165                 170                 175

Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr Gly Ile Asp Ser Glu Tyr
            180                 185                 190

Glu Lys Pro Glu Ala Pro Glu Leu Val Leu Lys Thr Asp Ser Cys Asp
        195                 200                 205

Val Asn Asp Cys Val Gln Gln Val Val Glu Leu Leu Gln Glu Arg Asp
    210                 215                 220

Ile Val Pro Val Asp Ala Ser Tyr Glu Val Lys Glu Leu Tyr Val Pro
225                 230                 235                 240

Glu Asn Lys Leu His Leu Ala Lys Thr Asp Ala Glu Thr Leu Pro Ala
                245                 250                 255

Leu Lys Ile Asn Lys Val Asp Met Gln Trp Val Gln Val Leu Ala Glu
            260                 265                 270

Gly Trp Ala Thr Pro Leu Asn Gly Phe Met Arg Glu Arg Glu Tyr Leu
        275                 280                 285

Gln Cys Leu His Phe Asp Cys Leu Leu Asp Gly Gly Val Ile Asn Leu
    290                 295                 300

Ser Val Pro Ile Val Leu Thr Ala Thr His Glu Asp Lys Glu Arg Leu
```

305 310 315 320

Asp Gly Cys Thr Ala Phe Ala Leu Met Tyr Glu Gly Arg Arg Val Ala
325 330 335

Ile Leu Arg Asn Pro Glu Phe Phe Glu His Arg Lys Glu Glu Arg Cys
340 345 350

Ala Arg Gln Trp Gly Thr Thr Cys Lys Asn His Pro Tyr Ile Lys Met
355 360 365

Val Met Glu Gln Gly Asp Trp Leu Ile Gly Gly Asp Leu Gln Val Leu
370 375 380

Asp Arg Val Tyr Trp Asn Asp Gly Leu Asp Gln Tyr Arg Leu Thr Pro
385 390 395 400

Thr Glu Leu Lys Gln Lys Phe Lys Asp Met Asn Ala Asp Ala Val Phe
405 410 415

Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met
420 425 430

Gln Asp Thr His Lys Gln Leu Leu Glu Arg Gly Tyr Arg Arg Pro Val
435 440 445

Leu Leu Leu His Pro Leu Gly Gly Trp Thr Lys Asp Asp Asp Val Pro
450 455 460

Leu Met Trp Arg Met Lys Gln His Ala Ala Val Leu Glu Glu Gly Val
465 470 475 480

Leu Asn Pro Glu Thr Thr Val Val Ala Ile Phe Pro Ser Pro Met Met
485 490 495

Tyr Ala Gly Pro Thr Glu Val Gln Trp His Cys Arg Ala Arg Met Val
500 505 510

Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Pro
515 520 525

His Pro Glu Thr Gly Lys Asp Leu Tyr Glu Pro Ser His Gly Ala Lys
530 535 540

```
Val Leu Thr Met Ala Pro Gly Leu Ile Thr Leu Glu Ile Val Pro Phe
545                 550                 555                 560


Arg Val Ala Ala Tyr Asn Lys Lys Lys Lys Arg Met Asp Tyr Tyr Asp
                565                 570                 575


Ser Glu His His Glu Asp Phe Glu Phe Ile Ser Gly Thr Arg Met Arg
            580                 585                 590


Lys Leu Ala Arg Glu Gly Gln Lys Pro Pro Glu Gly Phe Met Ala Pro
        595                 600                 605


Lys Ala Trp Thr Val Leu Thr Glu Tyr Tyr Lys Ser Leu Glu Lys Ala
    610                 615                 620


<210> 303
<211> 614
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 45; "

<220>
<221> source
<223> /note="Gene Symbol: PAPSS2; "

<220>
<221> source
<223> /note="Gene Name:
      3'-phosphoadenosine 5'-phosphosulfate synthase 2; "

<220>
<221> source
<223> /note="Uniprot ID:  O95340; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000354436"

<400> 303
Met Ser Gly Ile Lys Lys Gln Lys Thr Glu Asn Gln Gln Lys Ser Thr
1               5                   10                  15


Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln
            20                  25                  30
```

```
Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr
        35                  40                  45

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

Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn
65                  70                  75                  80

Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg
                85                  90                  95

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

Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp
        115                 120                 125

Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe
    130                 135                 140

Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp Val
145                 150                 155                 160

Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr
                165                 170                 175

Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Arg Val Leu
            180                 185                 190

Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu
        195                 200                 205

Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile
    210                 215                 220

His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu
225                 230                 235                 240

Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp
                245                 250                 255

Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met
```

260 265 270

Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp
275 280 285

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

Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys Phe Val Leu Ala His
305 310 315 320

Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala Glu Phe Tyr Glu His
325 330 335

Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly Thr Thr Cys Thr Lys
340 345 350

His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val Gly
355 360 365

Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp Asn Asp Gly Leu Asp
370 375 380

Gln Tyr Arg Leu Thr Pro Leu Glu Leu Lys Gln Lys Cys Lys Glu Met
385 390 395 400

Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn
405 410 415

Gly His Ala Leu Leu Met Gln Asp Thr Arg Arg Arg Leu Leu Glu Arg
420 425 430

Gly Tyr Lys His Pro Val Leu Leu Leu His Pro Leu Gly Gly Trp Thr
435 440 445

Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met Lys Gln His Ala Ala
450 455 460

Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser Thr Ile Val Ala Ile
465 470 475 480

Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr Glu Val Gln Trp His
485 490 495

```
Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg
            500                 505                 510

Asp Pro Ala Gly Met Pro His Pro Glu Thr Lys Lys Asp Leu Tyr Glu
        515                 520                 525

Pro Thr His Gly Gly Lys Val Leu Ser Met Ala Pro Gly Leu Thr Ser
    530                 535                 540

Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr Asn Lys Ala Lys Lys
545                 550                 555                 560

Ala Met Asp Phe Tyr Asp Pro Ala Arg His Asn Glu Phe Asp Phe Ile
                565                 570                 575

Ser Gly Thr Arg Met Arg Lys Leu Ala Arg Glu Gly Glu Asn Pro Pro
            580                 585                 590

Asp Gly Phe Met Ala Pro Lys Ala Trp Lys Val Leu Thr Asp Tyr Tyr
        595                 600                 605

Arg Ser Leu Glu Lys Asn
    610


<210> 304
<211> 619
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 45; "

<220>
<221> source
<223> /note="Gene Symbol: PAPSS2; "

<220>
<221> source
<223> /note="Gene Name:
      3'-phosphoadenosine 5'-phosphosulfate synthase 2; "

<220>
<221> source
<223> /note="Uniprot ID:  O95340; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000406157"

<400> 304
Met Ser Gly Ile Lys Lys Gln Lys Thr Glu Asn Gln Gln Lys Ser Thr
1 5 10 15

Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln
20 25 30

Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr
35 40 45

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

Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn
65 70 75 80

Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg
85 90 95

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

Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp
115 120 125

Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe
130 135 140

Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp Val
145 150 155 160

Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr
165 170 175

Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Arg Val Leu
180 185 190

Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu
195 200 205

Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile

```
    210                 215                 220

His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu
225                 230                 235                 240

Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp
                245                 250                 255

Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met
            260                 265                 270

Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp
        275                 280                 285

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

Leu Pro Val Ser Ala Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys
305                 310                 315                 320

Phe Val Leu Ala His Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala
                325                 330                 335

Glu Phe Tyr Glu His Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly
            340                 345                 350

Thr Thr Cys Thr Lys His Pro His Ile Lys Met Val Met Glu Ser Gly
        355                 360                 365

Asp Trp Leu Val Gly Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp
    370                 375                 380

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

Lys Cys Lys Glu Met Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg
                405                 410                 415

Asn Pro Val His Asn Gly His Ala Leu Leu Met Gln Asp Thr Arg Arg
            420                 425                 430

Arg Leu Leu Glu Arg Gly Tyr Lys His Pro Val Leu Leu Leu His Pro
        435                 440                 445
```

```
Leu Gly Gly Trp Thr Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met
    450                 455                 460

Lys Gln His Ala Ala Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser
465                 470                 475                 480

Thr Ile Val Ala Ile Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr
                485                 490                 495

Glu Val Gln Trp His Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe
            500                 505                 510

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

Lys Asp Leu Tyr Glu Pro Thr His Gly Gly Lys Val Leu Ser Met Ala
    530                 535                 540

Pro Gly Leu Thr Ser Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr
545                 550                 555                 560

Asn Lys Ala Lys Lys Ala Met Asp Phe Tyr Asp Pro Ala Arg His Asn
                565                 570                 575

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

Gly Glu Asn Pro Pro Asp Gly Phe Met Ala Pro Lys Ala Trp Lys Val
        595                 600                 605

Leu Thr Asp Tyr Tyr Arg Ser Leu Glu Lys Asn
    610                 615


<210> 305
<211> 429
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 46; "

<220>
<221> source
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<223> /note="Gene Symbol: PDPK1; "

<220>
<221> source
<223> /note="Gene Name:
3-phosphoinositide dependent prt kinase 1; "

<220>
<221> source
<223> /note="Uniprot ID: O15530; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000268673"

<400> 305

```
Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
1               5                   10                  15


Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
            20                  25                  30


Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
        35                  40                  45


Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
    50                  55                  60


Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
65                  70                  75                  80


Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
                85                  90                  95


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


Asn Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr
        115                 120                 125


Glu Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile
    130                 135                 140


Ile Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu
145                 150                 155                 160


Tyr Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu
```

```
                165                 170                 175

Lys Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu
            180                 185                 190

Asp Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro
        195                 200                 205

Leu Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His
    210                 215                 220

Gln Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu
225                 230                 235                 240

Asp Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe
                245                 250                 255

Gly Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala
            260                 265                 270

Ser Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr
        275                 280                 285

Ile His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser
    290                 295                 300

Glu Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro
305                 310                 315                 320

Trp His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val
                325                 330                 335

Asp Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr
            340                 345                 350

Glu Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys
        355                 360                 365

Gly Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe
    370                 375                 380

Lys Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp
385                 390                 395                 400
```

```
Pro Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp
                405                 410                 415


Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
            420                 425


<210> 306
<211> 556
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 46; "

<220>
<221> source
<223> /note="Gene Symbol: PDPK1; "

<220>
<221> source
<223> /note="Gene Name:
      3-phosphoinositide dependent prt kinase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  O15530; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000344220"

<400> 306
Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
1               5                   10                  15


Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
            20                  25                  30


Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
        35                  40                  45


Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
    50                  55                  60


Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
65                  70                  75                  80
```

```
Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
                85                  90                  95

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

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
        115                 120                 125

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
    130                 135                 140

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
145                 150                 155                 160

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
                165                 170                 175

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
            180                 185                 190

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
        195                 200                 205

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
    210                 215                 220

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
225                 230                 235                 240

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
                245                 250                 255

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
            260                 265                 270

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
        275                 280                 285

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys
    290                 295                 300

Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp
```

305 310 315 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu
325 330 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln
340 345 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp
355 360 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly
370 375 380

Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser
385 390 395 400

Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile
405 410 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu
420 425 430

Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp
435 440 445

His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp
450 455 460

Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu
465 470 475 480

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly
485 490 495

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys
500 505 510

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro
515 520 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg
530 535 540

```
Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
545                 550                 555


<210> 307
<211> 529
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 46; "

<220>
<221> source
<223> /note="Gene Symbol: PDPK1; "

<220>
<221> source
<223> /note="Gene Name:
      3-phosphoinositide dependent prt kinase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373876"

<400> 307
Met Val Arg Thr Gln Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly
1               5                   10                  15


Gly Ser Arg Gln Gly Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg
            20                  25                  30


Pro Gly Ala Gly Ser Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg
        35                  40                  45


Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly
    50                  55                  60


Ser Phe Ser Thr Val Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu
65                  70                  75                  80


Tyr Ala Ile Lys Ile Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys
                85                  90                  95


Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met Ser Arg Leu Asp His
            100                 105                 110
```

```
Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu
        115                 120                 125

Tyr Phe Gly Leu Ser Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile
    130                 135                 140

Arg Lys Ile Gly Ser Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala
145                 150                 155                 160

Glu Ile Val Ser Ala Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His
                165                 170                 175

Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile
            180                 185                 190

Gln Ile Thr Asp Phe Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys
        195                 200                 205

Gln Ala Arg Ala Asn Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro
    210                 215                 220

Glu Leu Leu Thr Glu Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala
225                 230                 235                 240

Leu Gly Cys Ile Ile Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg
                245                 250                 255

Ala Gly Asn Glu Tyr Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr
            260                 265                 270

Asp Phe Pro Glu Lys Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys
        275                 280                 285

Leu Leu Val Leu Asp Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu
    290                 295                 300

Gly Tyr Gly Pro Leu Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp
305                 310                 315                 320

Glu Asn Leu His Gln Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro
                325                 330                 335

Ala Met Ser Glu Asp Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu
```

```
            340                 345                 350

Leu Ser Gln Phe Gly Cys Met Gln Val Ser Ser Ser Ser Ser Ser His
        355                 360                 365

Ser Leu Ser Ala Ser Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn
    370                 375                 380

Ile Glu Gln Tyr Ile His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp
385                 390                 395                 400

Leu Gln Phe Ser Glu Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala
                405                 410                 415

Gly Gly Asn Pro Trp His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys
            420                 425                 430

Met Gly Pro Val Asp Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln
        435                 440                 445

Leu Leu Leu Thr Glu Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn
    450                 455                 460

Lys Val Leu Lys Gly Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu
465                 470                 475                 480

Ala Lys Asn Phe Lys Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr
                485                 490                 495

Tyr Leu Met Asp Pro Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile
            500                 505                 510

Gln Glu Val Trp Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val
        515                 520                 525

Gln
```

<210> 308
<211> 454
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 46; "

<220>
<221> source
<223> /note="Gene Symbol: PDPK1; "

<220>
<221> source
<223> /note="Gene Name:
3-phosphoinositide dependent prt kinase 1; "

<220>
<221> source
<223> /note="Uniprot ID: O15530; "

<220>
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<223> /note="ENSP ID: ENSP00000395357"

<400> 308

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

Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
            20                  25                  30

Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
        35                  40                  45

Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
    50                  55                  60

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
65                  70                  75                  80

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
                85                  90                  95

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

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
        115                 120                 125

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
    130                 135                 140
```

```
Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
145                 150                 155                 160

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
                165                 170                 175

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
            180                 185                 190

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
        195                 200                 205

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
    210                 215                 220

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
225                 230                 235                 240

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
                245                 250                 255

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
            260                 265                 270

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
        275                 280                 285

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys
    290                 295                 300

Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp
305                 310                 315                 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu
                325                 330                 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln
            340                 345                 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp
        355                 360                 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly
```

```
    370                 375                 380

Cys Met Gln Val Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser
385                 390                 395                 400

Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile
                405                 410                 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu
            420                 425                 430

Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Cys
        435                 440                 445

Leu Thr Gly Arg Ile Ile
    450


<210> 309
<211> 35
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 46; "

<220>
<221> source
<223> /note="Gene Symbol: PDPK1; "

<220>
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<223> /note="Gene Name:
      3-phosphoinositide dependent prt kinase 1; "

<220>
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<223> /note="ENSP ID: ENSP00000455025"

<400> 309
Met Ala Arg Thr Thr Ser Gln Leu Arg Asn Arg Pro Gly Leu Pro Pro
1               5                   10                  15

Gly Thr Gly Ser Leu Ala Pro Pro Pro Ala Arg Glu Ala Glu Gly Ala
            20                  25                  30

Ser Ser Cys
        35
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<210> 310
<211> 40
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
3-phosphoinositide dependent prt kinase 1; "

<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 310
Xaa His His Ser Glu Leu Glu Thr Ser Ile Leu Tyr Phe Arg Arg Ser
1 5 10 15

Leu Ser Trp Asn Met Thr Phe Gln Lys Asn Ser Ser Leu Arg Gln Glu
20 25 30

Thr Ser Trp Arg Asn Phe Trp Phe
35 40

<210> 311
<211> 88
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<223> /note="Gene Name:
3-phosphoinositide dependent prt kinase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455492"

<400> 311
Met Lys Ile Cys Thr Ser Arg Ser Gln Ile Leu Glu Gln Gln Lys Ser
1 5 10 15

Tyr Pro Gln Arg Ala Asn Lys Pro Gly Pro Thr His Ser Trp Glu Gln
20 25 30

Arg Ser Thr Phe Leu Gln Ser Cys Ser Arg Arg Ser Pro Pro Val Arg
35 40 45

Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln Leu Val Ala Gly Leu
50 55 60

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

Lys Leu Glu Tyr Asp Phe Pro Glu
85

<210> 312
<211> 149
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: PDPK1; "

<220>
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<223> /note="Gene Name:
3-phosphoinositide dependent prt kinase 1; "

<220>
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<223> /note="ENSP ID: ENSP00000455551"

<400> 312
Met Val Arg Thr Gln Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly
1 5 10 15

```
Gly Ser Arg Gln Gly Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg
            20                  25                  30

Pro Gly Ala Gly Ser Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg
        35                  40                  45

Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly
    50                  55                  60

Ser Phe Ser Thr Val Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu
65                  70                  75                  80

Tyr Ala Ile Lys Ile Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys
                85                  90                  95

Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met Ser Arg Leu Asp His
            100                 105                 110

Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu
        115                 120                 125

Tyr Phe Gly Leu Ser Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile
    130                 135                 140

Arg Lys Ile Gly Ser
145
```

<210> 313
<211> 55
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: PDPK1; "

<220>
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<223> /note="Gene Name:
3-phosphoinositide dependent prt kinase 1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000455684"

<400> 313
Met Ala Arg Thr Thr Ser Gln Leu Ile Leu Asp Asp Ser Gly Arg Glu
1   5   10   15

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

Pro Val Ala Val Leu Ser Val Val Gly Ser Pro Trp Glu Ala Glu Cys
        35   40   45

Ala Gly Ser Pro Arg Gly Lys
    50   55

<210> 314
<211> 500
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
      4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="Uniprot ID: P80404; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000268251"

<400> 314
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1   5   10   15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
            20   25   30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
        35   40   45

```
Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile
    50                  55                  60

Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser
65                  70                  75                  80

Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
                85                  90                  95

Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser His Pro Ala Leu
            100                 105                 110

Leu Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg
        115                 120                 125

Pro Ala Leu Gly Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg
    130                 135                 140

Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr
145                 150                 155                 160

Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe
                165                 170                 175

Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Gln Glu
            180                 185                 190

Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Gly Cys Pro Asp Tyr
        195                 200                 205

Ser Ile Leu Ser Phe Met Gly Ala Phe His Gly Arg Thr Met Gly Cys
    210                 215                 220

Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
225                 230                 235                 240

Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
                245                 250                 255

Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Arg Cys Leu Glu Glu
            260                 265                 270
```

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

Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
    290                 295                 300

Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Gly
305                 310                 315                 320

Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
                325                 330                 335

Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
            340                 345                 350

Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe His Lys Glu
        355                 360                 365

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly
    370                 375                 380

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

Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu
                405                 410                 415

Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg
            420                 425                 430

Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser
        435                 440                 445

Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu
    450                 455                 460

Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe
465                 470                 475                 480

Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu
                485                 490                 495
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Ala Asp Phe Lys
500

<210> 315
<211> 500
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 47; "

<220>
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<223> /note="Gene Symbol: ABAT; "

<220>
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<223> /note="Gene Name:
4-aminobutyrate aminotransferase; "

<220>
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<223> /note="Uniprot ID: P80404; "

<220>
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<223> /note="ENSP ID: ENSP00000379845"

<400> 315
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1 5 10 15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
20 25 30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
35 40 45

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

Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser
65 70 75 80

Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
85 90 95

Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser His Pro Ala Leu
100 105 110

```
Leu Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg
        115                 120                 125

Pro Ala Leu Gly Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg
    130                 135                 140

Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr
145                 150                 155                 160

Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe
                165                 170                 175

Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Gln Glu
            180                 185                 190

Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Gly Cys Pro Asp Tyr
        195                 200                 205

Ser Ile Leu Ser Phe Met Gly Ala Phe His Gly Arg Thr Met Gly Cys
    210                 215                 220

Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
225                 230                 235                 240

Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
                245                 250                 255

Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Arg Cys Leu Glu Glu
            260                 265                 270

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

Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
    290                 295                 300

Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Gly
305                 310                 315                 320

Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
                325                 330                 335
```

```
Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
            340                 345                 350

Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe His Lys Glu
        355                 360                 365

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly
    370                 375                 380

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

Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu
                405                 410                 415

Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg
            420                 425                 430

Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser
        435                 440                 445

Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu
    450                 455                 460

Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe
465                 470                 475                 480

Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu
                485                 490                 495

Ala Asp Phe Lys
            500


<210> 316
<211> 500
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "
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<220>
<221> source
<223> /note="Gene Name:
4-aminobutyrate aminotransferase; "

<220>
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<223> /note="Uniprot ID: P80404; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000411916"

<400> 316

```
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                  10                  15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
            20                  25                  30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
        35                  40                  45

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

Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser
65                  70                  75                  80

Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
                85                  90                  95

Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser His Pro Ala Leu
            100                 105                 110

Leu Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg
        115                 120                 125

Pro Ala Leu Gly Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg
    130                 135                 140

Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr
145                 150                 155                 160

Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe
                165                 170                 175
```

```
Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Gln Glu
            180                 185                 190

Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Gly Cys Pro Asp Tyr
        195                 200                 205

Ser Ile Leu Ser Phe Met Gly Ala Phe His Gly Arg Thr Met Gly Cys
    210                 215                 220

Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
225                 230                 235                 240

Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
                245                 250                 255

Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Arg Cys Leu Glu Glu
            260                 265                 270

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

Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
    290                 295                 300

Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Gly
305                 310                 315                 320

Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
                325                 330                 335

Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
            340                 345                 350

Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe His Lys Glu
        355                 360                 365

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly
    370                 375                 380

Asp Pro Ser Lys Asn Leu Leu Leu Ala Glu Val Ile Asn Ile Ile Lys
385                 390                 395                 400
```

```
Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu
                405                 410                 415

Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg
            420                 425                 430

Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser
        435                 440                 445

Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu
    450                 455                 460

Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe
465                 470                 475                 480

Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu
                485                 490                 495

Ala Asp Phe Lys
            500


<210> 317
<211> 91
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
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<223> /note="Gene Name:
      4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454415"

<400> 317
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                   10                  15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Asn Pro Gly Ser Arg His Ile
```

```
            20                  25                  30

Ser Gln Ala Ala Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro
        35                  40                  45

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

Gln Leu Asn Ile Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn
65                  70                  75                  80

Tyr Glu Glu Ser Arg Gly Asn Tyr Leu Val Asp
                85                  90


<210> 318
<211> 515
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
      4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454963"

<400> 318
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                   10                  15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
            20                  25                  30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
        35                  40                  45

Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile
    50                  55                  60
```

```
Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser
65                  70                  75                  80

Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
                85                  90                  95

Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser His Pro Ala Leu
            100                 105                 110

Leu Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg
        115                 120                 125

Pro Ala Leu Gly Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg
    130                 135                 140

Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr
145                 150                 155                 160

Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe
                165                 170                 175

Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Gln Glu
            180                 185                 190

Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Gly Cys Pro Asp Tyr
        195                 200                 205

Ser Ile Leu Ser Phe Met Gly Ala Phe His Gly Arg Thr Met Gly Cys
    210                 215                 220

Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
225                 230                 235                 240

Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
                245                 250                 255

Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Arg Cys Leu Glu Glu
            260                 265                 270

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

```
Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
    290                 295                 300

Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Gly
305                 310                 315                 320

Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
                325                 330                 335

Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
            340                 345                 350

Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe His Lys Glu
        355                 360                 365

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly
    370                 375                 380

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

Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu
                405                 410                 415

Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg
            420                 425                 430

Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser
        435                 440                 445

Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Ala Leu Pro Ala
    450                 455                 460

Cys Asp Phe Glu Lys Pro Arg Ser Ser Pro Thr Ser Cys Leu Phe Gln
465                 470                 475                 480

Val Trp Cys Trp Val Ala Val Val Thr Asn Pro Phe Val Ser Val Pro
                485                 490                 495

Arg Trp Ser Ser Gly Ile Thr Thr Leu Thr Cys Ser Ser Ile Phe Ser
            500                 505                 510

Val Thr Ser
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515

<210> 319
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455184"

<400> 319
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1 5 10 15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala
20 25 30

<210> 320
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
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<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455198"

<400> 320

```
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                   10                  15

Ser Tyr Arg Leu Leu Val Pro Gly Val Asn Glu Thr Ala Glu Tyr Asn
            20                  25                  30

Ser Glu Cys Arg Gly Cys Ala Phe Phe Leu Gln Leu Arg Arg Glu Pro
        35                  40                  45

Arg Gln Leu Pro Gly
    50
```

<210> 321
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455502"

<400> 321

```
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                   10                  15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
            20                  25                  30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
        35                  40                  45

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

Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser
65                  70                  75                  80
```

```
Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
                85                  90                  95

Tyr Ser Gln Ile Ser Ser Val Pro Ile Glu Ser His Cys His Pro Gly
            100                 105                 110

Trp Ser Ala Val Ala
        115


<210> 322
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
      4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456267"

<400> 322
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                   10                  15

Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
            20                  25                  30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
        35                  40                  45

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

Ile
65
```

<210> 323
<211> 515
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456330"

<400> 323
Met Trp Trp Gln His Ala Lys Gly Val Pro Val Pro Gln Gly Val Met
1 5 10 15

Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His Ser
20 25 30

Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala Ala
35 40 45

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

Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile Ile
65 70 75 80

Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser Arg
85 90 95

Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu Tyr
100 105 110

Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser His Pro Ala Leu Leu
115 120 125

Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg Pro
130 135 140

```
Ala Leu Gly Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg Gln
145                 150                 155                 160

Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr Met
                165                 170                 175

Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe Met
            180                 185                 190

Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Gln Glu Glu
        195                 200                 205

Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Gly Cys Pro Asp Tyr Ser
    210                 215                 220

Ile Leu Ser Phe Met Gly Ala Phe His Gly Arg Thr Met Gly Cys Leu
225                 230                 235                 240

Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser Phe
                245                 250                 255

Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu Glu
            260                 265                 270

Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Arg Cys Leu Glu Glu Val
        275                 280                 285

Glu Asp Leu Ile Val Lys Tyr Arg Lys Lys Lys Lys Thr Val Ala Gly
    290                 295                 300

Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala Ser
305                 310                 315                 320

Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Gly Cys
                325                 330                 335

Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly Lys
            340                 345                 350

Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val Met
        355                 360                 365
```

```
Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe His Lys Glu Glu
    370                 375                 380

Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly Asp
385                 390                 395                 400

Pro Ser Lys Asn Leu Leu Leu Ala Glu Val Ile Asn Ile Ile Lys Arg
                405                 410                 415

Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu Thr
            420                 425                 430

Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg Val
        435                 440                 445

Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser Ile
    450                 455                 460

Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu Gly
465                 470                 475                 480

Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe Arg
                485                 490                 495

Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu Ala
            500                 505                 510

Asp Phe Lys
        515


<210> 324
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 47; "

<220>
<221> source
<223> /note="Gene Symbol: ABAT; "

<220>
<221> source
<223> /note="Gene Name:
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4-aminobutyrate aminotransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456392"

<400> 324
Met Gln Leu Arg Gly Trp Gln His Ala Lys Gly Val Pro Val Pro Gln
1   5   10   15

Gly Val Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe
            20   25   30

Gln His Ser Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln
        35   40   45

Ala Ala Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met
    50   55   60

Lys Thr Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu
65   70   75   80

Asn Ile Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr
                85   90   95

<210> 325
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 48; "

<220>
<221> source
<223> /note="Gene Symbol: HOGA1; "

<220>
<221> source
<223> /note="Gene Name:
4-hydroxy-2-oxoglutarate aldolase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359676"

<220>
<221> MOD_RES
<222> (1)..(1)

<223> Any amino acid

<400> 325
Xaa Ser Gly Gly Asp Val Thr Arg Ile Gly Leu Ile Val His Lys Thr
1   5   10   15

Arg Lys Gln Asp Phe Gln Val Leu Ala Gly Ser Ala Gly Phe Leu Met
            20   25   30

Ala Ser Tyr Ala Leu Gly Ala Val Gly Gly Val Cys Ala Leu Ala Asn
        35   40   45

Val Leu Gly Ala Gln Val Cys Gln Leu Glu Arg Leu Cys Cys Thr Gly
    50   55   60

Gln Trp Glu Asp Ala Gln Lys Leu Gln His Arg Leu Ile Glu Pro Asn
65   70   75   80

Ala Ala Lys Ile Leu
                85

<210> 326
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 48; "

<220>
<221> source
<223> /note="Gene Symbol: HOGA1; "

<220>
<221> source
<223> /note="Gene Name:
      4-hydroxy-2-oxoglutarate aldolase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q86XE5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359680"

<400> 326
Met Leu Gly Pro Gln Val Trp Ser Ser Val Arg Gln Gly Leu Ser Arg
1   5   10   15

```
Ser Leu Ser Arg Asn Val Gly Val Trp Ala Ser Gly Glu Gly Lys Lys
            20                  25                  30

Val Asp Ile Ala Gly Ile Tyr Pro Pro Val Thr Thr Pro Phe Thr Ala
        35                  40                  45

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

Gly Thr Phe Pro Phe Arg Gly Phe Val Val Gln Gly Ser Asn Gly Glu
65                  70                  75                  80

Phe Pro Phe Leu Thr Ser Ser Glu Arg Leu Glu Val Val Ser Arg Val
                85                  90                  95

Arg Gln Ala Met Pro Lys Asn Arg Leu Leu Leu Ala Gly Ser Gly Cys
            100                 105                 110

Glu Ser Thr Gln Ala Thr Val Glu Met Thr Val Ser Met Ala Gln Val
        115                 120                 125

Gly Ala Asp Ala Ala Met Val Val Thr Pro Cys Tyr Tyr Arg Gly Arg
    130                 135                 140

Met Ser Ser Ala Ala Leu Ile His His Tyr Thr Lys Val Ala Asp Leu
145                 150                 155                 160

Ser Pro Ile Pro Val Val Leu Tyr Ser Val Pro Ala Asn Thr Gly Leu
                165                 170                 175

Asp Leu Pro Val Asp Ala Val Val Thr Leu Ser Gln His Pro Asn Ile
            180                 185                 190

Val Gly Met Lys Asp Ser Gly Gly Asp Val Thr Arg Ile Gly Leu Ile
        195                 200                 205

Val His Lys Thr Arg Lys Gln Asp Phe Gln Val Leu Ala Gly Ser Ala
    210                 215                 220

Gly Phe Leu Met Ala Ser Tyr Ala Leu Gly Ala Val Gly Gly Val Cys
225                 230                 235                 240
```

```
Ala Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu Arg Leu
                245                 250                 255

Cys Cys Thr Gly Gln Trp Glu Asp Ala Gln Lys Leu Gln His Arg Leu
            260                 265                 270

Ile Glu Pro Asn Ala Ala Val Thr Arg Arg Phe Gly Ile Pro Gly Leu
        275                 280                 285

Lys Lys Ile Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys Arg Ala
    290                 295                 300

Pro Leu Gln Glu Leu Ser Pro Ala Glu Glu Glu Ala Leu Arg Met Asp
305                 310                 315                 320

Phe Thr Ser Asn Gly Trp Leu
                325
```

<210> 327
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 48; "

<220>
<221> source
<223> /note="Gene Symbol: HOGA1; "

<220>
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<223> /note="Gene Name:
4-hydroxy-2-oxoglutarate aldolase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q86XE5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359681"

<400> 327

```
Met Leu Gly Pro Gln Val Trp Ser Ser Val Arg Gln Gly Leu Ser Arg
1               5                   10                  15

Ser Leu Ser Arg Asn Val Gly Val Trp Ala Ser Gly Glu Gly Lys Lys
            20                  25                  30
```

```
Val Asp Ile Ala Gly Ile Tyr Pro Pro Val Thr Thr Pro Phe Thr Ala
        35                  40                  45

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

Gly Thr Phe Pro Phe Arg Gly Ala Val Gly Gly Val Cys Ala Leu Ala
65                  70                  75                  80

Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu Arg Leu Cys Cys Thr
                85                  90                  95

Gly Gln Trp Glu Asp Ala Gln Lys Leu Gln His Arg Leu Ile Glu Pro
            100                 105                 110

Asn Ala Ala Val Thr Arg Arg Phe Gly Ile Pro Gly Leu Lys Lys Ile
        115                 120                 125

Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys Arg Ala Pro Leu Gln
    130                 135                 140

Glu Leu Ser Pro Ala Glu Glu Glu Ala Leu Arg Met Asp Phe Thr Ser
145                 150                 155                 160

Asn Gly Trp Leu
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<210> 328
<211> 393
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 49; "

<220>
<221> source
<223> /note="Gene Symbol: HPD; "

<220>
<221> source
<223> /note="Gene Name:
4-hydroxyphenylpyruvate
dioxygenase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000289004"

<400> 328
Met Thr Thr Tyr Ser Asp Lys Gly Ala Lys Pro Glu Arg Gly Arg Phe
1   5   10   15

Leu His Phe His Ser Val Thr Phe Trp Val Gly Asn Ala Lys Gln Ala
            20   25   30

Thr Ser Phe Tyr Cys Ser Lys Met Gly Phe Glu Pro Leu Ala Tyr Arg
        35   40   45

Gly Leu Glu Thr Gly Ser Arg Glu Val Val Ser His Val Ile Lys Gln
    50   55   60

Gly Lys Ile Val Phe Val Leu Ser Ser Ala Leu Asn Pro Trp Asn Lys
65   70   75   80

Glu Met Gly Asp His Leu Val Lys His Gly Asp Gly Val Lys Asp Ile
                85   90   95

Ala Phe Glu Val Glu Asp Cys Asp Tyr Ile Val Gln Lys Ala Arg Glu
            100   105   110

Arg Gly Ala Lys Ile Met Arg Glu Pro Trp Val Glu Gln Asp Lys Phe
        115   120   125

Gly Lys Val Lys Phe Ala Val Leu Gln Thr Tyr Gly Asp Thr Thr His
    130   135   140

Thr Leu Val Glu Lys Met Asn Tyr Ile Gly Gln Phe Leu Pro Gly Tyr
145   150   155   160

Glu Ala Pro Ala Phe Met Asp Pro Leu Leu Pro Lys Leu Pro Lys Cys
                165   170   175

Ser Leu Glu Met Ile Asp His Ile Val Gly Asn Gln Pro Asp Gln Glu
            180   185   190

Met Val Ser Ala Ser Glu Trp Tyr Leu Lys Asn Leu Gln Phe His Arg
        195   200   205

```
Phe Trp Ser Val Asp Asp Thr Gln Val His Thr Glu Tyr Ser Ser Leu
    210                 215                 220

Arg Ser Ile Val Val Ala Asn Tyr Glu Glu Ser Ile Lys Met Pro Ile
225                 230                 235                 240

Asn Glu Pro Ala Pro Gly Lys Lys Lys Ser Gln Ile Gln Glu Tyr Val
                245                 250                 255

Asp Tyr Asn Gly Gly Ala Gly Val Gln His Ile Ala Leu Lys Thr Glu
            260                 265                 270

Asp Ile Ile Thr Ala Ile Arg His Leu Arg Glu Arg Gly Leu Glu Phe
        275                 280                 285

Leu Ser Val Pro Ser Thr Tyr Tyr Lys Gln Leu Arg Glu Lys Leu Lys
    290                 295                 300

Thr Ala Lys Ile Lys Val Lys Glu Asn Ile Asp Ala Leu Glu Glu Leu
305                 310                 315                 320

Lys Ile Leu Val Asp Tyr Asp Glu Lys Gly Tyr Leu Leu Gln Ile Phe
                325                 330                 335

Thr Lys Pro Val Gln Asp Arg Pro Thr Leu Phe Leu Glu Val Ile Gln
            340                 345                 350

Arg His Asn His Gln Gly Phe Gly Ala Gly Asn Phe Asn Ser Leu Phe
        355                 360                 365

Lys Ala Phe Glu Glu Glu Gln Asn Leu Arg Gly Asn Leu Thr Asn Met
    370                 375                 380

Glu Thr Asn Gly Val Val Pro Gly Met
385                 390


<210> 329
<211> 354
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 49; "
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<220>
<221> source
<223> /note="Gene Symbol: HPD; "

<220>
<221> source
<223> /note="Gene Name:
4-hydroxyphenylpyruvate
dioxygenase; "

<220>
<221> source
<223> /note="Uniprot ID: P32754; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000441677"

<400> 329
Met Gly Phe Glu Pro Leu Ala Tyr Arg Gly Leu Glu Thr Gly Ser Arg
1   5   10   15

Glu Val Val Ser His Val Ile Lys Gln Gly Lys Ile Val Phe Val Leu
            20   25   30

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

Lys His Gly Asp Gly Val Lys Asp Ile Ala Phe Glu Val Glu Asp Cys
    50   55   60

Asp Tyr Ile Val Gln Lys Ala Arg Glu Arg Gly Ala Lys Ile Met Arg
65   70   75   80

Glu Pro Trp Val Glu Gln Asp Lys Phe Gly Lys Val Lys Phe Ala Val
                85   90   95

Leu Gln Thr Tyr Gly Asp Thr Thr His Thr Leu Val Glu Lys Met Asn
            100   105   110

Tyr Ile Gly Gln Phe Leu Pro Gly Tyr Glu Ala Pro Ala Phe Met Asp
        115   120   125

Pro Leu Leu Pro Lys Leu Pro Lys Cys Ser Leu Glu Met Ile Asp His
    130   135   140

Ile Val Gly Asn Gln Pro Asp Gln Glu Met Val Ser Ala Ser Glu Trp
145   150   155   160

Tyr Leu Lys Asn Leu Gln Phe His Arg Phe Trp Ser Val Asp Asp Thr
165 170 175

Gln Val His Thr Glu Tyr Ser Ser Leu Arg Ser Ile Val Val Ala Asn
180 185 190

Tyr Glu Glu Ser Ile Lys Met Pro Ile Asn Glu Pro Ala Pro Gly Lys
195 200 205

Lys Lys Ser Gln Ile Gln Glu Tyr Val Asp Tyr Asn Gly Gly Ala Gly
210 215 220

Val Gln His Ile Ala Leu Lys Thr Glu Asp Ile Ile Thr Ala Ile Arg
225 230 235 240

His Leu Arg Glu Arg Gly Leu Glu Phe Leu Ser Val Pro Ser Thr Tyr
245 250 255

Tyr Lys Gln Leu Arg Glu Lys Leu Lys Thr Ala Lys Ile Lys Val Lys
260 265 270

Glu Asn Ile Asp Ala Leu Glu Glu Leu Lys Ile Leu Val Asp Tyr Asp
275 280 285

Glu Lys Gly Tyr Leu Leu Gln Ile Phe Thr Lys Pro Val Gln Asp Arg
290 295 300

Pro Thr Leu Phe Leu Glu Val Ile Gln Arg His Asn His Gln Gly Phe
305 310 315 320

Gly Ala Gly Asn Phe Asn Ser Leu Phe Lys Ala Phe Glu Glu Glu Gln
325 330 335

Asn Leu Arg Gly Asn Leu Thr Asn Met Glu Thr Asn Gly Val Val Pro
340 345 350

Gly Met

<210> 330
<211> 371
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 50; "

<220>
<221> source
<223> /note="Gene Symbol: HPDL; "

<220>
<221> source
<223> /note="Gene Name:
4-hydroxyphenylpyruvate dioxygenase-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q96IR7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000335060"

<400> 330

```
Met Ala Ala Pro Ala Leu Arg Leu Cys His Ile Ala Phe His Val Pro
1               5                  10                  15

Ala Gly Gln Pro Leu Ala Arg Asn Leu Gln Arg Leu Phe Gly Phe Gln
            20                  25                  30

Pro Leu Ala Ser Arg Glu Val Asp Gly Trp Arg Gln Leu Ala Leu Arg
        35                  40                  45

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

Pro Leu Tyr Gly Leu Asp Pro Arg His Ala Val Pro Ser Ala Thr Asn
65                  70                  75                  80

Leu Cys Phe Asp Val Ala Asp Ala Gly Ala Ala Thr Arg Glu Leu Ala
                85                  90                  95

Ala Leu Gly Cys Ser Val Pro Val Pro Pro Val Arg Val Arg Asp Ala
            100                 105                 110

Gln Gly Ala Ala Thr Tyr Ala Val Val Ser Ser Pro Ala Gly Ile Leu
        115                 120                 125

Ser Leu Thr Leu Leu Glu Arg Ala Gly Tyr Arg Gly Pro Phe Leu Pro
```

```
    130                 135                 140

Gly Phe Arg Pro Val Ser Ser Ala Pro Gly Pro Gly Trp Val Ser Arg
145                 150                 155                 160

Val Asp His Leu Thr Leu Ala Cys Thr Pro Gly Ser Ser Pro Thr Leu
                165                 170                 175

Leu Arg Trp Phe His Asp Cys Leu Gly Phe Cys His Leu Pro Leu Ser
            180                 185                 190

Pro Gly Glu Asp Pro Glu Leu Gly Leu Glu Met Thr Ala Gly Phe Gly
        195                 200                 205

Leu Gly Gly Leu Arg Leu Thr Ala Leu Gln Ala Gln Pro Gly Ser Ile
    210                 215                 220

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

Gln Asp Gln Val Glu Gln Phe Leu Ala Arg His Lys Gly Pro Gly Leu
                245                 250                 255

Gln His Val Gly Leu Tyr Thr Pro Asn Ile Val Glu Ala Thr Glu Gly
            260                 265                 270

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

Gln Gln Pro Gly Lys Glu Arg Gln Ile Arg Ala Ala Gly His Glu Pro
    290                 295                 300

His Leu Leu Ala Arg Gln Gly Ile Leu Leu Asp Gly Asp Lys Gly Lys
305                 310                 315                 320

Phe Leu Leu Gln Val Phe Thr Lys Ser Leu Phe Thr Glu Asp Thr Phe
                325                 330                 335

Phe Leu Glu Leu Ile Gln Arg Gln Gly Ala Thr Gly Phe Gly Gln Gly
            340                 345                 350

Asn Ile Arg Ala Leu Trp Gln Ser Val Gln Glu Gln Ser Ala Arg Ser
        355                 360                 365
```

Gln Glu Ala
    370

<210> 331
<211> 201
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
      5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TCD5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000245552"

<400> 331
Met Ala Arg Ser Val Arg Val Leu Val Asp Met Asp Gly Val Leu Ala
1   5   10   15

Asp Phe Glu Ala Gly Leu Leu Arg Gly Phe Arg Arg Arg Phe Pro Glu
            20   25   30

Glu Pro His Val Pro Leu Glu Gln Arg Arg Gly Phe Leu Ala Arg Glu
        35   40   45

Gln Tyr Arg Ala Leu Arg Pro Asp Leu Ala Asp Lys Val Ala Ser Val
    50   55   60

Tyr Glu Ala Pro Gly Phe Phe Leu Asp Leu Glu Pro Ile Pro Gly Ala
65   70   75   80

Leu Asp Ala Val Arg Glu Met Asn Asp Leu Pro Asp Thr Gln Val Phe
                85   90   95

```
Ile Cys Thr Ser Pro Leu Leu Lys Tyr His His Cys Val Gly Glu Lys
            100                 105                 110

Tyr Arg Trp Val Glu Gln His Leu Gly Pro Gln Phe Val Glu Arg Ile
        115                 120                 125

Ile Leu Thr Arg Asp Lys Thr Val Val Leu Gly Asp Leu Leu Ile Asp
    130                 135                 140

Asp Lys Asp Thr Val Arg Gly Gln Glu Glu Thr Pro Ser Trp Glu His
145                 150                 155                 160

Ile Leu Phe Thr Cys Cys His Asn Arg His Leu Val Leu Pro Pro Thr
                165                 170                 175

Arg Arg Arg Leu Leu Ser Trp Ser Asp Asn Trp Arg Glu Ile Leu Asp
            180                 185                 190

Ser Lys Arg Gly Ala Ala Gln Arg Glu
        195                 200


<210> 332
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
      5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461927"

<400> 332
Met Ala Arg Ser Val Arg Val Leu Val Asp Met Asp Gly Val Leu Ala
1               5                   10                  15

Asp Phe Glu Ala Gly Leu Leu Arg Gly Phe Arg Arg Arg Phe Pro Glu
            20                  25                  30
```

```
Glu Pro His Val Pro Leu Glu Gln Arg Arg Gly Phe Leu Ala Arg Glu
        35                  40                  45

Gln Tyr Arg Ala Leu Arg Pro Asp Leu Ala Asp Lys Val Ala Ser Val
    50                  55                  60

Tyr Glu Ala Pro Gly Phe Phe Leu Asp Leu Glu Pro Ile Pro Gly Ala
65                  70                  75                  80

Leu Asp Ala Val Arg Glu Met Asn Asp Leu Pro Asp Thr Gln Val Phe
                85                  90                  95

Ile Cys Thr Ser Pro Leu Leu Lys Tyr His His Cys Val Gly Glu Lys
            100                 105                 110

Tyr Arg Trp Val Glu Gln His Leu Gly Pro Gln Phe Val Glu Arg Ile
        115                 120                 125

Ile Leu Thr Arg Asp Lys Thr Val Val Leu Gly Asp Leu Leu Ile Asp
    130                 135                 140

Asp Lys Asp Thr Val Arg Gly Gly Asp Pro Lys Leu Gly Ala His Leu
145                 150                 155                 160

Val His Leu Leu Pro Gln Ser Ala Pro Gly Pro Ala Pro Asp Lys Glu
                165                 170                 175

Thr Ala Ala Leu Leu Glu
            180


<210> 333
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
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<223> /note="Gene Name:
5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TCD5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462123"

<400> 333
Met Ala Arg Ser Val Arg Val Leu Val Asp Met Asp Gly Val Leu Ala
1 5 10 15

Asp Phe Glu Ala Gly Leu Leu Arg Gly Phe Arg Arg Arg Phe Pro Glu
20 25 30

Glu Pro His Val Pro Leu Glu Gln Arg Arg Gly Phe Leu Ala Arg Glu
35 40 45

Gln Tyr Arg Ala Leu Arg Pro Asp Leu Ala Asp Lys Val Ala Ser Val
50 55 60

Tyr Glu Ala Pro Gly Phe Phe Leu Asp Leu Glu Pro Ile Pro Gly Ala
65 70 75 80

Leu Asp Ala Val Arg Glu Met Asn Asp Leu Pro Asp Pro Leu Leu Lys
85 90 95

Tyr His His Cys Val Gly Glu Lys Val Trp Leu Pro Arg Pro Tyr Ser
100 105 110

Ala Arg Gly Ala Ala
115

<210> 334
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462455"

<400> 334
Met Asn Asp Leu Pro Asp Thr Gln Val Phe Ile Cys Thr Ser Pro Leu
1 5 10 15

Leu Lys Tyr His His Cys Val Gly Glu Lys Val Trp Leu Pro Arg Pro
20 25 30

Tyr Ser Ala Arg Gly Ala Ala
35

<210> 335
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462697"

<400> 335
Val Asp Met Asp Gly Val Leu Ala Asp Phe Glu Ala Gly Leu Leu Arg
1 5 10 15

Gly Phe Arg Arg Arg Phe Pro Glu Glu Pro His Val Pro Leu Glu Gln
20 25 30

Arg Arg Gly Phe Leu Ala Arg Glu Gln Tyr Arg Ala Leu Arg Pro Asp
35 40 45

```
Leu Ala Asp Lys Val Ala Ser Val Tyr Glu Ala Pro Gly Phe Phe Leu
    50                  55                  60

Asp Leu Glu Pro Ile Pro Gly Ala Leu Asp Ala Val Arg Glu Met Asn
65                  70                  75                  80

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

Tyr His His Cys Val Gly Glu Lys Glu Glu Thr Pro Ser Trp Glu His
            100                 105                 110

Ile Leu Phe Thr Cys Cys His Asn Arg His Leu Val Leu Pro Pro Thr
        115                 120                 125

Arg Arg Arg Leu Leu Ser Trp Ser Asp Asn Trp Arg Glu Ile Leu Asp
    130                 135                 140

Ser Lys Arg Gly Ala Ala Gln Arg Glu
145                 150


<210> 336
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
      5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462712"

<400> 336
Met Asn Asp Leu Pro Asp Thr Gln Val Phe Ile Cys Thr Ser Pro Leu
1               5                   10                  15

Leu Lys Tyr His His Cys Val Gly Glu Lys Tyr Arg Trp Val Glu Gln
            20                  25                  30
```

```
His Leu Gly Pro Gln Phe Val Glu Arg Ile Ile Leu Thr Arg Asp Lys
        35                  40                  45

Thr Val Val Leu Gly Asp Leu Leu Ile Asp Asp Lys Asp Thr Val Arg
    50                  55                  60

Gly Gln Glu Glu Thr Pro Ser Trp Glu His Ile Leu Phe Thr Cys Cys
65                  70                  75                  80

His Asn Arg His Leu Val Leu Pro Pro Thr Arg Arg Arg Leu Leu Ser
                85                  90                  95

Trp Ser Asp Asn Trp Arg Glu Ile Leu Asp Ser Lys Arg Gly Ala Ala
            100                 105                 110

Gln Arg Glu
        115


<210> 337
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
      5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462981"

<400> 337
Met Asn Asp Leu Pro Asp Thr Gln Val Phe Ile Cys Thr Ser Pro Leu
1               5                   10                  15

Leu Lys Tyr His His Cys Val Gly Glu Lys Val Trp Leu Pro Arg Pro
            20                  25                  30
```

Tyr Ser Ala Arg Gly Ala Ala
35

<210> 338
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 51; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C; "

<220>
<221> source
<223> /note="Gene Name:
5', 3'-nucleotidase, cytosolic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463947"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 338
Xaa Ala Pro Gly Phe Phe Leu Asp Leu Glu Pro Ile Pro Gly Ala Leu
1 5 10 15

Asp Ala Val Arg Glu Met Asn Asp Leu Pro Asp Thr Gln Val Phe Ile
20 25 30

Cys Thr Ser Pro Leu Leu Lys Tyr His His Cys Val Gly Glu Lys Ala
35 40 45

Arg Arg Arg Pro Gln Ala Gly Ser Thr Ser Cys Ser Pro Ala Ala Thr
50 55 60

Ile Gly Thr Trp Ser Cys Pro Arg Gln Gly Asp Gly Cys Ser Pro Gly
65 70 75 80

Val Thr Thr Gly Gly Arg Ser
85

<210> 339
<211> 203
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 52; "

<220>
<221> source
<223> /note="Gene Symbol: MTHFS; "

<220>
<221> source
<223> /note="Gene Name:
5,10-m 356ethenyltetrahydrofolate synthetase
(5-formyltetrahydrofolate cyclo-ligase); "

<220>
<221> source
<223> /note="Uniprot ID: P49914; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000258874"

<400> 339
Met Ala Ala Ala Ala Val Ser Ser Ala Lys Arg Ser Leu Arg Gly Glu
1   5   10   15

Leu Lys Gln Arg Leu Arg Ala Met Ser Ala Glu Glu Arg Leu Arg Gln
            20   25   30

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

Ser Lys Arg Ile Ser Ile Phe Leu Ser Met Gln Asp Glu Ile Glu Thr
    50   55   60

Glu Glu Ile Ile Lys Asp Ile Phe Gln Arg Gly Lys Ile Cys Phe Ile
65   70   75   80

Pro Arg Tyr Arg Phe Gln Ser Asn His Met Asp Met Val Arg Ile Glu
                85   90   95

Ser Pro Glu Glu Ile Ser Leu Leu Pro Lys Thr Ser Trp Asn Ile Pro
            100   105   110

Gln Pro Gly Glu Gly Asp Val Arg Glu Glu Ala Leu Ser Thr Gly Gly

```
        115                 120                 125

Leu Asp Leu Ile Phe Met Pro Gly Leu Gly Phe Asp Lys His Gly Asn
    130                 135                 140

Arg Leu Gly Arg Gly Lys Gly Tyr Tyr Asp Ala Tyr Leu Lys Arg Cys
145                 150                 155                 160

Leu Gln His Gln Glu Val Lys Pro Tyr Thr Leu Ala Leu Ala Phe Lys
                165                 170                 175

Glu Gln Ile Cys Leu Gln Val Pro Val Asn Glu Asn Asp Met Lys Val
            180                 185                 190

Asp Glu Val Leu Tyr Glu Asp Ser Ser Thr Ala
        195                 200


<210> 340
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 52; "

<220>
<221> source
<223> /note="Gene Symbol: MTHFS; "

<220>
<221> source
<223> /note="Gene Name:
      5,10-methenyltetrahydrofolate synthetase
      (5-formyltetrahydrofolate cyclo-ligase); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454318"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 340
Xaa Val Lys Pro Tyr Thr Leu Ala Leu Ala Phe Lys Glu Gln Ile Cys
1               5                   10                  15
```

```
Leu Gln Val Pro Val Asn Glu Asn Asp Met Lys Val Asp Glu Val Leu
            20                  25                  30


Tyr Glu Asp Ser Ser Thr Ala
        35


<210> 341
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 52; "

<220>
<221> source
<223> /note="Gene Symbol: MTHFS; "

<220>
<221> source
<223> /note="Gene Name:
      5,10-methenyltetrahydrofolate synthetase
      (5-formyltetrahydrofolate cyclo-ligase); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454626"

<400> 341
Met Ala Ala Ala Ala Val Ser Ser Ala Lys Arg Ser Leu Arg Gly Glu
1               5                   10                  15


Leu Lys Gln Arg Leu Arg Ala Met Ser Ala Glu Glu Arg Leu Arg Gln
            20                  25                  30


Ser Arg Val Leu Ser Gln Lys Val Arg Gly Arg Pro
        35                  40


<210> 342
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 52; "

<220>
<221> source
<223> /note="Gene Symbol: MTHFS; "
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<220>
<221> source
<223> /note="Gene Name:
5,10-methenyltetrahydrofolate synthetase
(5-formyltetrahydrofolate cyclo-ligase); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489076"

<400> 342
Met Pro Gly Thr Val Gly Thr Ala Gly His Leu Tyr His Pro Arg Gln
1 5 10 15

Trp Arg Cys Arg Leu Arg Gly Pro Gly Glu Gly Pro Gly Ser Gly Arg
20 25 30

Ser Gly Gly Arg Ala Ala Thr Ala Pro Arg His Arg Ser Pro Asn Arg
35 40 45

Gly Gly Arg Ala Gly Pro Arg Gly Pro His Glu Gly Trp Val Pro Arg
50 55 60

Ala Arg Gly Glu Val Ile Ala His Ser Glu Tyr Gln Lys Ser Lys Arg
65 70 75 80

Ile Ser Ile Phe Leu Ser Met Gln Asp Glu Ile Glu Thr Glu Glu Ile
85 90 95

Ile Lys Asp Ile Phe Gln Arg Gly Lys Ile Cys Phe Ile Pro Arg Tyr
100 105 110

Arg Phe Gln Ser Asn His Met Asp Met Val Arg Ile Glu Ser Pro Glu
115 120 125

Glu Ile Ser Leu Leu Pro Lys Thr Ser Trp Asn Ile Pro Gln Pro Gly
130 135 140

Glu Gly Asp Val Arg Glu Glu Ala Leu Ser Thr Gly Gly Leu Asp Leu
145 150 155 160

Ile Phe Met Pro Gly Leu Gly Phe Asp Lys His Gly Asn Arg Leu Gly
165 170 175

Arg Gly Lys Gly Tyr Tyr Asp Ala Tyr Leu Lys Arg Cys Leu Gln His
180 185 190

```
Gln Glu Val Lys Pro Tyr Thr Leu Ala Leu Ala Phe Lys Glu Gln Ile
        195                 200                 205


Cys Leu Gln Val Pro Val Asn Glu Asn Asp Met Lys Val Asp Glu Val
    210                 215                 220


Leu Tyr Glu Asp Ser Ser Thr Ala
225                 230


<210> 343
<211> 228
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 53; "

<220>
<221> source
<223> /note="Gene Symbol: NT5M; "

<220>
<221> source
<223> /note="Gene Name:
      5',3'-nucleotidase,
      mitochondrial; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NPB1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373674"

<400> 343
Met Ile Arg Leu Gly Gly Trp Cys Ala Arg Arg Leu Cys Ser Ala Ala
1               5                   10                  15


Val Pro Ala Gly Arg Arg Gly Ala Ala Gly Gly Leu Gly Leu Ala Gly
            20                  25                  30


Gly Arg Ala Leu Arg Val Leu Val Asp Met Asp Gly Val Leu Ala Asp
        35                  40                  45


Phe Glu Gly Gly Phe Leu Arg Lys Phe Arg Ala Arg Phe Pro Asp Gln
    50                  55                  60
```

```
Pro Phe Ile Ala Leu Glu Asp Arg Arg Gly Phe Trp Val Ser Glu Gln
65                  70                  75                  80

Tyr Gly Arg Leu Arg Pro Gly Leu Ser Glu Lys Ala Ile Ser Ile Trp
                85                  90                  95

Glu Ser Lys Asn Phe Phe Phe Glu Leu Glu Pro Leu Pro Gly Ala Val
            100                 105                 110

Glu Ala Val Lys Glu Met Ala Ser Leu Gln Asn Thr Asp Val Phe Ile
        115                 120                 125

Cys Thr Ser Pro Ile Lys Met Phe Lys Tyr Cys Pro Tyr Glu Lys Tyr
    130                 135                 140

Ala Trp Val Glu Lys Tyr Phe Gly Pro Asp Phe Leu Glu Gln Ile Val
145                 150                 155                 160

Leu Thr Arg Asp Lys Thr Val Val Ser Ala Asp Leu Leu Ile Asp Asp
                165                 170                 175

Arg Pro Asp Ile Thr Gly Ala Glu Pro Thr Pro Ser Trp Glu His Val
            180                 185                 190

Leu Phe Thr Ala Cys His Asn Gln His Leu Gln Leu Gln Pro Pro Arg
        195                 200                 205

Arg Arg Leu His Ser Trp Ala Asp Asp Trp Lys Ala Ile Leu Asp Ser
    210                 215                 220

Lys Arg Pro Cys
225


<210> 344
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 53; "

<220>
<221> source
<223> /note="Gene Symbol: NT5M; "
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<220>
<221> source
<223> /note="Gene Name:
5',3'-nucleotidase,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463674"

<400> 344
Met Ile Arg Leu Gly Gly Trp Cys Ala Arg Arg Leu Cys Ser Ala Ala
1 5 10 15

Val Pro Ala Gly Arg Arg Gly Ala Ala Gly Gly Leu Gly Leu Ala Gly
20 25 30

Gly Arg Ala Leu Arg Val Leu Val Asp Met Asp Gly Val Leu Ala Asp
35 40 45

Phe Glu Gly Gly Phe Leu Arg Lys Phe Arg Ala Arg Phe Pro Asp Gln
50 55 60

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

Tyr Gly Arg Leu Arg Pro Gly Leu Ser Ser Trp Pro Cys
85 90

<210> 345
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 53; "

<220>
<221> source
<223> /note="Gene Symbol: NT5M; "

<220>
<221> source
<223> /note="Gene Name:
5',3'-nucleotidase,
mitochondrial; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000464303"

<400> 345
Met Ile Arg Leu Gly Gly Trp Cys Ala Arg Arg Leu Cys Ser Ala Ala
1 5 10 15

Val Pro Ala Gly Arg Arg Gly Ala Ala Gly Gly Leu Gly Leu Ala Gly
20 25 30

Gly Arg Ala Leu Arg Val Leu Val Asp Met Asp Gly Val Leu Ala Asp
35 40 45

Phe Glu Gly Gly Phe Leu Arg Lys Phe Arg Ala Arg Phe Pro Asp Gln
50 55 60

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

Tyr Gly Arg Leu Arg Pro Gly Leu Ser Val Ser Val Pro Ala Pro Pro
85 90 95

Arg Ala Gly Pro Pro Ser Arg Pro Glu Pro Gln Thr Pro Pro Leu Arg
100 105 110

Arg

<210> 346
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 53; "

<220>
<221> source
<223> /note="Gene Symbol: NT5M; "

<220>
<221> source
<223> /note="Gene Name:
5',3'-nucleotidase,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467567"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 346
Xaa Gly Val Leu Ala Asp Phe Glu Gly Gly Phe Leu Arg Lys Phe Arg
1   5   10   15

Ala Arg Phe Pro Asp Gln Pro Phe Ile Ala Leu Glu Asp Arg Arg Gly
            20   25   30

Phe Trp Val Ser Glu Gln Tyr Gly Arg Leu Arg Pro Gly Leu Ser Ser
        35   40   45

Trp Pro Cys
    50

<210> 347
<211> 234
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 53; "

<220>
<221> source
<223> /note="Gene Symbol: NT5M; "

<220>
<221> source
<223> /note="Gene Name:
      5',3'-nucleotidase,
      mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481269"

<400> 347
Met Ile Arg Leu Gly Gly Trp Cys Ala Arg Arg Leu Cys Ser Ala Ala
1   5   10   15

Val Pro Ala Gly Arg Arg Gly Ala Ala Gly Gly Leu Gly Leu Ala Gly
            20   25   30

Gly Arg Ala Leu Arg Val Leu Val Asp Met Asp Gly Val Leu Ala Asp

```
        35                  40                  45

Phe Glu Gly Gly Phe Leu Arg Lys Phe Arg Ala Arg Phe Pro Asp Gln
    50                  55                  60

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

Tyr Gly Arg Leu Arg Pro Gly Leu Ser Glu Lys Ala Ile Ser Ile Trp
                85                  90                  95

Glu Ser Lys Asn Phe Phe Phe Glu Leu Glu Pro Leu Pro Gly Ala Val
            100                 105                 110

Glu Ala Val Lys Glu Met Ala Ser Leu Gln Asn Thr Asp Val Phe Ile
        115                 120                 125

Cys Thr Ser Pro Ile Lys Met Phe Lys Tyr Cys Pro Tyr Glu Lys Tyr
    130                 135                 140

Ala Trp Val Glu Lys Tyr Phe Gly Pro Asp Phe Leu Glu Gln Ile Val
145                 150                 155                 160

Leu Thr Arg Asp Lys Thr Val Val Ser Ala Asp Leu Leu Ile Asp Asp
                165                 170                 175

Arg Pro Asp Ile Thr Gly Lys Trp Pro Ala Thr Gly Ala Glu Pro Thr
            180                 185                 190

Pro Ser Trp Glu His Val Leu Phe Thr Ala Cys His Asn Gln His Leu
        195                 200                 205

Gln Leu Gln Pro Pro Arg Arg Arg Leu His Ser Trp Ala Asp Asp Trp
    210                 215                 220

Lys Ala Ile Leu Asp Ser Lys Arg Pro Cys
225                 230
```

<210> 348
<211> 1706
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 54; "

<220>
<221> source
<223> /note="Gene Symbol: XRN1; "

<220>
<221> source
<223> /note="Gene Name:
5'-3' exoribonuclease 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZH2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000264951"

<400> 348

```
Met Gly Val Pro Lys Phe Tyr Arg Trp Ile Ser Glu Arg Tyr Pro Cys
1               5                  10                  15

Leu Ser Glu Val Val Lys Glu His Gln Ile Pro Glu Phe Asp Asn Leu
            20                  25                  30

Tyr Leu Asp Met Asn Gly Ile Ile His Gln Cys Ser His Pro Asn Asp
        35                  40                  45

Asp Asp Val His Phe Arg Ile Ser Asp Asp Lys Ile Phe Thr Asp Ile
    50                  55                  60

Phe His Tyr Leu Glu Val Leu Phe Arg Ile Ile Lys Pro Arg Lys Val
65                  70                  75                  80

Phe Phe Met Ala Val Asp Gly Val Ala Pro Arg Ala Lys Met Asn Gln
                85                  90                  95

Gln Arg Gly Arg Arg Phe Arg Ser Ala Lys Glu Ala Glu Asp Lys Ile
            100                 105                 110

Lys Lys Ala Ile Glu Lys Gly Glu Thr Leu Pro Thr Glu Ala Arg Phe
        115                 120                 125

Asp Ser Asn Cys Ile Thr Pro Gly Thr Glu Phe Met Ala Arg Leu His
    130                 135                 140
```

```
Glu His Leu Lys Tyr Phe Val Asn Met Lys Ile Ser Thr Asp Lys Ser
145                 150                 155                 160

Trp Gln Gly Val Thr Ile Tyr Phe Ser Gly His Glu Thr Pro Gly Glu
                165                 170                 175

Gly Glu His Lys Ile Met Glu Phe Ile Arg Ser Glu Lys Ala Lys Pro
            180                 185                 190

Asp His Asp Pro Asn Thr Arg His Cys Leu Tyr Gly Leu Asp Ala Asp
        195                 200                 205

Leu Ile Met Leu Gly Leu Thr Ser His Glu Ala His Phe Ser Leu Leu
    210                 215                 220

Arg Glu Glu Val Arg Phe Gly Gly Lys Lys Thr Gln Arg Val Cys Ala
225                 230                 235                 240

Pro Glu Glu Thr Thr Phe His Leu Leu His Leu Ser Leu Met Arg Glu
                245                 250                 255

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

Tyr Asp Ile Glu Arg Ile Ile Asp Asp Trp Ile Leu Met Gly Phe Leu
        275                 280                 285

Val Gly Asn Asp Phe Ile Pro His Leu Pro His Leu His Ile Asn His
    290                 295                 300

Asp Ala Leu Pro Leu Leu Tyr Gly Thr Tyr Val Thr Ile Leu Pro Glu
305                 310                 315                 320

Leu Gly Gly Tyr Ile Asn Glu Ser Gly His Leu Asn Leu Pro Arg Phe
                325                 330                 335

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

Glu Val Phe Val Asp Leu Lys Trp Phe Glu Ser Lys Val Gly Asn Lys
        355                 360                 365

Tyr Leu Asn Glu Ala Ala Gly Val Ala Ala Glu Glu Ala Arg Asn Tyr
```

370 375 380

Lys Glu Lys Lys Lys Leu Lys Gly Gln Glu Asn Ser Leu Cys Trp Thr
385 390 395 400

Ala Leu Asp Lys Asn Glu Gly Glu Met Ile Thr Ser Lys Asp Asn Leu
405 410 415

Glu Asp Glu Thr Glu Asp Asp Asp Leu Phe Glu Thr Glu Phe Arg Gln
420 425 430

Tyr Lys Arg Thr Tyr Tyr Met Thr Lys Met Gly Val Asp Val Val Ser
435 440 445

Asp Asp Phe Leu Ala Asp Gln Ala Ala Cys Tyr Val Gln Ala Ile Gln
450 455 460

Trp Ile Leu His Tyr Tyr Tyr His Gly Val Gln Ser Trp Ser Trp Tyr
465 470 475 480

Tyr Pro Tyr His Tyr Ala Pro Phe Leu Ser Asp Ile His Asn Ile Ser
485 490 495

Thr Leu Lys Ile His Phe Glu Leu Gly Lys Pro Phe Lys Pro Phe Glu
500 505 510

Gln Leu Leu Ala Val Leu Pro Ala Ala Ser Lys Asn Leu Leu Pro Ala
515 520 525

Cys Tyr Gln His Leu Met Thr Asn Glu Asp Ser Pro Ile Ile Glu Tyr
530 535 540

Tyr Pro Pro Asp Phe Lys Thr Asp Leu Asn Gly Lys Gln Gln Glu Trp
545 550 555 560

Glu Ala Val Val Leu Ile Pro Phe Ile Asp Glu Lys Arg Leu Leu Glu
565 570 575

Ala Met Glu Thr Cys Asn His Ser Leu Lys Lys Glu Glu Arg Lys Arg
580 585 590

Asn Gln His Ser Glu Cys Leu Met Cys Trp Tyr Asp Arg Asp Thr Glu
595 600 605

```
Phe Ile Tyr Pro Ser Pro Trp Pro Glu Lys Phe Pro Ala Ile Glu Arg
    610                 615                 620

Cys Cys Thr Arg Tyr Lys Ile Ile Ser Leu Asp Ala Trp Arg Val Asp
625                 630                 635                 640

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

Cys Gly Phe Pro Thr Leu Lys His Ile Arg His Lys Phe Phe Leu Lys
            660                 665                 670

Lys Ser Gly Val Gln Val Phe Gln Gln Ser Ser Arg Gly Glu Asn Met
        675                 680                 685

Met Leu Glu Ile Leu Val Asp Ala Glu Ser Asp Glu Leu Thr Val Glu
    690                 695                 700

Asn Val Ala Ser Ser Val Leu Gly Lys Ser Val Phe Val Asn Trp Pro
705                 710                 715                 720

His Leu Glu Glu Ala Arg Val Val Ala Val Ser Asp Gly Glu Thr Lys
                725                 730                 735

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

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

Asn Trp Ala Lys Glu Val Gln Gly Ile Ser Glu His Tyr Leu Arg Arg
    770                 775                 780

Lys Gly Ile Ile Ile Asn Glu Thr Ser Ala Val Val Tyr Ala Gln Leu
785                 790                 795                 800

Leu Thr Gly Arg Lys Tyr Gln Ile Asn Gln Asn Gly Glu Val Arg Leu
                805                 810                 815

Glu Lys Gln Trp Ser Lys Gln Val Val Pro Phe Val Tyr Gln Thr Ile
            820                 825                 830
```

```
Val Lys Asp Ile Arg Ala Phe Asp Ser Arg Phe Ser Asn Ile Lys Thr
        835                 840                 845

Leu Asp Asp Leu Phe Pro Leu Arg Ser Met Val Phe Met Leu Gly Thr
    850                 855                 860

Pro Tyr Tyr Gly Cys Thr Gly Glu Val Gln Asp Ser Gly Asp Val Ile
865                 870                 875                 880

Thr Glu Gly Arg Ile Arg Val Ile Phe Ser Ile Pro Cys Glu Pro Asn
                885                 890                 895

Leu Asp Ala Leu Ile Gln Asn Gln His Lys Tyr Ser Ile Lys Tyr Asn
            900                 905                 910

Pro Gly Tyr Val Leu Ala Ser Arg Leu Gly Val Ser Gly Tyr Leu Val
        915                 920                 925

Ser Arg Phe Thr Gly Ser Ile Phe Ile Gly Arg Gly Ser Arg Arg Asn
    930                 935                 940

Pro His Gly Asp His Lys Ala Asn Val Gly Leu Asn Leu Lys Phe Asn
945                 950                 955                 960

Lys Lys Asn Glu Glu Val Pro Gly Tyr Thr Lys Lys Val Gly Ser Glu
                965                 970                 975

Trp Met Tyr Ser Ser Ala Ala Glu Gln Leu Leu Ala Glu Tyr Leu Glu
            980                 985                 990

Arg Ala Pro Glu Leu Phe Ser Tyr  Ile Ala Lys Asn Ser  Gln Glu
Asp
        995                 1000                1005

Val Phe  Tyr Glu Asp Asp Ile  Trp Pro Gly Glu Asn  Glu Asn Gly
    1010                1015                1020

Ala Glu  Lys Val Gln Glu Ile  Ile Thr Trp Leu Lys  Gly His Pro
    1025                1030                1035

Val Ser  Thr Leu Ser Arg Ser  Ser Cys Asp Leu Gln  Ile Leu Asp
    1040                1045                1050
```

Ala Ala Ile Val Glu Lys Ile Glu Glu Glu Val Glu Lys Cys Lys
1055 1060 1065

Gln Arg Lys Asn Asn Lys Lys Val Arg Val Thr Val Lys Pro His
1070 1075 1080

Leu Leu Tyr Arg Pro Leu Glu Gln Gln His Gly Val Ile Pro Asp
1085 1090 1095

Arg Asp Ala Glu Phe Cys Leu Phe Asp Arg Val Val Asn Val Arg
1100 1105 1110

Glu Asn Phe Ser Val Pro Val Gly Leu Arg Gly Thr Ile Ile Gly
1115 1120 1125

Ile Lys Gly Ala Asn Arg Glu Ala Asp Val Leu Phe Glu Val Leu
1130 1135 1140

Phe Asp Glu Glu Phe Pro Gly Gly Leu Thr Ile Arg Cys Ser Pro
1145 1150 1155

Gly Arg Gly Tyr Arg Leu Pro Thr Ser Ala Leu Val Asn Leu Ser
1160 1165 1170

His Gly Ser Arg Ser Glu Thr Gly Asn Gln Lys Leu Thr Ala Ile
1175 1180 1185

Val Lys Pro Gln Pro Ala Val His Gln His Ser Ser Ser Ser Ser
1190 1195 1200

Val Ser Ser Gly His Leu Gly Ala Leu Asn His Ser Pro Gln Ser
1205 1210 1215

Leu Phe Val Pro Thr Gln Val Pro Thr Lys Asp Asp Asp Glu Phe
1220 1225 1230

Cys Asn Ile Trp Gln Ser Leu Gln Gly Ser Gly Lys Met Gln Tyr
1235 1240 1245

Phe Gln Pro Thr Ile Gln Glu Lys Gly Ala Val Leu Pro Gln Glu
1250 1255 1260

```
Ile Ser  Gln Val Asn Gln His  His Lys Ser Gly Phe  Asn Asp Asn
    1265                1270                1275

Ser Val  Lys Tyr Gln Gln Arg  Lys His Asp Pro His  Arg Lys Phe
    1280                1285                1290

Lys Glu  Glu Cys Lys Ser Pro  Lys Ala Glu Cys Trp  Ser Gln Lys
    1295                1300                1305

Met Ser  Asn Lys Gln Pro Asn  Ser Gly Ile Glu Asn  Phe Leu Ala
    1310                1315                1320

Ser Leu  Asn Ile Ser Lys Glu  Asn Glu Val Gln Ser  Ser His His
    1325                1330                1335

Gly Glu  Pro Pro Ser Glu Glu  His Leu Ser Pro Gln  Ser Phe Ala
    1340                1345                1350

Met Gly  Thr Arg Met Leu Lys  Glu Ile Leu Lys Ile  Asp Gly Ser
    1355                1360                1365

Asn Thr  Val Asp His Lys Asn  Glu Ile Lys Gln Ile  Ala Asn Glu
    1370                1375                1380

Ile Pro  Val Ser Ser Asn Arg  Arg Asp Glu Tyr Gly  Leu Pro Ser
    1385                1390                1395

Gln Pro  Lys Gln Asn Lys Lys  Leu Ala Ser Tyr Met  Asn Lys Pro
    1400                1405                1410

His Ser  Ala Asn Glu Tyr His  Asn Val Gln Ser Met  Asp Asn Met
    1415                1420                1425

Cys Trp  Pro Ala Pro Ser Gln  Ile Pro Pro Val Ser  Thr Pro Val
    1430                1435                1440

Thr Glu  Leu Ser Arg Ile Cys  Ser Leu Val Gly Met  Pro Gln Pro
    1445                1450                1455

Asp Phe  Ser Phe Leu Arg Met  Pro Gln Thr Met Thr  Val Cys Gln
    1460                1465                1470

Val Lys  Leu Ser Asn Gly Leu  Leu Val His Gly Pro  Gln Cys His
```

1475 1480 1485

Ser Glu Asn Glu Ala Lys Glu Lys Ala Ala Leu Phe Ala Leu Gln
1490 1495 1500

Gln Leu Gly Ser Leu Gly Met Asn Phe Pro Leu Pro Ser Gln Val
1505 1510 1515

Phe Ala Asn Tyr Pro Ser Ala Val Pro Pro Gly Thr Ile Pro Pro
1520 1525 1530

Ala Phe Pro Pro Pro Thr Gly Trp Asp His Tyr Gly Ser Asn Tyr
1535 1540 1545

Ala Leu Gly Ala Ala Asn Ile Met Pro Ser Ser Ser His Leu Phe
1550 1555 1560

Gly Ser Met Pro Trp Gly Pro Ser Val Pro Val Pro Gly Lys Pro
1565 1570 1575

Phe His His Thr Leu Tyr Ser Gly Thr Met Pro Met Ala Gly Gly
1580 1585 1590

Ile Pro Gly Gly Val His Asn Gln Phe Ile Pro Leu Gln Val Thr
1595 1600 1605

Lys Lys Arg Val Ala Asn Lys Lys Asn Phe Glu Asn Lys Glu Ala
1610 1615 1620

Gln Ser Ser Gln Ala Thr Pro Val Gln Thr Ser Gln Pro Asp Ser
1625 1630 1635

Ser Asn Ile Val Lys Val Ser Pro Arg Glu Ser Ser Ser Ala Ser
1640 1645 1650

Leu Lys Ser Ser Pro Ile Ala Gln Pro Ala Ser Ser Phe Gln Val
1655 1660 1665

Glu Thr Ala Ser Gln Gly His Ser Ile Ser His His Lys Ser Thr
1670 1675 1680

Pro Ile Ser Ser Ser Arg Arg Lys Ser Arg Lys Leu Ala Val Asn
1685 1690 1695

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Phe Gly  Val Ser Lys Pro Ser  Glu
    1700                1705


<210> 349
<211> 1694
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<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: XRN1; "

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<223> /note="Gene Name:
      5'-3' exoribonuclease 1; "

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<223> /note="Uniprot ID:  Q8IZH2; "

<220>
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<400> 349
Met Gly Val Pro Lys Phe Tyr Arg Trp Ile Ser Glu Arg Tyr Pro Cys
1               5                  10                  15


Leu Ser Glu Val Val Lys Glu His Gln Ile Pro Glu Phe Asp Asn Leu
            20                  25                  30


Tyr Leu Asp Met Asn Gly Ile Ile His Gln Cys Ser His Pro Asn Asp
        35                  40                  45


Asp Asp Val His Phe Arg Ile Ser Asp Asp Lys Ile Phe Thr Asp Ile
    50                  55                  60


Phe His Tyr Leu Glu Val Leu Phe Arg Ile Ile Lys Pro Arg Lys Val
65                  70                  75                  80


Phe Phe Met Ala Val Asp Gly Val Ala Pro Arg Ala Lys Met Asn Gln
                85                  90                  95
```

```
Gln Arg Gly Arg Arg Phe Arg Ser Ala Lys Glu Ala Glu Asp Lys Ile
            100                 105                 110

Lys Lys Ala Ile Glu Lys Gly Glu Thr Leu Pro Thr Glu Ala Arg Phe
        115                 120                 125

Asp Ser Asn Cys Ile Thr Pro Gly Thr Glu Phe Met Ala Arg Leu His
    130                 135                 140

Glu His Leu Lys Tyr Phe Val Asn Met Lys Ile Ser Thr Asp Lys Ser
145                 150                 155                 160

Trp Gln Gly Val Thr Ile Tyr Phe Ser Gly His Glu Thr Pro Gly Glu
                165                 170                 175

Gly Glu His Lys Ile Met Glu Phe Ile Arg Ser Glu Lys Ala Lys Pro
            180                 185                 190

Asp His Asp Pro Asn Thr Arg His Cys Leu Tyr Gly Leu Asp Ala Asp
        195                 200                 205

Leu Ile Met Leu Gly Leu Thr Ser His Glu Ala His Phe Ser Leu Leu
    210                 215                 220

Arg Glu Glu Val Arg Phe Gly Gly Lys Lys Thr Gln Arg Val Cys Ala
225                 230                 235                 240

Pro Glu Glu Thr Thr Phe His Leu Leu His Leu Ser Leu Met Arg Glu
                245                 250                 255

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

Tyr Asp Ile Glu Arg Ile Ile Asp Asp Trp Ile Leu Met Gly Phe Leu
        275                 280                 285

Val Gly Asn Asp Phe Ile Pro His Leu Pro His Leu His Ile Asn His
    290                 295                 300

Asp Ala Leu Pro Leu Leu Tyr Gly Thr Tyr Val Thr Ile Leu Pro Glu
305                 310                 315                 320

Leu Gly Gly Tyr Ile Asn Glu Ser Gly His Leu Asn Leu Pro Arg Phe
```

```
                325                 330                 335

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

Glu Val Phe Val Asp Leu Lys Trp Phe Glu Ser Lys Val Gly Asn Lys
        355                 360                 365

Tyr Leu Asn Glu Ala Ala Gly Val Ala Ala Glu Glu Ala Arg Asn Tyr
    370                 375                 380

Lys Glu Lys Lys Lys Leu Lys Gly Gln Glu Asn Ser Leu Cys Trp Thr
385                 390                 395                 400

Ala Leu Asp Lys Asn Glu Gly Glu Met Ile Thr Ser Lys Asp Asn Leu
                405                 410                 415

Glu Asp Glu Thr Glu Asp Asp Asp Leu Phe Glu Thr Glu Phe Arg Gln
            420                 425                 430

Tyr Lys Arg Thr Tyr Tyr Met Thr Lys Met Gly Val Asp Val Val Ser
        435                 440                 445

Asp Asp Phe Leu Ala Asp Gln Ala Ala Cys Tyr Val Gln Ala Ile Gln
    450                 455                 460

Trp Ile Leu His Tyr Tyr Tyr His Gly Val Gln Ser Trp Ser Trp Tyr
465                 470                 475                 480

Tyr Pro Tyr His Tyr Ala Pro Phe Leu Ser Asp Ile His Asn Ile Ser
                485                 490                 495

Thr Leu Lys Ile His Phe Glu Leu Gly Lys Pro Phe Lys Pro Phe Glu
            500                 505                 510

Gln Leu Leu Ala Val Leu Pro Ala Ala Ser Lys Asn Leu Leu Pro Ala
        515                 520                 525

Cys Tyr Gln His Leu Met Thr Asn Glu Asp Ser Pro Ile Ile Glu Tyr
    530                 535                 540

Tyr Pro Pro Asp Phe Lys Thr Asp Leu Asn Gly Lys Gln Gln Glu Trp
545                 550                 555                 560
```

Glu Ala Val Val Leu Ile Pro Phe Ile Asp Glu Lys Arg Leu Leu Glu
565 570 575

Ala Met Glu Thr Cys Asn His Ser Leu Lys Lys Glu Glu Arg Lys Arg
580 585 590

Asn Gln His Ser Glu Cys Leu Met Cys Trp Tyr Asp Arg Asp Thr Glu
595 600 605

Phe Ile Tyr Pro Ser Pro Trp Pro Glu Lys Phe Pro Ala Ile Glu Arg
610 615 620

Cys Cys Thr Arg Tyr Lys Ile Ile Ser Leu Asp Ala Trp Arg Val Asp
625 630 635 640

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

Cys Gly Phe Pro Thr Leu Lys His Ile Arg His Lys Phe Phe Leu Lys
660 665 670

Lys Ser Gly Val Gln Val Phe Gln Gln Ser Ser Arg Gly Glu Asn Met
675 680 685

Met Leu Glu Ile Leu Val Asp Ala Glu Ser Asp Glu Leu Thr Val Glu
690 695 700

Asn Val Ala Ser Ser Val Leu Gly Lys Ser Val Phe Val Asn Trp Pro
705 710 715 720

His Leu Glu Glu Ala Arg Val Val Ala Val Ser Asp Gly Glu Thr Lys
725 730 735

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

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

Asn Trp Ala Lys Glu Val Gln Gly Ile Ser Glu His Tyr Leu Arg Arg
770 775 780

```
Lys Gly Ile Ile Ile Asn Glu Thr Ser Ala Val Val Tyr Ala Gln Leu
785                 790                 795                 800

Leu Thr Gly Arg Lys Tyr Gln Ile Asn Gln Asn Gly Glu Val Arg Leu
                805                 810                 815

Glu Lys Gln Trp Ser Lys Gln Val Val Pro Phe Val Tyr Gln Thr Ile
            820                 825                 830

Val Lys Asp Ile Arg Ala Phe Asp Ser Arg Phe Ser Asn Ile Lys Thr
        835                 840                 845

Leu Asp Asp Leu Phe Pro Leu Arg Ser Met Val Phe Met Leu Gly Thr
    850                 855                 860

Pro Tyr Tyr Gly Cys Thr Gly Glu Val Gln Asp Ser Gly Asp Val Ile
865                 870                 875                 880

Thr Glu Gly Arg Ile Arg Val Ile Phe Ser Ile Pro Cys Glu Pro Asn
                885                 890                 895

Leu Asp Ala Leu Ile Gln Asn Gln His Lys Tyr Ser Ile Lys Tyr Asn
            900                 905                 910

Pro Gly Tyr Val Leu Ala Ser Arg Leu Gly Val Ser Gly Tyr Leu Val
        915                 920                 925

Ser Arg Phe Thr Gly Ser Ile Phe Ile Gly Arg Gly Ser Arg Arg Asn
    930                 935                 940

Pro His Gly Asp His Lys Ala Asn Val Gly Leu Asn Leu Lys Phe Asn
945                 950                 955                 960

Lys Lys Asn Glu Glu Val Pro Gly Tyr Thr Lys Lys Val Gly Ser Glu
                965                 970                 975

Trp Met Tyr Ser Ser Ala Ala Glu Gln Leu Leu Ala Glu Tyr Leu Glu
            980                 985                 990

Arg Ala Pro Glu Leu Phe Ser Tyr  Ile Ala Lys Asn Ser  Gln Glu
Asp
        995                 1000                1005
```

```
Val Phe  Tyr Glu Asp Asp Ile  Trp Pro Gly Glu Asn  Glu Asn Gly
    1010                1015                1020

Ala Glu  Lys Val Gln Glu Ile  Ile Thr Trp Leu Lys  Gly His Pro
    1025                1030                1035

Val Ser  Thr Leu Ser Arg Ser  Ser Cys Asp Leu Gln  Ile Leu Asp
    1040                1045                1050

Ala Ala  Ile Val Glu Lys Ile  Glu Glu Glu Val Glu  Lys Cys Lys
    1055                1060                1065

Gln Arg  Lys Asn Asn Lys Lys  Val Arg Val Thr Val  Lys Pro His
    1070                1075                1080

Leu Leu  Tyr Arg Pro Leu Glu  Gln Gln His Gly Val  Ile Pro Asp
    1085                1090                1095

Arg Asp  Ala Glu Phe Cys Leu  Phe Asp Arg Val Val  Asn Val Arg
    1100                1105                1110

Glu Asn  Phe Ser Val Pro Val  Gly Leu Arg Gly Thr  Ile Ile Gly
    1115                1120                1125

Ile Lys  Gly Ala Asn Arg Glu  Ala Asp Val Leu Phe  Glu Val Leu
    1130                1135                1140

Phe Asp  Glu Glu Phe Pro Gly  Gly Leu Thr Ile Arg  Cys Ser Pro
    1145                1150                1155

Gly Arg  Gly Tyr Arg Leu Pro  Thr Ser Ala Leu Val  Asn Leu Ser
    1160                1165                1170

His Gly  Ser Arg Ser Glu Thr  Gly Asn Gln Lys Leu  Thr Ala Ile
    1175                1180                1185

Val Lys  Pro Gln Pro Ala Val  His Gln His Ser Ser  Ser Ser Ser
    1190                1195                1200

Val Ser  Ser Gly His Leu Gly  Ala Leu Asn His Ser  Pro Gln Ser
    1205                1210                1215
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```
Leu Phe  Val Pro Thr Gln Val  Pro Thr Lys Asp Asp  Asp Glu Phe
    1220                1225                1230

Cys Asn  Ile Trp Gln Ser Leu  Gln Gly Ser Gly Lys  Met Gln Tyr
    1235                1240                1245

Phe Gln  Pro Thr Ile Gln Glu  Lys Gly Ala Val Leu  Pro Gln Glu
    1250                1255                1260

Ile Ser  Gln Val Asn Gln His  His Lys Ser Gly Phe  Asn Asp Asn
    1265                1270                1275

Ser Val  Lys Tyr Gln Gln Arg  Lys His Asp Pro His  Arg Lys Phe
    1280                1285                1290

Lys Glu  Glu Cys Lys Ser Pro  Lys Ala Glu Cys Trp  Ser Gln Lys
    1295                1300                1305

Met Ser  Asn Lys Gln Pro Asn  Ser Gly Ile Glu Asn  Phe Leu Ala
    1310                1315                1320

Ser Leu  Asn Ile Ser Lys Glu  Asn Glu Val Gln Ser  Ser His His
    1325                1330                1335

Gly Glu  Pro Pro Ser Glu Glu  His Leu Ser Pro Gln  Ser Phe Ala
    1340                1345                1350

Met Lys  Gly Thr Arg Met Leu  Lys Glu Ile Leu Lys  Ile Asp Gly
    1355                1360                1365

Ser Asn  Thr Val Asp His Lys  Asn Glu Ile Lys Gln  Ile Ala Asn
    1370                1375                1380

Glu Ile  Pro Val Ser Ser Asn  Arg Arg Asp Glu Tyr  Gly Leu Pro
    1385                1390                1395

Ser Gln  Pro Lys Gln Asn Lys  Lys Leu Ala Ser Tyr  Met Asn Lys
    1400                1405                1410

Pro His  Ser Ala Asn Glu Tyr  His Asn Val Gln Ser  Met Asp Asn
    1415                1420                1425

Met Cys  Trp Pro Ala Pro Ser  Gln Ile Pro Pro Val  Ser Thr Pro
```

1430 1435 1440

Val Thr Glu Leu Ser Arg Ile Cys Ser Leu Val Gly Met Pro Gln
1445 1450 1455

Pro Asp Phe Ser Phe Leu Arg Met Pro Gln Thr Met Thr Val Cys
1460 1465 1470

Gln Val Lys Leu Ser Asn Gly Leu Leu Val His Gly Pro Gln Cys
1475 1480 1485

His Ser Glu Asn Glu Ala Lys Glu Lys Ala Ala Leu Phe Ala Leu
1490 1495 1500

Gln Gln Leu Gly Ser Leu Gly Met Asn Phe Pro Leu Pro Ser Gln
1505 1510 1515

Val Phe Ala Asn Tyr Pro Ser Ala Val Pro Pro Gly Thr Ile Pro
1520 1525 1530

Pro Ala Phe Pro Pro Pro Thr Ala Asn Ile Met Pro Ser Ser Ser
1535 1540 1545

His Leu Phe Gly Ser Met Pro Trp Gly Pro Ser Val Pro Val Pro
1550 1555 1560

Gly Lys Pro Phe His His Thr Leu Tyr Ser Gly Thr Met Pro Met
1565 1570 1575

Ala Gly Gly Ile Pro Gly Gly Val His Asn Gln Phe Ile Pro Leu
1580 1585 1590

Gln Val Thr Lys Lys Arg Val Ala Asn Lys Lys Asn Phe Glu Asn
1595 1600 1605

Lys Glu Ala Gln Ser Ser Gln Ala Thr Pro Val Gln Thr Ser Gln
1610 1615 1620

Pro Asp Ser Ser Asn Ile Val Lys Val Ser Pro Arg Glu Ser Ser
1625 1630 1635

Ser Ala Ser Leu Lys Ser Ser Pro Ile Ala Gln Pro Ala Ser Ser
1640 1645 1650

```
Phe Gln  Val Glu Thr Ala Ser  Gln Gly His Ser Ile  Ser His His
    1655                 1660                 1665


Lys Ser  Thr Pro Ile Ser Ser  Ser Arg Arg Lys Ser  Arg Lys Leu
    1670                 1675                 1680


Ala Val  Asn Phe Gly Val Ser  Lys Pro Ser Glu
    1685                 1690


<210> 350
<211> 459
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<213> Homo sapiens

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<220>
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<223> /note="Uniprot ID:  Q8IZH2; "

<220>
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Met Gly Val Pro Lys Phe Tyr Arg Trp Ile Ser Glu Arg Tyr Pro Cys
1               5                  10                  15


Leu Ser Glu Val Val Lys Glu His Gln Ile Pro Glu Phe Asp Asn Leu
            20                  25                  30


Tyr Leu Asp Met Asn Gly Ile Ile His Gln Cys Ser His Pro Asn Asp
        35                  40                  45


Asp Asp Val His Phe Arg Ile Ser Asp Asp Lys Ile Phe Thr Asp Ile
    50                  55                  60
```

```
Phe His Tyr Leu Glu Val Leu Phe Arg Ile Ile Lys Pro Arg Lys Val
65                  70                  75                  80

Phe Phe Met Ala Val Asp Gly Val Ala Pro Arg Ala Lys Met Asn Gln
                85                  90                  95

Gln Arg Gly Arg Arg Phe Arg Ser Ala Lys Glu Ala Glu Asp Lys Ile
            100                 105                 110

Lys Lys Ala Ile Glu Lys Gly Glu Thr Leu Pro Thr Glu Ala Arg Phe
        115                 120                 125

Asp Ser Asn Cys Ile Thr Pro Gly Thr Glu Phe Met Ala Arg Leu His
    130                 135                 140

Glu His Leu Lys Tyr Phe Val Asn Met Lys Ile Ser Thr Asp Lys Ser
145                 150                 155                 160

Trp Gln Gly Val Thr Ile Tyr Phe Ser Gly His Glu Thr Pro Gly Glu
                165                 170                 175

Gly Glu His Lys Ile Met Glu Phe Ile Arg Ser Glu Lys Ala Lys Pro
            180                 185                 190

Asp His Asp Pro Asn Thr Arg His Cys Leu Tyr Gly Leu Asp Ala Asp
        195                 200                 205

Leu Ile Met Leu Gly Leu Thr Ser His Glu Ala His Phe Ser Leu Leu
    210                 215                 220

Arg Glu Glu Val Arg Phe Gly Gly Lys Lys Thr Gln Arg Val Cys Ala
225                 230                 235                 240

Pro Glu Glu Thr Thr Phe His Leu Leu His Leu Ser Leu Met Arg Glu
                245                 250                 255

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

Tyr Asp Ile Glu Arg Ile Ile Asp Asp Trp Ile Leu Met Gly Phe Leu
        275                 280                 285

Val Gly Asn Asp Phe Ile Pro His Leu Pro His Leu His Ile Asn His
```

```
    290                 295                 300

Asp Ala Leu Pro Leu Leu Tyr Gly Thr Tyr Val Thr Ile Leu Pro Glu
305                 310                 315                 320

Leu Gly Gly Tyr Ile Asn Glu Ser Gly His Leu Asn Leu Pro Arg Phe
                325                 330                 335

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

Glu Val Phe Val Asp Leu Lys Trp Phe Glu Ser Lys Val Gly Asn Lys
        355                 360                 365

Tyr Leu Asn Glu Ala Ala Gly Val Ala Ala Glu Glu Ala Arg Asn Tyr
    370                 375                 380

Lys Glu Lys Lys Lys Leu Lys Gly Gln Glu Asn Ser Leu Cys Trp Thr
385                 390                 395                 400

Ala Leu Asp Lys Asn Glu Gly Glu Met Ile Thr Ser Lys Asp Asn Leu
                405                 410                 415

Glu Asp Glu Thr Glu Asp Asp Asp Leu Phe Glu Thr Glu Phe Arg Gln
            420                 425                 430

Tyr Lys Arg Thr Tyr Tyr Met Thr Lys Met Gly Val Asp Val Val Ser
        435                 440                 445

Glu Tyr Val Phe Ala Asn Ala Phe Ile Leu Lys
    450                 455


<210> 351
<211> 63
<212> PRT
<213> Homo sapiens

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<223> /note="Gene Symbol: XRN1; "

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<222> (1)..(1)
<223> Any amino acid

<400> 351
Xaa Glu Glu Cys Lys Ser Pro Lys Ala Glu Cys Trp Ser Gln Lys Met
1 5 10 15

Ser Asn Lys Gln Pro Asn Ser Gly Ile Glu Asn Phe Leu Ala Ser Leu
20 25 30

Asn Ile Ser Lys Glu Asn Glu Val Gln Ser Ser His His Gly Glu Pro
35 40 45

Pro Ser Glu Glu His Leu Ser Pro Gln Ser Phe Ala Met Lys Arg
50 55 60

<210> 352
<211> 1160
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<222> (1)..(1)

<223> Any amino acid

<400> 352

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Xaa Thr Asn Glu Asp Ser Pro Ile Ile Glu Tyr Tyr Pro Pro Asp Phe
1               5                  10                  15

Lys Thr Asp Leu Asn Gly Lys Gln Gln Glu Trp Glu Ala Val Val Leu
            20                  25                  30

Ile Pro Phe Ile Asp Glu Arg Leu Leu Glu Ala Met Glu Thr Cys Asn
        35                  40                  45

His Ser Leu Lys Lys Glu Glu Arg Lys Arg Asn Gln His Ser Glu Cys
    50                  55                  60

Leu Met Cys Trp Tyr Asp Arg Asp Thr Glu Phe Ile Tyr Pro Ser Pro
65                  70                  75                  80

Trp Pro Glu Lys Phe Pro Ala Ile Glu Arg Cys Cys Thr Arg Tyr Lys
                85                  90                  95

Ile Ile Ser Leu Asp Ala Trp Arg Val Asp Ile Asn Lys Asn Lys Ile
            100                 105                 110

Thr Arg Ile Asp Gln Lys Ala Leu Tyr Phe Cys Gly Phe Pro Thr Leu
        115                 120                 125

Lys His Ile Arg His Lys Phe Phe Leu Lys Lys Ser Gly Val Gln Val
    130                 135                 140

Phe Gln Gln Ser Ser Arg Gly Glu Asn Met Met Leu Glu Ile Leu Val
145                 150                 155                 160

Asp Ala Glu Ser Asp Glu Leu Thr Val Glu Asn Val Ala Ser Ser Val
                165                 170                 175

Leu Gly Lys Ser Val Phe Val Asn Trp Pro His Leu Glu Glu Ala Arg
            180                 185                 190

Val Val Ala Val Ser Asp Gly Glu Thr Lys Phe Tyr Leu Glu Glu Pro
        195                 200                 205

Pro Gly Thr Gln Lys Leu Tyr Ser Gly Arg Thr Ala Pro Pro Ser Lys
    210                 215                 220
```

```
Val Val His Leu Gly Asp Lys Glu Gln Ser Asn Trp Ala Lys Glu Val
225                 230                 235                 240

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

Glu Thr Ser Ala Val Val Tyr Ala Gln Leu Leu Thr Gly Arg Lys Tyr
            260                 265                 270

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

Gln Val Val Pro Phe Val Tyr Gln Thr Ile Val Lys Asp Ile Arg Ala
    290                 295                 300

Phe Asp Ser Arg Phe Ser Asn Ile Lys Thr Leu Asp Asp Leu Phe Pro
305                 310                 315                 320

Leu Arg Ser Met Val Phe Met Leu Gly Thr Pro Tyr Tyr Gly Cys Thr
                325                 330                 335

Gly Glu Val Gln Asp Ser Gly Asp Val Ile Thr Glu Gly Arg Ile Arg
            340                 345                 350

Val Ile Phe Ser Ile Pro Cys Glu Pro Asn Leu Asp Ala Leu Ile Gln
        355                 360                 365

Asn Gln His Lys Tyr Ser Ile Lys Tyr Asn Pro Gly Tyr Val Leu Ala
    370                 375                 380

Ser Arg Leu Gly Val Ser Gly Tyr Leu Val Ser Arg Phe Thr Gly Ser
385                 390                 395                 400

Ile Phe Ile Gly Arg Gly Ser Arg Arg Asn Pro His Gly Asp His Lys
                405                 410                 415

Ala Asn Val Gly Leu Asn Leu Lys Phe Asn Lys Lys Asn Glu Glu Val
            420                 425                 430

Pro Gly Tyr Thr Lys Lys Val Gly Ser Glu Trp Met Tyr Ser Ser Ala
        435                 440                 445
```

```
Ala Glu Gln Leu Leu Ala Glu Tyr Leu Glu Arg Ala Pro Glu Leu Phe
    450                 455                 460

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

Ile Trp Pro Gly Glu Asn Glu Asn Gly Ala Glu Lys Val Gln Glu Ile
                485                 490                 495

Ile Thr Trp Leu Lys Gly His Pro Val Ser Thr Leu Ser Arg Ser Ser
            500                 505                 510

Cys Asp Leu Gln Ile Leu Asp Ala Ala Ile Val Glu Lys Ile Glu Glu
        515                 520                 525

Glu Val Glu Lys Cys Lys Gln Arg Lys Asn Asn Lys Lys Val Arg Val
    530                 535                 540

Thr Val Lys Pro His Leu Leu Tyr Arg Pro Leu Glu Gln Gln His Gly
545                 550                 555                 560

Val Ile Pro Asp Arg Asp Ala Glu Phe Cys Leu Phe Asp Arg Val Val
                565                 570                 575

Asn Val Arg Glu Asn Phe Ser Val Pro Val Gly Leu Arg Gly Thr Ile
            580                 585                 590

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

Leu Phe Asp Glu Glu Phe Pro Gly Gly Leu Thr Ile Arg Cys Ser Pro
    610                 615                 620

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

Gly Ser Arg Ser Glu Thr Gly Asn Gln Lys Leu Thr Ala Ile Val Lys
                645                 650                 655

Pro Gln Pro Ala Val His Gln His Ser Ser Ser Ser Ser Val Ser Ser
            660                 665                 670
```

```
Gly His Leu Gly Ala Leu Asn His Ser Pro Gln Ser Leu Phe Val Pro
        675                 680                 685

Thr Gln Val Pro Thr Lys Asp Asp Asp Glu Phe Cys Asn Ile Trp Gln
    690                 695                 700

Ser Leu Gln Gly Ser Gly Lys Met Gln Tyr Phe Gln Pro Thr Ile Gln
705                 710                 715                 720

Glu Lys Gly Ala Val Leu Pro Gln Glu Ile Ser Gln Val Asn Gln His
                725                 730                 735

His Lys Ser Gly Phe Asn Asp Asn Ser Val Lys Tyr Gln Gln Arg Lys
            740                 745                 750

His Asp Pro His Arg Lys Phe Lys Glu Glu Cys Lys Ser Pro Lys Ala
        755                 760                 765

Glu Cys Trp Ser Gln Lys Met Ser Asn Lys Gln Pro Asn Ser Gly Ile
    770                 775                 780

Glu Asn Phe Leu Ala Ser Leu Asn Ile Ser Lys Glu Asn Glu Val Gln
785                 790                 795                 800

Ser Ser His His Gly Glu Pro Pro Ser Glu Glu His Leu Ser Pro Gln
                805                 810                 815

Ser Phe Ala Met Lys Gly Thr Arg Met Leu Lys Glu Ile Leu Lys Ile
            820                 825                 830

Asp Gly Ser Asn Thr Val Asp His Lys Asn Glu Ile Lys Gln Ile Ala
        835                 840                 845

Asn Glu Ile Pro Val Ser Ser Asn Arg Arg Asp Glu Tyr Gly Leu Pro
    850                 855                 860

Ser Gln Pro Lys Gln Asn Lys Lys Leu Ala Ser Tyr Met Asn Lys Pro
865                 870                 875                 880

His Ser Ala Asn Glu Tyr His Asn Val Gln Ser Met Asp Asn Met Cys
                885                 890                 895

Trp Pro Ala Pro Ser Gln Ile Pro Pro Val Ser Thr Pro Val Thr Glu
```

900 905 910

Leu Ser Arg Ile Cys Ser Leu Val Gly Met Pro Gln Pro Asp Phe Ser
915 920 925

Phe Leu Arg Met Pro Gln Thr Met Thr Val Cys Gln Val Lys Leu Ser
930 935 940

Asn Gly Leu Leu Val His Gly Pro Gln Cys His Ser Glu Asn Glu Ala
945 950 955 960

Lys Glu Lys Ala Ala Leu Phe Ala Leu Gln Gln Leu Gly Ser Leu Gly
965 970 975

Met Asn Phe Pro Leu Pro Ser Gln Val Phe Ala Asn Tyr Pro Ser Ala
980 985 990

Val Pro Pro Gly Thr Ile Pro Pro Ala Phe Pro Pro Pro Thr Ala Asn
995 1000 1005

Ile Met Pro Ser Ser Ser His Leu Phe Gly Ser Met Pro Trp Gly
1010 1015 1020

Pro Ser Val Pro Val Pro Gly Lys Pro Phe His His Thr Leu Tyr
1025 1030 1035

Ser Gly Thr Met Pro Met Ala Gly Gly Ile Pro Gly Gly Val His
1040 1045 1050

Asn Gln Phe Ile Pro Leu Gln Val Thr Lys Lys Arg Val Ala Asn
1055 1060 1065

Lys Lys Asn Phe Glu Asn Lys Glu Ala Gln Ser Ser Gln Ala Thr
1070 1075 1080

Pro Val Gln Thr Ser Gln Pro Asp Ser Ser Asn Ile Val Lys Val
1085 1090 1095

Ser Pro Arg Glu Ser Ser Ser Ala Ser Leu Lys Ser Ser Pro Ile
1100 1105 1110

Ala Gln Pro Ala Ser Ser Phe Gln Val Glu Thr Ala Ser Gln Gly

```
    1115                1120                1125

His Ser  Ile Ser His His Lys  Ser Thr Pro Ile Ser  Ser Ser Arg
    1130                1135                1140

Arg Lys  Ser Arg Lys Leu Ala  Val Asn Phe Gly Val  Ser Lys Pro
    1145                1150                1155

Ser Glu
    1160


<210> 353
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 54; "

<220>
<221> source
<223> /note="Gene Symbol: XRN1; "

<220>
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<223> /note="Gene Name:
      5'-3' exoribonuclease 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420634"

<400> 353
Met Ala Arg Leu His Glu His Leu Lys Tyr Phe Val Asn Met Lys Ile
1               5                   10                  15

Ser Thr Asp Lys Ser Trp Gln Gly Val Thr Ile Tyr Phe Ser Gly His
            20                  25                  30

Glu Thr Pro Gly Glu Gly Glu His Lys Ile Met Glu Phe Ile Arg Ser
        35                  40                  45

Glu Lys Ala Lys Pro Asp His Asp Pro Asn Thr Arg His Cys Leu Tyr
    50                  55                  60

Gly Leu Asp Ala Asp Leu Ile Met Leu Gly Leu Thr Ser His Glu Ala
65                  70                  75                  80
```

```
His Phe Ser Leu Leu Arg Glu Glu Val Arg Phe Gly Gly Lys Lys Thr
                85                  90                  95

Gln Arg Val Cys Ala Pro Glu Glu Thr Thr Phe His Leu Leu His Leu
            100                 105                 110

Ser Leu Met Arg Glu Tyr Ile Asp Tyr Glu Phe Ser Val Leu Lys Glu
        115                 120                 125

Lys Ile Thr Phe Lys Tyr Asp Ile Glu Arg Ile Ile Asp Asp Trp Ile
    130                 135                 140

Leu Met Gly Phe Leu Val Gly Asn Asp Phe Ile Pro His Leu Pro His
145                 150                 155                 160

Leu His Ile Asn His
                165


<210> 354
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 54; "

<220>
<221> source
<223> /note="Gene Symbol: XRN1; "

<220>
<221> source
<223> /note="Gene Name:
      5'-3' exoribonuclease 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420786"

<400> 354
Met Gly Val Pro Lys Phe Tyr Arg Trp Ile Ser Glu Arg Tyr Pro Cys
1               5                   10                  15

Leu Ser Glu Val Val Lys Glu His Gln Ile Pro Glu Phe Asp Asn Leu
            20                  25                  30

Tyr Leu Asp Met Asn Gly Ile Ile His Gln Cys Ser His Pro Asn Asp
```

```
        35                  40                  45

Asp Asp Val His Phe Arg Ile Ser Asp Asp Lys Ile Phe Thr Asp Ile
    50                  55                  60

Phe His Tyr Leu Glu Val Leu Phe Arg Ile Ile Lys Pro Arg Lys Val
65                  70                  75                  80

Phe Phe Met Ala Val Asp Gly Val Ala Pro Arg Ala Lys Met Asn Gln
                85                  90                  95

Gln Arg Gly Arg Arg Phe Arg Leu Cys Leu Asp
            100                 105


<210> 355
<211> 950
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 55; "

<220>
<221> source
<223> /note="Gene Symbol: XRN2; "

<220>
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<223> /note="Gene Name:
      5'-3' exoribonuclease 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H0D6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000366396"

<400> 355
Met Gly Val Pro Ala Phe Phe Arg Trp Leu Ser Arg Lys Tyr Pro Ser
1               5                   10                  15

Ile Ile Val Asn Cys Val Glu Glu Lys Pro Lys Glu Cys Asn Gly Val
            20                  25                  30

Lys Ile Pro Val Asp Ala Ser Lys Pro Asn Pro Asn Asp Val Glu Phe
        35                  40                  45
```

```
Asp Asn Leu Tyr Leu Asp Met Asn Gly Ile Ile His Pro Cys Thr His
    50                  55                  60

Pro Glu Asp Lys Pro Ala Pro Lys Asn Glu Asp Glu Met Met Val Ala
65                  70                  75                  80

Ile Phe Glu Tyr Ile Asp Arg Leu Phe Ser Ile Val Arg Pro Arg Arg
                85                  90                  95

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

Gln Gln Arg Ser Arg Arg Phe Arg Ala Ser Lys Glu Gly Met Glu Ala
        115                 120                 125

Ala Val Glu Lys Gln Arg Val Arg Glu Glu Ile Leu Ala Lys Gly Gly
    130                 135                 140

Phe Leu Pro Pro Glu Glu Ile Lys Glu Arg Phe Asp Ser Asn Cys Ile
145                 150                 155                 160

Thr Pro Gly Thr Glu Phe Met Asp Asn Leu Ala Lys Cys Leu Arg Tyr
                165                 170                 175

Tyr Ile Ala Asp Arg Leu Asn Asn Asp Pro Gly Trp Lys Asn Leu Thr
            180                 185                 190

Val Ile Leu Ser Asp Ala Ser Ala Pro Gly Glu Gly Glu His Lys Ile
        195                 200                 205

Met Asp Tyr Ile Arg Arg Gln Arg Ala Gln Pro Asn His Asp Pro Asn
    210                 215                 220

Thr His His Cys Leu Cys Gly Ala Asp Ala Asp Leu Ile Met Leu Gly
225                 230                 235                 240

Leu Ala Thr His Glu Pro Asn Phe Thr Ile Ile Arg Glu Glu Phe Lys
                245                 250                 255

Pro Asn Lys Pro Lys Pro Cys Gly Leu Cys Asn Gln Phe Gly His Glu
            260                 265                 270
```

```
Val Lys Asp Cys Glu Gly Leu Pro Arg Glu Lys Lys Gly Lys His Asp
        275                 280                 285

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

Arg Leu Asn Val Leu Arg Glu Tyr Leu Glu Arg Glu Leu Thr Met Ala
305                 310                 315                 320

Ser Leu Pro Phe Thr Phe Asp Val Glu Arg Ser Ile Asp Asp Trp Val
                325                 330                 335

Phe Met Cys Phe Phe Val Gly Asn Asp Phe Leu Pro His Leu Pro Ser
            340                 345                 350

Leu Glu Ile Arg Glu Asn Ala Ile Asp Arg Leu Val Asn Ile Tyr Lys
        355                 360                 365

Asn Val Val His Lys Thr Gly Gly Tyr Leu Thr Glu Ser Gly Tyr Val
    370                 375                 380

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

Asp Ser Ile Phe Lys Lys Arg Lys Asp Asp Glu Asp Ser Phe Arg Arg
                405                 410                 415

Arg Gln Lys Glu Lys Arg Lys Arg Met Lys Arg Asp Gln Pro Ala Phe
            420                 425                 430

Thr Pro Ser Gly Ile Leu Thr Pro His Ala Leu Gly Ser Arg Asn Ser
        435                 440                 445

Pro Gly Ser Gln Val Ala Ser Asn Pro Arg Gln Ala Ala Tyr Glu Met
    450                 455                 460

Arg Met Gln Asn Asn Ser Ser Pro Ser Ile Ser Pro Asn Thr Ser Phe
465                 470                 475                 480

Thr Ser Asp Gly Ser Pro Ser Pro Leu Gly Gly Ile Lys Arg Lys Ala
                485                 490                 495

Glu Asp Ser Asp Ser Glu Pro Glu Pro Glu Asp Asn Val Arg Leu Trp
```

```
            500                 505                 510

Glu Ala Gly Trp Lys Gln Arg Tyr Tyr Lys Asn Lys Phe Asp Val Asp
        515                 520                 525

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

Gly Leu Cys Trp Val Leu Arg Tyr Tyr Tyr Gln Gly Cys Ala Ser Trp
545                 550                 555                 560

Lys Trp Tyr Tyr Pro Phe His Tyr Ala Pro Phe Ala Ser Asp Phe Glu
                565                 570                 575

Gly Ile Ala Asp Met Pro Ser Asp Phe Glu Lys Gly Thr Lys Pro Phe
            580                 585                 590

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

Phe Leu Pro Pro Ser Trp Arg Lys Leu Met Ser Asp Pro Asp Ser Ser
    610                 615                 620

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

Lys Tyr Ala Trp Gln Gly Val Ala Leu Leu Pro Phe Val Asp Glu Arg
                645                 650                 655

Arg Leu Arg Ala Ala Leu Glu Glu Val Tyr Pro Asp Leu Thr Pro Glu
            660                 665                 670

Glu Thr Arg Arg Asn Ser Leu Gly Gly Asp Val Leu Phe Val Gly Lys
        675                 680                 685

His His Pro Leu His Asp Phe Ile Leu Glu Leu Tyr Gln Thr Gly Ser
    690                 695                 700

Thr Glu Pro Val Glu Val Pro Pro Glu Leu Cys His Gly Ile Gln Gly
705                 710                 715                 720

Lys Phe Ser Leu Asp Glu Glu Ala Ile Leu Pro Asp Gln Ile Val Cys
                725                 730                 735
```

```
Ser Pro Val Pro Met Leu Arg Asp Leu Thr Gln Asn Thr Val Val Ser
            740                 745                 750

Ile Asn Phe Lys Asp Pro Gln Phe Ala Glu Asp Tyr Ile Phe Lys Ala
        755                 760                 765

Val Met Leu Pro Gly Ala Arg Lys Pro Ala Ala Val Leu Lys Pro Ser
    770                 775                 780

Asp Trp Glu Lys Ser Ser Asn Gly Arg Gln Trp Lys Pro Gln Leu Gly
785                 790                 795                 800

Phe Asn Arg Asp Arg Arg Pro Val His Leu Asp Gln Ala Ala Phe Arg
                805                 810                 815

Thr Leu Gly His Val Met Pro Arg Gly Ser Gly Thr Gly Ile Tyr Ser
            820                 825                 830

Asn Ala Ala Pro Pro Pro Val Thr Tyr Gln Gly Asn Leu Tyr Arg Pro
        835                 840                 845

Leu Leu Arg Gly Gln Ala Gln Ile Pro Lys Leu Met Ser Asn Met Arg
    850                 855                 860

Pro Gln Asp Ser Trp Arg Gly Pro Pro Pro Leu Phe Gln Gln Gln Arg
865                 870                 875                 880

Phe Asp Arg Gly Val Gly Ala Glu Pro Leu Leu Pro Trp Asn Arg Met
                885                 890                 895

Leu Gln Thr Gln Asn Ala Ala Phe Gln Pro Asn Gln Tyr Gln Met Leu
            900                 905                 910

Ala Gly Pro Gly Gly Tyr Pro Pro Arg Arg Asp Asp Arg Gly Gly Arg
        915                 920                 925

Gln Gly Tyr Pro Arg Glu Gly Arg Lys Tyr Pro Leu Pro Pro Pro Ser
    930                 935                 940

Gly Arg Tyr Asn Trp Asn
945                 950
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<210> 356
<211> 592
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
5-aminoimidazole-4-carboxamide ribonucleotide
formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="Uniprot ID: P31939; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000236959"

<400> 356
Met Ala Pro Gly Gln Leu Ala Leu Phe Ser Val Ser Asp Lys Thr Gly
1   5   10   15

Leu Val Glu Phe Ala Arg Asn Leu Thr Ala Leu Gly Leu Asn Leu Val
            20   25   30

Ala Ser Gly Gly Thr Ala Lys Ala Leu Arg Asp Ala Gly Leu Ala Val
        35   40   45

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

Val Lys Thr Leu His Pro Ala Val His Ala Gly Ile Leu Ala Arg Asn
65   70   75   80

Ile Pro Glu Asp Asn Ala Asp Met Ala Arg Leu Asp Phe Asn Leu Ile
                85   90   95

Arg Val Val Ala Cys Asn Leu Tyr Pro Phe Val Lys Thr Val Ala Ser
            100   105   110

```
Pro Gly Val Thr Val Glu Glu Ala Val Glu Gln Ile Asp Ile Gly Gly
        115                 120                 125

Val Thr Leu Leu Arg Ala Ala Ala Lys Asn His Ala Arg Val Thr Val
    130                 135                 140

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

Ser Glu Ser Lys Asp Thr Ser Leu Glu Thr Arg Arg Gln Leu Ala Leu
                165                 170                 175

Lys Ala Phe Thr His Thr Ala Gln Tyr Asp Glu Ala Ile Ser Asp Tyr
            180                 185                 190

Phe Arg Lys Gln Tyr Ser Lys Gly Val Ser Gln Met Pro Leu Arg Tyr
        195                 200                 205

Gly Met Asn Pro His Gln Thr Pro Ala Gln Leu Tyr Thr Leu Gln Pro
    210                 215                 220

Lys Leu Pro Ile Thr Val Leu Asn Gly Ala Pro Gly Phe Ile Asn Leu
225                 230                 235                 240

Cys Asp Ala Leu Asn Ala Trp Gln Leu Val Lys Glu Leu Lys Glu Ala
                245                 250                 255

Leu Gly Ile Pro Ala Ala Ala Ser Phe Lys His Val Ser Pro Ala Gly
            260                 265                 270

Ala Ala Val Gly Ile Pro Leu Ser Glu Asp Glu Ala Lys Val Cys Met
        275                 280                 285

Val Tyr Asp Leu Tyr Lys Thr Leu Thr Pro Ile Ser Ala Ala Tyr Ala
    290                 295                 300

Arg Ala Arg Gly Ala Asp Arg Met Ser Ser Phe Gly Asp Phe Val Ala
305                 310                 315                 320

Leu Ser Asp Val Cys Asp Val Pro Thr Ala Lys Ile Ile Ser Arg Glu
                325                 330                 335

Val Ser Asp Gly Ile Ile Ala Pro Gly Tyr Glu Glu Glu Ala Leu Thr
```

```
            340                 345                 350

Ile Leu Ser Lys Lys Lys Asn Gly Asn Tyr Cys Val Leu Gln Met Asp
        355                 360                 365

Gln Ser Tyr Lys Pro Asp Glu Asn Glu Val Arg Thr Leu Phe Gly Leu
    370                 375                 380

His Leu Ser Gln Lys Arg Asn Asn Gly Val Val Asp Lys Ser Leu Phe
385                 390                 395                 400

Ser Asn Val Val Thr Lys Asn Lys Asp Leu Pro Glu Ser Ala Leu Arg
                405                 410                 415

Asp Leu Ile Val Ala Thr Ile Ala Val Lys Tyr Thr Gln Ser Asn Ser
            420                 425                 430

Val Cys Tyr Ala Lys Asn Gly Gln Val Ile Gly Ile Gly Ala Gly Gln
        435                 440                 445

Gln Ser Arg Ile His Cys Thr Arg Leu Ala Gly Asp Lys Ala Asn Tyr
    450                 455                 460

Trp Trp Leu Arg His His Pro Gln Val Leu Ser Met Lys Phe Lys Thr
465                 470                 475                 480

Gly Val Lys Arg Ala Glu Ile Ser Asn Ala Ile Asp Gln Tyr Val Thr
                485                 490                 495

Gly Thr Ile Gly Glu Asp Glu Asp Leu Ile Lys Trp Lys Ala Leu Phe
            500                 505                 510

Glu Glu Val Pro Glu Leu Leu Thr Glu Ala Glu Lys Lys Glu Trp Val
        515                 520                 525

Glu Lys Leu Thr Glu Val Ser Ile Ser Ser Asp Ala Phe Phe Pro Phe
    530                 535                 540

Arg Asp Asn Val Asp Arg Ala Lys Arg Ser Gly Val Ala Tyr Ile Ala
545                 550                 555                 560

Ala Pro Ser Gly Ser Ala Ala Asp Lys Val Val Ile Glu Ala Cys Asp
                565                 570                 575
```

Glu Leu Gly Ile Ile Leu Ala His Thr Asn Leu Arg Leu Phe His His
580 585 590

<210> 357
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
5-aminoimidazole-4-carboxamide ribonucleotide
formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388675"

<400> 357
Met Ala Pro Gly Gln Leu Ala Leu Phe Ser Val Ser Asp Lys Thr Gly
1 5 10 15

Leu Val Glu Phe Ala Arg Asn Leu Thr Ala Leu Gly Leu Asn Leu Val
20 25 30

Ala Ser Gly Gly Thr Ala Lys Ala Leu Arg Asp Ala Gly Leu Ala Val
35 40 45

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

Val Lys Thr Leu His Pro Ala Val His Ala Glu Leu Leu Pro Ala Ile
65 70 75 80

Ser Ile Pro Leu

<210> 358
<211> 43
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
5-aminoimidazole-4-carboxamide ribonucleotide
formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394317"

<400> 358
Met Ala Pro Gly Gln Leu Gly Glu Ala Leu Ala Glu Arg Arg Gly Leu
1 5 10 15

Arg Pro Arg Leu Arg Pro Pro Thr Leu Pro Pro Trp Arg Arg Pro Ala
20 25 30

Gly Pro Gly Thr Ala Gly Ala Ala Leu Arg Asp
35 40

<210> 359
<211> 231
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
5-aminoimidazole-4-carboxamide ribonucleotide
formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401936"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 359
Xaa Ile Phe Leu Gln Val Ser Asp Gly Ile Ile Ala Pro Gly Tyr Glu
1 5 10 15

Glu Glu Ala Leu Thr Ile Leu Ser Lys Lys Lys Asn Gly Asn Tyr Cys
20 25 30

Val Leu Gln Met Asp Gln Ser Tyr Lys Pro Asp Glu Asn Glu Val Arg
35 40 45

Thr Leu Phe Gly Leu His Leu Ser Gln Lys Arg Asn Asn Gly Val Val
50 55 60

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

Glu Ser Ala Leu Arg Asp Leu Ile Val Ala Thr Ile Ala Val Lys Tyr
85 90 95

Thr Gln Ser Asn Ser Val Cys Tyr Ala Lys Asn Gly Gln Val Ile Gly
100 105 110

Ile Gly Ala Gly Gln Gln Ser Arg Ile His Cys Thr Arg Leu Ala Gly
115 120 125

Asp Lys Ala Asn Tyr Trp Trp Leu Arg His His Pro Gln Val Leu Ser
130 135 140

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

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

Trp Lys Ala Leu Phe Glu Glu Val Pro Glu Leu Leu Thr Glu Ala Glu
180 185 190

Lys Lys Glu Trp Val Glu Lys Leu Thr Glu Val Ser Ile Ser Ser Asp
195 200 205

Ala Phe Phe Pro Phe Arg Asp Asn Val Asp Arg Ala Lys Arg Val Ser
210 215 220

Met Glu Leu Gly Ala Phe Ala
225 230

<210> 360
<211> 170
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
5-aminoimidazole-4-carboxamide ribonucleotide
formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402393"

<400> 360
Met Leu Gly Gly Arg Val Lys Thr Leu His Pro Ala Val His Ala Gly
1 5 10 15

Ile Leu Ala Arg Asn Ile Pro Glu Asp Asn Ala Asp Met Ala Arg Leu
20 25 30

Asp Phe Asn Leu Ile Arg Val Val Ala Cys Asn Leu Tyr Pro Phe Val
35 40 45

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

Ile Asp Ile Gly Gly Val Thr Leu Leu Arg Ala Ala Ala Lys Asn His
65 70 75 80

Ala Arg Val Thr Val Val Cys Glu Pro Glu Asp Tyr Val Val Val Ser
85 90 95

```
Thr Glu Met Gln Ser Ser Glu Ser Lys Asp Thr Ser Leu Glu Thr Arg
            100                 105                 110

Arg Gln Leu Ala Leu Lys Ala Phe Thr His Thr Ala Gln Tyr Asp Glu
        115                 120                 125

Ala Ile Ser Asp Tyr Phe Arg Lys Gln Tyr Ser Lys Gly Val Ser Gln
    130                 135                 140

Met Pro Leu Arg Tyr Gly Met Asn Pro His Gln Thr Pro Ala Gln Leu
145                 150                 155                 160

Tyr Thr Leu Gln Pro Lys Leu Pro Ile Thr
                165                 170


<210> 361
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
      5-aminoimidazole-4-carboxamide ribonucleotide
      formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000406792"

<400> 361
Met Ala Pro Gly Gln Leu Gly Glu Ala Leu Ala Glu Arg Arg Gly Leu
1               5                   10                  15

Arg Pro Arg Leu Arg Pro Pro Thr Leu Pro Pro Trp Arg Arg Pro Ala
            20                  25                  30

Gly Pro Gly Thr Ala Gly Ala Ala Leu Arg Asp
        35                  40


<210> 362
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<211> 591
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 56; "

<220>
<221> source
<223> /note="Gene Symbol: ATIC; "

<220>
<221> source
<223> /note="Gene Name:
5-aminoimidazole-4-carboxamide ribonucleotide
formyltransferase/IMP cyclohydrolase; "

<220>
<221> source
<223> /note="Uniprot ID: P31939; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000415935"

<400> 362

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

```
Thr Leu Leu Arg Ala Ala Ala Lys Asn His Ala Arg Val Thr Val Val
    130                 135                 140

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

Glu Ser Lys Asp Thr Ser Leu Glu Thr Arg Arg Gln Leu Ala Leu Lys
                165                 170                 175

Ala Phe Thr His Thr Ala Gln Tyr Asp Glu Ala Ile Ser Asp Tyr Phe
            180                 185                 190

Arg Lys Gln Tyr Ser Lys Gly Val Ser Gln Met Pro Leu Arg Tyr Gly
        195                 200                 205

Met Asn Pro His Gln Thr Pro Ala Gln Leu Tyr Thr Leu Gln Pro Lys
    210                 215                 220

Leu Pro Ile Thr Val Leu Asn Gly Ala Pro Gly Phe Ile Asn Leu Cys
225                 230                 235                 240

Asp Ala Leu Asn Ala Trp Gln Leu Val Lys Glu Leu Lys Glu Ala Leu
                245                 250                 255

Gly Ile Pro Ala Ala Ala Ser Phe Lys His Val Ser Pro Ala Gly Ala
            260                 265                 270

Ala Val Gly Ile Pro Leu Ser Glu Asp Glu Ala Lys Val Cys Met Val
        275                 280                 285

Tyr Asp Leu Tyr Lys Thr Leu Thr Pro Ile Ser Ala Ala Tyr Ala Arg
    290                 295                 300

Ala Arg Gly Ala Asp Arg Met Ser Ser Phe Gly Asp Phe Val Ala Leu
305                 310                 315                 320

Ser Asp Val Cys Asp Val Pro Thr Ala Lys Ile Ile Ser Arg Glu Val
                325                 330                 335

Ser Asp Gly Ile Ile Ala Pro Gly Tyr Glu Glu Glu Ala Leu Thr Ile
            340                 345                 350
```

Leu Ser Lys Lys Lys Asn Gly Asn Tyr Cys Val Leu Gln Met Asp Gln
355 360 365

Ser Tyr Lys Pro Asp Glu Asn Glu Val Arg Thr Leu Phe Gly Leu His
370 375 380

Leu Ser Gln Lys Arg Asn Asn Gly Val Val Asp Lys Ser Leu Phe Ser
385 390 395 400

Asn Val Val Thr Lys Asn Lys Asp Leu Pro Glu Ser Ala Leu Arg Asp
405 410 415

Leu Ile Val Ala Thr Ile Ala Val Lys Tyr Thr Gln Ser Asn Ser Val
420 425 430

Cys Tyr Ala Lys Asn Gly Gln Val Ile Gly Ile Gly Ala Gly Gln Gln
435 440 445

Ser Arg Ile His Cys Thr Arg Leu Ala Gly Asp Lys Ala Asn Tyr Trp
450 455 460

Trp Leu Arg His His Pro Gln Val Leu Ser Met Lys Phe Lys Thr Gly
465 470 475 480

Val Lys Arg Ala Glu Ile Ser Asn Ala Ile Asp Gln Tyr Val Thr Gly
485 490 495

Thr Ile Gly Glu Asp Glu Asp Leu Ile Lys Trp Lys Ala Leu Phe Glu
500 505 510

Glu Val Pro Glu Leu Leu Thr Glu Ala Glu Lys Lys Glu Trp Val Glu
515 520 525

Lys Leu Thr Glu Val Ser Ile Ser Ser Asp Ala Phe Phe Pro Phe Arg
530 535 540

Asp Asn Val Asp Arg Ala Lys Arg Ser Gly Val Ala Tyr Ile Ala Ala
545 550 555 560

Pro Ser Gly Ser Ala Ala Asp Lys Val Val Ile Glu Ala Cys Asp Glu
565 570 575

```
Leu Gly Ile Ile Leu Ala His Thr Asn Leu Arg Leu Phe His His
            580                 585                 590


<210> 363
<211> 640
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 57; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS1; "

<220>
<221> source
<223> /note="Gene Name:
      5'-aminolevulinate synthase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P13196; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000309259"

<400> 363
Met Glu Ser Val Val Arg Arg Cys Pro Phe Leu Ser Arg Val Pro Gln
1               5                  10                  15


Ala Phe Leu Gln Lys Ala Gly Lys Ser Leu Leu Phe Tyr Ala Gln Asn
            20                  25                  30


Cys Pro Lys Met Met Glu Val Gly Ala Lys Pro Ala Pro Arg Ala Leu
        35                  40                  45


Ser Thr Ala Ala Val His Tyr Gln Gln Ile Lys Glu Thr Pro Pro Ala
    50                  55                  60


Ser Glu Lys Asp Lys Thr Ala Lys Ala Lys Val Gln Gln Thr Pro Asp
65                  70                  75                  80


Gly Ser Gln Gln Ser Pro Asp Gly Thr Gln Leu Pro Ser Gly His Pro
                85                  90                  95


Leu Pro Ala Thr Ser Gln Gly Thr Ala Ser Lys Cys Pro Phe Leu Ala
            100                 105                 110
```

```
Ala Gln Met Asn Gln Arg Gly Ser Ser Val Phe Cys Lys Ala Ser Leu
        115                 120                 125

Glu Leu Gln Glu Asp Val Gln Glu Met Asn Ala Val Arg Lys Glu Val
    130                 135                 140

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

Gly Asp Pro Ser Gly Leu Leu Lys Asn Phe Gln Asp Ile Met Gln Lys
                165                 170                 175

Gln Arg Pro Glu Arg Val Ser His Leu Leu Gln Asp Asn Leu Pro Lys
            180                 185                 190

Ser Val Ser Thr Phe Gln Tyr Asp Arg Phe Phe Glu Lys Lys Ile Asp
        195                 200                 205

Glu Lys Lys Asn Asp His Thr Tyr Arg Val Phe Lys Thr Val Asn Arg
    210                 215                 220

Arg Ala His Ile Phe Pro Met Ala Asp Asp Tyr Ser Asp Ser Leu Ile
225                 230                 235                 240

Thr Lys Lys Gln Val Ser Val Trp Cys Ser Asn Asp Tyr Leu Gly Met
                245                 250                 255

Ser Arg His Pro Arg Val Cys Gly Ala Val Met Asp Thr Leu Lys Gln
            260                 265                 270

His Gly Ala Gly Ala Gly Gly Thr Arg Asn Ile Ser Gly Thr Ser Lys
        275                 280                 285

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

Ala Ala Leu Leu Phe Ser Ser Cys Phe Val Ala Asn Asp Ser Thr Leu
305                 310                 315                 320

Phe Thr Leu Ala Lys Met Met Pro Gly Cys Glu Ile Tyr Ser Asp Ser
                325                 330                 335
```

```
Gly Asn His Ala Ser Met Ile Gln Gly Ile Arg Asn Ser Arg Val Pro
            340                 345                 350

Lys Tyr Ile Phe Arg His Asn Asp Val Ser His Leu Arg Glu Leu Leu
        355                 360                 365

Gln Arg Ser Asp Pro Ser Val Pro Lys Ile Val Ala Phe Glu Thr Val
    370                 375                 380

His Ser Met Asp Gly Ala Val Cys Pro Leu Glu Glu Leu Cys Asp Val
385                 390                 395                 400

Ala His Glu Phe Gly Ala Ile Thr Phe Val Asp Glu Val His Ala Val
                405                 410                 415

Gly Leu Tyr Gly Ala Arg Gly Gly Gly Ile Gly Asp Arg Asp Gly Val
            420                 425                 430

Met Pro Lys Met Asp Ile Ile Ser Gly Thr Leu Gly Lys Ala Phe Gly
        435                 440                 445

Cys Val Gly Gly Tyr Ile Ala Ser Thr Ser Ser Leu Ile Asp Thr Val
    450                 455                 460

Arg Ser Tyr Ala Ala Gly Phe Ile Phe Thr Thr Ser Leu Pro Pro Met
465                 470                 475                 480

Leu Leu Ala Gly Ala Leu Glu Ser Val Arg Ile Leu Lys Ser Ala Glu
                485                 490                 495

Gly Arg Val Leu Arg Arg Gln His Gln Arg Asn Val Lys Leu Met Arg
            500                 505                 510

Gln Met Leu Met Asp Ala Gly Leu Pro Val Val His Cys Pro Ser His
        515                 520                 525

Ile Ile Pro Val Arg Val Ala Asp Ala Ala Lys Asn Thr Glu Val Cys
    530                 535                 540

Asp Glu Leu Met Ser Arg His Asn Ile Tyr Val Gln Ala Ile Asn Tyr
545                 550                 555                 560
```

```
Pro Thr Val Pro Arg Gly Glu Glu Leu Leu Arg Ile Ala Pro Thr Pro
                565                 570                 575

His His Thr Pro Gln Met Met Asn Tyr Phe Leu Glu Asn Leu Leu Val
            580                 585                 590

Thr Trp Lys Gln Val Gly Leu Glu Leu Lys Pro His Ser Ser Ala Glu
        595                 600                 605

Cys Asn Phe Cys Arg Arg Pro Leu His Phe Glu Val Met Ser Glu Arg
    610                 615                 620

Glu Lys Ser Tyr Phe Ser Gly Leu Ser Lys Leu Val Ser Ala Gln Ala
625                 630                 635                 640
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<210> 364
<211> 640
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 57; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS1; "

<220>
<221> source
<223> /note="Gene Name:
5'-aminolevulinate synthase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P13196; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378416"

<400> 364

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Met Glu Ser Val Val Arg Arg Cys Pro Phe Leu Ser Arg Val Pro Gln
1               5                   10                  15

Ala Phe Leu Gln Lys Ala Gly Lys Ser Leu Leu Phe Tyr Ala Gln Asn
            20                  25                  30

Cys Pro Lys Met Met Glu Val Gly Ala Lys Pro Ala Pro Arg Ala Leu
        35                  40                  45
```

```
Ser Thr Ala Ala Val His Tyr Gln Gln Ile Lys Glu Thr Pro Pro Ala
    50                  55                  60

Ser Glu Lys Asp Lys Thr Ala Lys Ala Lys Val Gln Gln Thr Pro Asp
65                  70                  75                  80

Gly Ser Gln Gln Ser Pro Asp Gly Thr Gln Leu Pro Ser Gly His Pro
                85                  90                  95

Leu Pro Ala Thr Ser Gln Gly Thr Ala Ser Lys Cys Pro Phe Leu Ala
            100                 105                 110

Ala Gln Met Asn Gln Arg Gly Ser Ser Val Phe Cys Lys Ala Ser Leu
        115                 120                 125

Glu Leu Gln Glu Asp Val Gln Glu Met Asn Ala Val Arg Lys Glu Val
    130                 135                 140

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

Gly Asp Pro Ser Gly Leu Leu Lys Asn Phe Gln Asp Ile Met Gln Lys
                165                 170                 175

Gln Arg Pro Glu Arg Val Ser His Leu Leu Gln Asp Asn Leu Pro Lys
            180                 185                 190

Ser Val Ser Thr Phe Gln Tyr Asp Arg Phe Phe Glu Lys Lys Ile Asp
        195                 200                 205

Glu Lys Lys Asn Asp His Thr Tyr Arg Val Phe Lys Thr Val Asn Arg
    210                 215                 220

Arg Ala His Ile Phe Pro Met Ala Asp Asp Tyr Ser Asp Ser Leu Ile
225                 230                 235                 240

Thr Lys Lys Gln Val Ser Val Trp Cys Ser Asn Asp Tyr Leu Gly Met
                245                 250                 255

Ser Arg His Pro Arg Val Cys Gly Ala Val Met Asp Thr Leu Lys Gln
            260                 265                 270
```

```
His Gly Ala Gly Ala Gly Gly Thr Arg Asn Ile Ser Gly Thr Ser Lys
        275                 280                 285

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

Ala Ala Leu Leu Phe Ser Ser Cys Phe Val Ala Asn Asp Ser Thr Leu
305                 310                 315                 320

Phe Thr Leu Ala Lys Met Met Pro Gly Cys Glu Ile Tyr Ser Asp Ser
                325                 330                 335

Gly Asn His Ala Ser Met Ile Gln Gly Ile Arg Asn Ser Arg Val Pro
            340                 345                 350

Lys Tyr Ile Phe Arg His Asn Asp Val Ser His Leu Arg Glu Leu Leu
        355                 360                 365

Gln Arg Ser Asp Pro Ser Val Pro Lys Ile Val Ala Phe Glu Thr Val
    370                 375                 380

His Ser Met Asp Gly Ala Val Cys Pro Leu Glu Glu Leu Cys Asp Val
385                 390                 395                 400

Ala His Glu Phe Gly Ala Ile Thr Phe Val Asp Glu Val His Ala Val
                405                 410                 415

Gly Leu Tyr Gly Ala Arg Gly Gly Gly Ile Gly Asp Arg Asp Gly Val
            420                 425                 430

Met Pro Lys Met Asp Ile Ile Ser Gly Thr Leu Gly Lys Ala Phe Gly
        435                 440                 445

Cys Val Gly Gly Tyr Ile Ala Ser Thr Ser Ser Leu Ile Asp Thr Val
    450                 455                 460

Arg Ser Tyr Ala Ala Gly Phe Ile Phe Thr Thr Ser Leu Pro Pro Met
465                 470                 475                 480

Leu Leu Ala Gly Ala Leu Glu Ser Val Arg Ile Leu Lys Ser Ala Glu
                485                 490                 495
```

```
Gly Arg Val Leu Arg Arg Gln His Gln Arg Asn Val Lys Leu Met Arg
            500                 505                 510

Gln Met Leu Met Asp Ala Gly Leu Pro Val Val His Cys Pro Ser His
        515                 520                 525

Ile Ile Pro Val Arg Val Ala Asp Ala Ala Lys Asn Thr Glu Val Cys
    530                 535                 540

Asp Glu Leu Met Ser Arg His Asn Ile Tyr Val Gln Ala Ile Asn Tyr
545                 550                 555                 560

Pro Thr Val Pro Arg Gly Glu Glu Leu Leu Arg Ile Ala Pro Thr Pro
                565                 570                 575

His His Thr Pro Gln Met Met Asn Tyr Phe Leu Glu Asn Leu Leu Val
            580                 585                 590

Thr Trp Lys Gln Val Gly Leu Glu Leu Lys Pro His Ser Ser Ala Glu
        595                 600                 605

Cys Asn Phe Cys Arg Arg Pro Leu His Phe Glu Val Met Ser Glu Arg
    610                 615                 620

Glu Lys Ser Tyr Phe Ser Gly Leu Ser Lys Leu Val Ser Ala Gln Ala
625                 630                 635                 640


<210> 365
<211> 237
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 57; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS1; "

<220>
<221> source
<223> /note="Gene Name:
      5'-aminolevulinate synthase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417352"
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 365
Xaa Arg Val Pro Lys Tyr Ile Phe Arg His Asn Asp Val Ser His Leu
1 5 10 15

Arg Glu Leu Leu Gln Arg Ser Asp Pro Ser Val Pro Lys Ile Val Ala
20 25 30

Phe Glu Thr Val His Ser Met Asp Gly Lys Ala Phe Gly Cys Val Gly
35 40 45

Gly Tyr Ile Ala Ser Thr Ser Ser Leu Ile Asp Thr Val Arg Ser Tyr
50 55 60

Ala Ala Gly Phe Ile Phe Thr Thr Ser Leu Pro Pro Met Leu Leu Ala
65 70 75 80

Gly Ala Leu Glu Ser Val Arg Ile Leu Lys Ser Ala Glu Gly Arg Val
85 90 95

Leu Arg Arg Gln His Gln Arg Asn Val Lys Leu Met Arg Gln Met Leu
100 105 110

Met Asp Ala Gly Leu Pro Val Val His Cys Pro Ser His Ile Ile Pro
115 120 125

Val Arg Val Ala Asp Ala Ala Lys Asn Thr Glu Val Cys Asp Glu Leu
130 135 140

Met Ser Arg His Asn Ile Tyr Val Gln Ala Ile Asn Tyr Pro Thr Val
145 150 155 160

Pro Arg Gly Glu Glu Leu Leu Arg Ile Ala Pro Thr Pro His His Thr
165 170 175

Pro Gln Met Met Asn Tyr Phe Leu Glu Asn Leu Leu Val Thr Trp Lys
180 185 190

Gln Val Gly Leu Glu Leu Lys Pro His Ser Ser Ala Glu Cys Asn Phe

```
        195                 200                 205

Cys Arg Arg Pro Leu His Phe Glu Val Met Ser Glu Arg Glu Lys Ser
    210                 215                 220

Tyr Phe Ser Gly Leu Ser Lys Leu Val Ser Ala Gln Ala
225                 230                 235


<210> 366
<211> 640
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 57; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS1; "

<220>
<221> source
<223> /note="Gene Name:
      5'-aminolevulinate synthase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P13196; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417719"

<400> 366
Met Glu Ser Val Val Arg Arg Cys Pro Phe Leu Ser Arg Val Pro Gln
1               5                   10                  15

Ala Phe Leu Gln Lys Ala Gly Lys Ser Leu Leu Phe Tyr Ala Gln Asn
            20                  25                  30

Cys Pro Lys Met Met Glu Val Gly Ala Lys Pro Ala Pro Arg Ala Leu
        35                  40                  45

Ser Thr Ala Ala Val His Tyr Gln Gln Ile Lys Glu Thr Pro Pro Ala
    50                  55                  60

Ser Glu Lys Asp Lys Thr Ala Lys Ala Lys Val Gln Gln Thr Pro Asp
65                  70                  75                  80
```

```
Gly Ser Gln Gln Ser Pro Asp Gly Thr Gln Leu Pro Ser Gly His Pro
                85                  90                  95

Leu Pro Ala Thr Ser Gln Gly Thr Ala Ser Lys Cys Pro Phe Leu Ala
            100                 105                 110

Ala Gln Met Asn Gln Arg Gly Ser Ser Val Phe Cys Lys Ala Ser Leu
        115                 120                 125

Glu Leu Gln Glu Asp Val Gln Glu Met Asn Ala Val Arg Lys Glu Val
    130                 135                 140

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

Gly Asp Pro Ser Gly Leu Leu Lys Asn Phe Gln Asp Ile Met Gln Lys
                165                 170                 175

Gln Arg Pro Glu Arg Val Ser His Leu Leu Gln Asp Asn Leu Pro Lys
            180                 185                 190

Ser Val Ser Thr Phe Gln Tyr Asp Arg Phe Phe Glu Lys Lys Ile Asp
        195                 200                 205

Glu Lys Lys Asn Asp His Thr Tyr Arg Val Phe Lys Thr Val Asn Arg
    210                 215                 220

Arg Ala His Ile Phe Pro Met Ala Asp Asp Tyr Ser Asp Ser Leu Ile
225                 230                 235                 240

Thr Lys Lys Gln Val Ser Val Trp Cys Ser Asn Asp Tyr Leu Gly Met
                245                 250                 255

Ser Arg His Pro Arg Val Cys Gly Ala Val Met Asp Thr Leu Lys Gln
            260                 265                 270

His Gly Ala Gly Ala Gly Gly Thr Arg Asn Ile Ser Gly Thr Ser Lys
        275                 280                 285

Phe His Val Asp Leu Glu Arg Glu Leu Ala Asp Leu His Gly Lys Asp
    290                 295                 300
```

```
Ala Ala Leu Leu Phe Ser Ser Cys Phe Val Ala Asn Asp Ser Thr Leu
305                 310                 315                 320

Phe Thr Leu Ala Lys Met Met Pro Gly Cys Glu Ile Tyr Ser Asp Ser
                325                 330                 335

Gly Asn His Ala Ser Met Ile Gln Gly Ile Arg Asn Ser Arg Val Pro
            340                 345                 350

Lys Tyr Ile Phe Arg His Asn Asp Val Ser His Leu Arg Glu Leu Leu
        355                 360                 365

Gln Arg Ser Asp Pro Ser Val Pro Lys Ile Val Ala Phe Glu Thr Val
    370                 375                 380

His Ser Met Asp Gly Ala Val Cys Pro Leu Glu Glu Leu Cys Asp Val
385                 390                 395                 400

Ala His Glu Phe Gly Ala Ile Thr Phe Val Asp Glu Val His Ala Val
                405                 410                 415

Gly Leu Tyr Gly Ala Arg Gly Gly Gly Ile Gly Asp Arg Asp Gly Val
            420                 425                 430

Met Pro Lys Met Asp Ile Ile Ser Gly Thr Leu Gly Lys Ala Phe Gly
        435                 440                 445

Cys Val Gly Gly Tyr Ile Ala Ser Thr Ser Ser Leu Ile Asp Thr Val
    450                 455                 460

Arg Ser Tyr Ala Ala Gly Phe Ile Phe Thr Thr Ser Leu Pro Pro Met
465                 470                 475                 480

Leu Leu Ala Gly Ala Leu Glu Ser Val Arg Ile Leu Lys Ser Ala Glu
                485                 490                 495

Gly Arg Val Leu Arg Arg Gln His Gln Arg Asn Val Lys Leu Met Arg
            500                 505                 510

Gln Met Leu Met Asp Ala Gly Leu Pro Val Val His Cys Pro Ser His
        515                 520                 525

Ile Ile Pro Val Arg Val Ala Asp Ala Ala Lys Asn Thr Glu Val Cys
```

```
    530                 535                 540

Asp Glu Leu Met Ser Arg His Asn Ile Tyr Val Gln Ala Ile Asn Tyr
545                 550                 555                 560

Pro Thr Val Pro Arg Gly Glu Glu Leu Leu Arg Ile Ala Pro Thr Pro
                565                 570                 575

His His Thr Pro Gln Met Met Asn Tyr Phe Leu Glu Asn Leu Leu Val
            580                 585                 590

Thr Trp Lys Gln Val Gly Leu Glu Leu Lys Pro His Ser Ser Ala Glu
        595                 600                 605

Cys Asn Phe Cys Arg Arg Pro Leu His Phe Glu Val Met Ser Glu Arg
    610                 615                 620

Glu Lys Ser Tyr Phe Ser Gly Leu Ser Lys Leu Val Ser Ala Gln Ala
625                 630                 635                 640


<210> 367
<211> 640
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 57; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS1; "

<220>
<221> source
<223> /note="Gene Name:
      5'-aminolevulinate synthase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P13196; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418779"

<400> 367
Met Glu Ser Val Val Arg Arg Cys Pro Phe Leu Ser Arg Val Pro Gln
1               5                   10                  15
```

```
Ala Phe Leu Gln Lys Ala Gly Lys Ser Leu Leu Phe Tyr Ala Gln Asn
            20                  25                  30

Cys Pro Lys Met Met Glu Val Gly Ala Lys Pro Ala Pro Arg Ala Leu
        35                  40                  45

Ser Thr Ala Ala Val His Tyr Gln Gln Ile Lys Glu Thr Pro Pro Ala
    50                  55                  60

Ser Glu Lys Asp Lys Thr Ala Lys Ala Lys Val Gln Gln Thr Pro Asp
65                  70                  75                  80

Gly Ser Gln Gln Ser Pro Asp Gly Thr Gln Leu Pro Ser Gly His Pro
                85                  90                  95

Leu Pro Ala Thr Ser Gln Gly Thr Ala Ser Lys Cys Pro Phe Leu Ala
            100                 105                 110

Ala Gln Met Asn Gln Arg Gly Ser Ser Val Phe Cys Lys Ala Ser Leu
        115                 120                 125

Glu Leu Gln Glu Asp Val Gln Glu Met Asn Ala Val Arg Lys Glu Val
    130                 135                 140

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

Gly Asp Pro Ser Gly Leu Leu Lys Asn Phe Gln Asp Ile Met Gln Lys
                165                 170                 175

Gln Arg Pro Glu Arg Val Ser His Leu Leu Gln Asp Asn Leu Pro Lys
            180                 185                 190

Ser Val Ser Thr Phe Gln Tyr Asp Arg Phe Phe Glu Lys Lys Ile Asp
        195                 200                 205

Glu Lys Lys Asn Asp His Thr Tyr Arg Val Phe Lys Thr Val Asn Arg
    210                 215                 220

Arg Ala His Ile Phe Pro Met Ala Asp Asp Tyr Ser Asp Ser Leu Ile
225                 230                 235                 240
```

```
Thr Lys Lys Gln Val Ser Val Trp Cys Ser Asn Asp Tyr Leu Gly Met
                245                 250                 255

Ser Arg His Pro Arg Val Cys Gly Ala Val Met Asp Thr Leu Lys Gln
            260                 265                 270

His Gly Ala Gly Ala Gly Gly Thr Arg Asn Ile Ser Gly Thr Ser Lys
        275                 280                 285

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

Ala Ala Leu Leu Phe Ser Ser Cys Phe Val Ala Asn Asp Ser Thr Leu
305                 310                 315                 320

Phe Thr Leu Ala Lys Met Met Pro Gly Cys Glu Ile Tyr Ser Asp Ser
                325                 330                 335

Gly Asn His Ala Ser Met Ile Gln Gly Ile Arg Asn Ser Arg Val Pro
            340                 345                 350

Lys Tyr Ile Phe Arg His Asn Asp Val Ser His Leu Arg Glu Leu Leu
        355                 360                 365

Gln Arg Ser Asp Pro Ser Val Pro Lys Ile Val Ala Phe Glu Thr Val
    370                 375                 380

His Ser Met Asp Gly Ala Val Cys Pro Leu Glu Glu Leu Cys Asp Val
385                 390                 395                 400

Ala His Glu Phe Gly Ala Ile Thr Phe Val Asp Glu Val His Ala Val
                405                 410                 415

Gly Leu Tyr Gly Ala Arg Gly Gly Gly Ile Gly Asp Arg Asp Gly Val
            420                 425                 430

Met Pro Lys Met Asp Ile Ile Ser Gly Thr Leu Gly Lys Ala Phe Gly
        435                 440                 445

Cys Val Gly Gly Tyr Ile Ala Ser Thr Ser Ser Leu Ile Asp Thr Val
    450                 455                 460

Arg Ser Tyr Ala Ala Gly Phe Ile Phe Thr Thr Ser Leu Pro Pro Met
```

```
465                 470                 475                 480

Leu Leu Ala Gly Ala Leu Glu Ser Val Arg Ile Leu Lys Ser Ala Glu
                485                 490                 495

Gly Arg Val Leu Arg Arg Gln His Gln Arg Asn Val Lys Leu Met Arg
            500                 505                 510

Gln Met Leu Met Asp Ala Gly Leu Pro Val Val His Cys Pro Ser His
        515                 520                 525

Ile Ile Pro Val Arg Val Ala Asp Ala Ala Lys Asn Thr Glu Val Cys
    530                 535                 540

Asp Glu Leu Met Ser Arg His Asn Ile Tyr Val Gln Ala Ile Asn Tyr
545                 550                 555                 560

Pro Thr Val Pro Arg Gly Glu Glu Leu Leu Arg Ile Ala Pro Thr Pro
                565                 570                 575

His His Thr Pro Gln Met Met Asn Tyr Phe Leu Glu Asn Leu Leu Val
            580                 585                 590

Thr Trp Lys Gln Val Gly Leu Glu Leu Lys Pro His Ser Ser Ala Glu
        595                 600                 605

Cys Asn Phe Cys Arg Arg Pro Leu His Phe Glu Val Met Ser Glu Arg
    610                 615                 620

Glu Lys Ser Tyr Phe Ser Gly Leu Ser Lys Leu Val Ser Ala Gln Ala
625                 630                 635                 640


<210> 368
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 57; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS1; "

<220>
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<221> source
<223> /note="Gene Name:
5'-aminolevulinate synthase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419423"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 368
Xaa Arg Arg Gln His Gln Arg Asn Val Lys Leu Met Arg Gln Met Leu
1 5 10 15

Met Asp Ala Gly Leu Pro Val Val His Cys Pro Ser His Ile Ile Pro
20 25 30

Val Arg Val Ala Asp Ala Ala Lys Asn Thr Glu Val Cys Asp Glu Leu
35 40 45

Met Ser Arg His Asn Ile Tyr Val Gln Ala Ile Asn Tyr Pro Thr Val
50 55 60

Pro Arg Gly Glu Glu Leu Leu Arg Ile Ala Pro Thr Pro His His Thr
65 70 75 80

Pro Gln Met Met Asn Tyr Phe Leu Gly Glu Tyr Leu Gly Ser Cys Trp
85 90 95

Cys Leu Thr Glu Glu Leu His Lys Ala Val Phe Ala Val Phe Ile Ile
100 105 110

Glu Ala Leu Gln Arg
115

<210> 369
<211> 587
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 58; "

<220>

<221> source
<223> /note="Gene Symbol: ALAS2; "

<220>
<221> source
<223> /note="Gene Name:
5'-aminolevulinate synthase 2; "

<220>
<221> source
<223> /note="Uniprot ID: P22557; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000332369"

<400> 369

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

```
Thr Tyr Arg Val Phe Lys Thr Val Asn Arg Trp Ala Asp Ala Tyr Pro
                165                 170                 175

Phe Ala Gln His Phe Ser Glu Ala Ser Val Ala Ser Lys Asp Val Ser
            180                 185                 190

Val Trp Cys Ser Asn Asp Tyr Leu Gly Met Ser Arg His Pro Gln Val
        195                 200                 205

Leu Gln Ala Thr Gln Glu Thr Leu Gln Arg His Gly Ala Gly Ala Gly
    210                 215                 220

Gly Thr Arg Asn Ile Ser Gly Thr Ser Lys Phe His Val Glu Leu Glu
225                 230                 235                 240

Gln Glu Leu Ala Glu Leu His Gln Lys Asp Ser Ala Leu Leu Phe Ser
                245                 250                 255

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

Leu Pro Gly Cys Glu Ile Tyr Ser Asp Ala Gly Asn His Ala Ser Met
        275                 280                 285

Ile Gln Gly Ile Arg Asn Ser Gly Ala Ala Lys Phe Val Phe Arg His
    290                 295                 300

Asn Asp Pro Asp His Leu Lys Lys Leu Leu Glu Lys Ser Asn Pro Lys
305                 310                 315                 320

Ile Pro Lys Ile Val Ala Phe Glu Thr Val His Ser Met Asp Gly Ala
                325                 330                 335

Ile Cys Pro Leu Glu Glu Leu Cys Asp Val Ser His Gln Tyr Gly Ala
            340                 345                 350

Leu Thr Phe Val Asp Glu Val His Ala Val Gly Leu Tyr Gly Ser Arg
        355                 360                 365

Gly Ala Gly Ile Gly Glu Arg Asp Gly Ile Met His Lys Ile Asp Ile
    370                 375                 380

Ile Ser Gly Thr Leu Gly Lys Ala Phe Gly Cys Val Gly Gly Tyr Ile
```

385 390 395 400

Ala Ser Thr Arg Asp Leu Val Asp Met Val Arg Ser Tyr Ala Ala Gly
405 410 415

Phe Ile Phe Thr Thr Ser Leu Pro Pro Met Val Leu Ser Gly Ala Leu
420 425 430

Glu Ser Val Arg Leu Leu Lys Gly Glu Glu Gly Gln Ala Leu Arg Arg
435 440 445

Ala His Gln Arg Asn Val Lys His Met Arg Gln Leu Leu Met Asp Arg
450 455 460

Gly Leu Pro Val Ile Pro Cys Pro Ser His Ile Ile Pro Ile Arg Val
465 470 475 480

Gly Asn Ala Ala Leu Asn Ser Lys Leu Cys Asp Leu Leu Leu Ser Lys
485 490 495

His Gly Ile Tyr Val Gln Ala Ile Asn Tyr Pro Thr Val Pro Arg Gly
500 505 510

Glu Glu Leu Leu Arg Leu Ala Pro Ser Pro His His Ser Pro Gln Met
515 520 525

Met Glu Asp Phe Val Glu Lys Leu Leu Leu Ala Trp Thr Ala Val Gly
530 535 540

Leu Pro Leu Gln Asp Val Ser Val Ala Ala Cys Asn Phe Cys Arg Arg
545 550 555 560

Pro Val His Phe Glu Leu Met Ser Glu Trp Glu Arg Ser Tyr Phe Gly
565 570 575

Asn Met Gly Pro Gln Tyr Val Thr Thr Tyr Ala
580 585

<210> 370
<211> 550
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 58; "

<220>
<221> source
<223> /note="Gene Symbol: ALAS2; "

<220>
<221> source
<223> /note="Gene Name:
5'-aminolevulinate synthase 2; "

<220>
<221> source
<223> /note="Uniprot ID: P22557; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000337131"

<400> 370

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Met Val Thr Ala Ala Met Leu Leu Gln Cys Cys Pro Val Leu Ala Arg
1               5                  10                  15

Gly Pro Thr Ser Leu Leu Gly Lys Val Val Lys Thr His Gln Phe Leu
            20                  25                  30

Phe Gly Ile Gly Arg Cys Pro Ile Leu Ala Thr Gln Gly Pro Asn Cys
        35                  40                  45

Ser Gln Ile His Leu Lys Ala Thr Lys Ala Gly Gly Asp Ser Pro Ser
    50                  55                  60

Trp Ala Lys Gly His Cys Pro Phe Met Leu Ser Glu Leu Gln Asp Gly
65                  70                  75                  80

Lys Ser Lys Ile Val Gln Lys Ala Ala Pro Glu Val Gln Glu Asp Val
                85                  90                  95

Lys Ala Phe Lys Thr Gly Asn Tyr Val Phe Ser Tyr Asp Gln Phe Phe
            100                 105                 110

Arg Asp Lys Ile Met Glu Lys Lys Gln Asp His Thr Tyr Arg Val Phe
        115                 120                 125

Lys Thr Val Asn Arg Trp Ala Asp Ala Tyr Pro Phe Ala Gln His Phe
    130                 135                 140
```

```
Ser Glu Ala Ser Val Ala Ser Lys Asp Val Ser Val Trp Cys Ser Asn
145                 150                 155                 160

Asp Tyr Leu Gly Met Ser Arg His Pro Gln Val Leu Gln Ala Thr Gln
                165                 170                 175

Glu Thr Leu Gln Arg His Gly Ala Gly Ala Gly Gly Thr Arg Asn Ile
            180                 185                 190

Ser Gly Thr Ser Lys Phe His Val Glu Leu Glu Gln Glu Leu Ala Glu
        195                 200                 205

Leu His Gln Lys Asp Ser Ala Leu Leu Phe Ser Ser Cys Phe Val Ala
    210                 215                 220

Asn Asp Ser Thr Leu Phe Thr Leu Ala Lys Ile Leu Pro Gly Cys Glu
225                 230                 235                 240

Ile Tyr Ser Asp Ala Gly Asn His Ala Ser Met Ile Gln Gly Ile Arg
                245                 250                 255

Asn Ser Gly Ala Ala Lys Phe Val Phe Arg His Asn Asp Pro Asp His
            260                 265                 270

Leu Lys Lys Leu Leu Glu Lys Ser Asn Pro Lys Ile Pro Lys Ile Val
        275                 280                 285

Ala Phe Glu Thr Val His Ser Met Asp Gly Ala Ile Cys Pro Leu Glu
    290                 295                 300

Glu Leu Cys Asp Val Ser His Gln Tyr Gly Ala Leu Thr Phe Val Asp
305                 310                 315                 320

Glu Val His Ala Val Gly Leu Tyr Gly Ser Arg Gly Ala Gly Ile Gly
                325                 330                 335

Glu Arg Asp Gly Ile Met His Lys Ile Asp Ile Ile Ser Gly Thr Leu
            340                 345                 350

Gly Lys Ala Phe Gly Cys Val Gly Gly Tyr Ile Ala Ser Thr Arg Asp
        355                 360                 365

Leu Val Asp Met Val Arg Ser Tyr Ala Ala Gly Phe Ile Phe Thr Thr
```

```
    370                 375                 380

Ser Leu Pro Pro Met Val Leu Ser Gly Ala Leu Glu Ser Val Arg Leu
385                 390                 395                 400

Leu Lys Gly Glu Glu Gly Gln Ala Leu Arg Arg Ala His Gln Arg Asn
                405                 410                 415

Val Lys His Met Arg Gln Leu Leu Met Asp Arg Gly Leu Pro Val Ile
            420                 425                 430

Pro Cys Pro Ser His Ile Ile Pro Ile Arg Val Gly Asn Ala Ala Leu
        435                 440                 445

Asn Ser Lys Leu Cys Asp Leu Leu Leu Ser Lys His Gly Ile Tyr Val
    450                 455                 460

Gln Ala Ile Asn Tyr Pro Thr Val Pro Arg Gly Glu Glu Leu Leu Arg
465                 470                 475                 480

Leu Ala Pro Ser Pro His His Ser Pro Gln Met Met Glu Asp Phe Val
                485                 490                 495

Glu Lys Leu Leu Leu Ala Trp Thr Ala Val Gly Leu Pro Leu Gln Asp
            500                 505                 510

Val Ser Val Ala Ala Cys Asn Phe Cys Arg Arg Pro Val His Phe Glu
        515                 520                 525

Leu Met Ser Glu Trp Glu Arg Ser Tyr Phe Gly Asn Met Gly Pro Gln
    530                 535                 540

Tyr Val Thr Thr Tyr Ala
545                 550


<210> 371
<211> 574
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 58; "

<220>
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<221> source
<223> /note="Gene Symbol: ALAS2; "

<220>
<221> source
<223> /note="Gene Name:
5'-aminolevulinate synthase 2; "

<220>
<221> source
<223> /note="Uniprot ID: P22557; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000379501"

<400> 371

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

```
Ala Tyr Pro Phe Ala Gln His Phe Ser Glu Ala Ser Val Ala Ser Lys
                165                 170                 175

Asp Val Ser Val Trp Cys Ser Asn Asp Tyr Leu Gly Met Ser Arg His
            180                 185                 190

Pro Gln Val Leu Gln Ala Thr Gln Glu Thr Leu Gln Arg His Gly Ala
        195                 200                 205

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

Glu Leu Glu Gln Glu Leu Ala Glu Leu His Gln Lys Asp Ser Ala Leu
225                 230                 235                 240

Leu Phe Ser Ser Cys Phe Val Ala Asn Asp Ser Thr Leu Phe Thr Leu
                245                 250                 255

Ala Lys Ile Leu Pro Gly Cys Glu Ile Tyr Ser Asp Ala Gly Asn His
            260                 265                 270

Ala Ser Met Ile Gln Gly Ile Arg Asn Ser Gly Ala Ala Lys Phe Val
        275                 280                 285

Phe Arg His Asn Asp Pro Asp His Leu Lys Lys Leu Leu Glu Lys Ser
    290                 295                 300

Asn Pro Lys Ile Pro Lys Ile Val Ala Phe Glu Thr Val His Ser Met
305                 310                 315                 320

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

Tyr Gly Ala Leu Thr Phe Val Asp Glu Val His Ala Val Gly Leu Tyr
            340                 345                 350

Gly Ser Arg Gly Ala Gly Ile Gly Glu Arg Asp Gly Ile Met His Lys
        355                 360                 365

Ile Asp Ile Ile Ser Gly Thr Leu Gly Lys Ala Phe Gly Cys Val Gly
    370                 375                 380

Gly Tyr Ile Ala Ser Thr Arg Asp Leu Val Asp Met Val Arg Ser Tyr
```

385 390 395 400

Ala Ala Gly Phe Ile Phe Thr Thr Ser Leu Pro Pro Met Val Leu Ser
405 410 415

Gly Ala Leu Glu Ser Val Arg Leu Leu Lys Gly Glu Glu Gly Gln Ala
420 425 430

Leu Arg Arg Ala His Gln Arg Asn Val Lys His Met Arg Gln Leu Leu
435 440 445

Met Asp Arg Gly Leu Pro Val Ile Pro Cys Pro Ser His Ile Ile Pro
450 455 460

Ile Arg Val Gly Asn Ala Ala Leu Asn Ser Lys Leu Cys Asp Leu Leu
465 470 475 480

Leu Ser Lys His Gly Ile Tyr Val Gln Ala Ile Asn Tyr Pro Thr Val
485 490 495

Pro Arg Gly Glu Glu Leu Leu Arg Leu Ala Pro Ser Pro His His Ser
500 505 510

Pro Gln Met Met Glu Asp Phe Val Glu Lys Leu Leu Leu Ala Trp Thr
515 520 525

Ala Val Gly Leu Pro Leu Gln Asp Val Ser Val Ala Ala Cys Asn Phe
530 535 540

Cys Arg Arg Pro Val His Phe Glu Leu Met Ser Glu Trp Glu Arg Ser
545 550 555 560

Tyr Phe Gly Asn Met Gly Pro Gln Tyr Val Thr Thr Tyr Ala
565 570

<210> 372
<211> 221
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 58; "

<220>

<221> source
<223> /note="Gene Symbol: ALAS2; "

<220>
<221> source
<223> /note="Gene Name:
5'-aminolevulinate synthase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000407204"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 372

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Xaa Leu Ser Phe Val Arg Pro Gln Cys Arg Ala Thr Asp Ser Pro Ser
1               5                  10                  15

Trp Ala Lys Gly His Cys Pro Phe Met Leu Ser Glu Leu Gln Asp Gly
            20                  25                  30

Lys Ser Lys Ile Val Gln Lys Ala Ala Pro Glu Val Gln Glu Asp Val
        35                  40                  45

Lys Ala Phe Lys Thr Asp Leu Pro Ser Ser Leu Val Ser Val Ser Leu
    50                  55                  60

Arg Lys Pro Phe Ser Gly Pro Gln Glu Gln Glu Gln Ile Ser Gly Lys
65                  70                  75                  80

Val Thr His Leu Ile Gln Asn Asn Met Pro Gly Asn Tyr Val Phe Ser
                85                  90                  95

Tyr Asp Gln Phe Phe Arg Asp Lys Ile Met Glu Lys Lys Gln Asp His
            100                 105                 110

Thr Tyr Arg Val Phe Lys Thr Val Asn Arg Trp Ala Asp Ala Tyr Pro
        115                 120                 125

Phe Ala Gln His Phe Ser Glu Ala Ser Val Ala Ser Lys Asp Val Ser
    130                 135                 140

Val Trp Cys Ser Asn Asp Tyr Leu Gly Met Ser Arg His Pro Gln Val
145                 150                 155                 160
```

```
Leu Gln Ala Thr Gln Glu Thr Leu Gln Arg His Gly Ala Gly Ala Gly
                165                 170                 175


Gly Thr Arg Asn Ile Ser Gly Thr Ser Lys Phe His Val Glu Leu Glu
            180                 185                 190


Gln Glu Leu Ala Glu Leu His Gln Lys Asp Ser Ala Leu Leu Phe Ser
        195                 200                 205


Ser Cys Phe Val Ala Asn Asp Ser Thr Leu Phe Thr Leu
    210                 215                 220


<210> 373
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 59; "

<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
      5-azacytidine induced 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H6S1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000335609"

<400> 373
Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1               5                   10                  15


Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
            20                  25                  30


Glu Ser Val Ala Ser His Phe Ala Leu Val Thr Ala Tyr Glu Asp Ile
        35                  40                  45
```

```
Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
    50                  55                  60

Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65                  70                  75                  80

Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
                85                  90                  95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
            100                 105                 110

Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu
        115                 120                 125

Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr
    130                 135                 140

Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val
145                 150                 155                 160

Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu
                165                 170                 175

Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys
            180                 185                 190

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

Leu Gln Lys Leu Ser Ile Ser Arg Val Ser Val Ala Gln Pro Gly Val
    210                 215                 220

Gln Trp Arg Asn His Gly Ile Ala
225                 230


<210> 374
<211> 243
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 59; "
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<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
5-azacytidine induced 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H6S1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389577"

<400> 374
Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1   5   10   15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
            20   25   30

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

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
    50   55   60

Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65   70   75   80

Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
                85   90   95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
            100   105   110

Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu
        115   120   125

Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr
    130   135   140

Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val
145   150   155   160

```
Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu
                165                 170                 175

Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys
            180                 185                 190

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

Leu Gln Lys Leu Ser Ile Ser Arg Gln Ser Ile Cys Ser Thr Ala Trp
    210                 215                 220

Ser Ala Val Ala Gln Ser Trp Asp Ser Met Asn Phe Glu Asp Cys Ser
225                 230                 235                 240

Leu Phe Ala
```

<210> 375
<211> 243
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 59; "

<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
5-azacytidine induced 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H6S1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391696"

<400> 375

```
Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1               5                   10                  15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
```

```
            20                  25                  30

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

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
    50                  55                  60

Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65                  70                  75                  80

Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
                85                  90                  95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
            100                 105                 110

Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu
        115                 120                 125

Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr
    130                 135                 140

Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val
145                 150                 155                 160

Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu
                165                 170                 175

Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys
            180                 185                 190

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

Leu Gln Lys Leu Ser Ile Ser Arg Gln Ser Ile Cys Ser Thr Ala Trp
    210                 215                 220

Ser Ala Val Ala Gln Ser Trp Asp Ser Met Asn Phe Glu Asp Cys Ser
225                 230                 235                 240

Leu Phe Ala
```

<210> 376
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 59; "

<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
5-azacytidine induced 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403133"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 376
Xaa Leu Lys Ser Arg Asp Leu Gln Lys Leu Ser Ile Ser Ser Asp Asn
1 5 10 15

Met Gln His Ala Tyr Trp Glu Leu Lys Arg Glu Met Ser Asn Leu His
20 25 30

Leu Val Thr Gln Val Gln Ala Glu Leu Leu Arg Lys Leu Lys Thr Ser
35 40 45

Thr Ala Ile Lys Lys Ala Leu Ser Gln Asn Arg Ala Met Arg Ser Thr
50 55 60

Ala Pro Val Leu Gly Thr His Gly Val Lys Asp Lys
65 70 75

<210> 377
<211> 215
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 59; "

<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
5-azacytidine induced 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412820"

<400> 377
Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1 5 10 15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
20 25 30

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

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
50 55 60

Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65 70 75 80

Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
85 90 95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
100 105 110

Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu
115 120 125

Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr
130 135 140

Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val
145 150 155 160

```
Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu
                165                 170                 175

Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys
            180                 185                 190

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

Leu Gln Lys Leu Ser Ile Ser
    210                 215
```

<210> 378
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 59; "

<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
5-azacytidine induced 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416380"

<400> 378

```
Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1               5                   10                  15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
            20                  25                  30

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

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
    50                  55                  60

Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65                  70                  75                  80
```

```
Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala
                85                  90                  95


<210> 379
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 59; "

<220>
<221> source
<223> /note="Gene Symbol: AZI2; "

<220>
<221> source
<223> /note="Gene Name:
      5-azacytidine induced 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H6S1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419371"

<400> 379
Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1               5                  10                  15


Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
            20                  25                  30


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


Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
    50                  55                  60


Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65                  70                  75                  80


Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
                85                  90                  95
```

```
Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
            100                 105                 110

Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu
        115                 120                 125

Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr
    130                 135                 140

Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val
145                 150                 155                 160

Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu
                165                 170                 175

Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys
            180                 185                 190

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

Leu Gln Lys Leu Ser Ile Ser Ser Asp Asn Met Gln His Ala Tyr Trp
    210                 215                 220

Glu Leu Lys Arg Glu Met Ser Asn Leu His Leu Val Thr Gln Val Gln
225                 230                 235                 240

Ala Glu Leu Leu Arg Lys Leu Lys Thr Ser Thr Ala Ile Lys Lys Ala
                245                 250                 255

Cys Ala Pro Val Gly Cys Ser Glu Asp Leu Gly Arg Asp Ser Thr Lys
            260                 265                 270

Leu His Leu Met Asn Phe Thr Ala Thr Tyr Thr Arg His Pro Pro Leu
        275                 280                 285

Leu Pro Asn Gly Lys Ala Leu Cys His Thr Thr Ser Ser Pro Leu Pro
    290                 295                 300

Gly Asp Val Lys Val Leu Ser Glu Lys Ala Ile Leu Gln Ser Trp Thr
305                 310                 315                 320

Asp Asn Glu Arg Ser Ile Pro Asn Asp Gly Thr Cys Phe Gln Glu His
```

325 330 335

Ser Ser Tyr Gly Arg Asn Ser Leu Glu Asp Asn Ser Trp Val Phe Pro
340 345 350

Ser Pro Pro Lys Ser Ser Glu Thr Ala Phe Gly Glu Thr Lys Thr Lys
355 360 365

Thr Leu Pro Leu Pro Asn Leu Pro Pro Leu His Tyr Leu Asp Gln His
370 375 380

Asn Gln Asn Cys Leu Tyr Lys Asn
385 390

<210> 380
<211> 354
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 60; "

<220>
<221> source
<223> /note="Gene Symbol: HMCES; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxymethylcytosine (hmC) binding, ES cell-specific;
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<220>
<221> source
<223> /note="Uniprot ID: Q96FZ2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000372955"

<400> 380
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1 5 10 15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
20 25 30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
35 40 45

```
Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
    50                  55                  60

Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro Ser
65                  70                  75                  80

Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
                85                  90                  95

Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro Leu
            100                 105                 110

Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
        115                 120                 125

Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
    130                 135                 140

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

Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
                165                 170                 175

Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
            180                 185                 190

Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
        195                 200                 205

Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser
    210                 215                 220

Lys Trp Leu Asp Phe Gly Glu Val Ser Thr Gln Glu Ala Leu Lys Leu
225                 230                 235                 240

Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
                245                 250                 255

Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
            260                 265                 270
```

```
Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Gln Arg Met Leu
        275                 280                 285

Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
    290                 295                 300

Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
305                 310                 315                 320

Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr Ala Gly Leu Leu Glu Gln
                325                 330                 335

Trp Leu Lys Arg Glu Lys Glu Glu Glu Pro Val Ala Lys Arg Pro Tyr
            340                 345                 350

Ser Gln
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<210> 381
<211> 354
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 60; "

<220>
<221> source
<223> /note="Gene Symbol: HMCES; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxymethylcytosine (hmC) binding, ES cell-specific;
"

<220>
<221> source
<223> /note="Uniprot ID: Q96FZ2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000374385"

<400> 381

```
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1               5                   10                  15
```

```
Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
            20                  25                  30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
        35                  40                  45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
    50                  55                  60

Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro Ser
65                  70                  75                  80

Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
                85                  90                  95

Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro Leu
            100                 105                 110

Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
        115                 120                 125

Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
    130                 135                 140

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

Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
                165                 170                 175

Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
            180                 185                 190

Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
        195                 200                 205

Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser
    210                 215                 220

Lys Trp Leu Asp Phe Gly Glu Val Ser Thr Gln Glu Ala Leu Lys Leu
225                 230                 235                 240

Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
```

```
                245                 250                 255

Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
            260                 265                 270

Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Gln Arg Met Leu
        275                 280                 285

Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
    290                 295                 300

Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
305                 310                 315                 320

Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr Ala Gly Leu Leu Glu Gln
                325                 330                 335

Trp Leu Lys Arg Glu Lys Glu Glu Glu Pro Val Ala Lys Arg Pro Tyr
            340                 345                 350

Ser Gln



<210> 382
<211> 312
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 60; "

<220>
<221> source
<223> /note="Gene Symbol: HMCES; "

<220>
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<223> /note="Gene Name:
      5-hydroxymethylcytosine (hmC) binding, ES cell-specific;
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<220>
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<223> /note="ENSP ID: ENSP00000392966"

<400> 382
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1               5                   10                  15
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```
Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
            20                  25                  30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
        35                  40                  45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
    50                  55                  60

Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro Ser
65                  70                  75                  80

Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
                85                  90                  95

Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Ser Gly Ser
            100                 105                 110

Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn
        115                 120                 125

Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro
    130                 135                 140

Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser
145                 150                 155                 160

Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp
                165                 170                 175

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

Gln Glu Ala Leu Lys Leu Ile His Pro Thr Glu Asn Ile Thr Phe His
        195                 200                 205

Ala Val Ser Ser Val Val Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys
    210                 215                 220

Leu Ala Pro Val Asp Leu Val Val Lys Lys Glu Leu Arg Ala Ser Gly
225                 230                 235                 240
```

```
Ser Ser Gln Arg Met Leu Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys
                245                 250                 255

Glu Asp Ser Lys Thr Pro Gln Lys Glu Glu Ser Asp Val Pro Gln Trp
            260                 265                 270

Ser Ser Gln Phe Leu Gln Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr
        275                 280                 285

Ala Gly Leu Leu Glu Gln Trp Leu Lys Arg Glu Lys Glu Glu Glu Pro
    290                 295                 300

Val Ala Lys Arg Pro Tyr Ser Gln
305                 310


<210> 383
<211> 140
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<400> 383
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1               5                   10                  15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
            20                  25                  30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
        35                  40                  45
```

```
Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Ser Gly Ser
    50                  55                  60

Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn
65                  70                  75                  80

Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro
                85                  90                  95

Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser
            100                 105                 110

Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp
        115                 120                 125

Gly Glu Glu Ala Val Ser Lys Trp Leu Asp Phe Gly
    130                 135                 140


<210> 384
<211> 282
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000423132"

<400> 384
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1               5                   10                  15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
            20                  25                  30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
```

```
        35                  40                  45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Val Pro Leu
    50                  55                  60

Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
65                  70                  75                  80

Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
                85                  90                  95

Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala Asp Ser
            100                 105                 110

Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
        115                 120                 125

Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
    130                 135                 140

Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
145                 150                 155                 160

Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser
                165                 170                 175

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

Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
        195                 200                 205

Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
    210                 215                 220

Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Gln Arg Met Leu
225                 230                 235                 240

Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
                245                 250                 255

Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
            260                 265                 270
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Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr
275 280

<210> 385
<211> 233
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<213> Homo sapiens

<220>
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<220>
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<220>
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5-hydroxymethylcytosine (hmC) binding, ES cell-specific;
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<220>
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<223> /note="ENSP ID: ENSP00000424594"

<400> 385
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1 5 10 15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
20 25 30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
35 40 45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
50 55 60

Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro Ser
65 70 75 80

Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
85 90 95

Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro Leu
100 105 110

```
Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
        115                 120                 125

Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
    130                 135                 140

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

Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
                165                 170                 175

Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
            180                 185                 190

Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
        195                 200                 205

Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser
    210                 215                 220

Lys Trp Leu Asp Phe Gly Glu Val Ser
225                 230


<210> 386
<211> 354
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<220>
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<221> source
<223> /note="ENSP ID: ENSP00000426215"

<400> 386
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1 5 10 15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
20 25 30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
35 40 45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
50 55 60

Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro Ser
65 70 75 80

Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
85 90 95

Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro Leu
100 105 110

Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
115 120 125

Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
130 135 140

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

Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
165 170 175

Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
180 185 190

Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
195 200 205

Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser

```
    210                 215                 220

Lys Trp Leu Asp Phe Gly Glu Val Ser Thr Gln Glu Ala Leu Lys Leu
225                 230                 235                 240

Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
                245                 250                 255

Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
            260                 265                 270

Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Gln Arg Met Leu
        275                 280                 285

Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
    290                 295                 300

Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
305                 310                 315                 320

Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr Ala Gly Leu Leu Glu Gln
                325                 330                 335

Trp Leu Lys Arg Glu Lys Glu Glu Glu Pro Val Ala Lys Arg Pro Tyr
            340                 345                 350

Ser Gln
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<210> 387
<211> 183
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 60; "

<220>
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<223> /note="Gene Symbol: HMCES; "

<220>
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<223> /note="Gene Name:
5-hydroxymethylcytosine (hmC) binding, ES cell-specific;
"

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426276"

<400> 387
Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
1   5   10   15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
            20   25   30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
        35   40   45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Ser Gly Ser
    50   55   60

Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn
65   70   75   80

Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro
                85   90   95

Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser
            100   105   110

Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp
        115   120   125

Gly Glu Glu Ala Val Ser Lys Trp Leu Asp Phe Gly Glu Val Ser Thr
    130   135   140

Gln Glu Ala Leu Lys Leu Ile His Pro Thr Glu Asn Ile Thr Phe His
145   150   155   160

Ala Val Ser Ser Val Val Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys
                165   170   175

Leu Ala Pro Val Asp Leu Val
            180

<210> 388
<211> 422
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 61; "

<220>
<221> source
<223> /note="Gene Symbol: HTR1A; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 1A,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P08908; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000316244"

<400> 388

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


Ala Pro Phe Glu Thr Gly Gly Asn Thr Thr Gly Ile Ser Asp Val Thr
            20                  25                  30


Val Ser Tyr Gln Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe
        35                  40                  45


Cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu
    50                  55                  60


Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val
65                  70                  75                  80


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


Gln Val Leu Asn Lys Trp Thr Leu Gly Gln Val Thr Cys Asp Leu Phe
            100                 105                 110


Ile Ala Leu Asp Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys
        115                 120                 125
```

```
Ala Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr
    130                 135                 140

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

Trp Leu Ile Gly Phe Leu Ile Ser Ile Pro Pro Met Leu Gly Trp Arg
                165                 170                 175

Thr Pro Glu Asp Arg Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp
            180                 185                 190

His Gly Tyr Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile Pro Leu
        195                 200                 205

Leu Leu Met Leu Val Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe
    210                 215                 220

Arg Ile Arg Lys Thr Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr
225                 230                 235                 240

Arg His Gly Ala Ser Pro Ala Pro Gln Pro Lys Lys Ser Val Asn Gly
                245                 250                 255

Glu Ser Gly Ser Arg Asn Trp Arg Leu Gly Val Glu Ser Lys Ala Gly
            260                 265                 270

Gly Ala Leu Cys Ala Asn Gly Ala Val Arg Gln Gly Asp Asp Gly Ala
        275                 280                 285

Ala Leu Glu Val Ile Glu Val His Arg Val Gly Asn Ser Lys Glu His
    290                 295                 300

Leu Pro Leu Pro Ser Glu Ala Gly Pro Thr Pro Cys Ala Pro Ala Ser
305                 310                 315                 320

Phe Glu Arg Lys Asn Glu Arg Asn Ala Glu Ala Lys Arg Lys Met Ala
                325                 330                 335

Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met Gly
            340                 345                 350

Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu
```

```
        355                 360                 365

Pro Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Leu Gly Ala Ile
    370                 375                 380

Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Val Ile Tyr
385                 390                 395                 400

Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe Lys Lys Ile Ile Lys
                405                 410                 415

Cys Lys Phe Cys Arg Gln
            420


<210> 389
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 61; "

<220>
<221> source
<223> /note="Gene Symbol: HTR1A; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 1A,
      G prt-coupled; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423433"

<400> 389
Met Asp Val Leu Ser Pro Gly Gln Gly Asn Asn Thr Thr Ser Pro Pro
1               5                   10                  15

Ala Pro Phe Glu Thr Gly Gly Asn Thr Thr Gly Ile Ser Asp Val Thr
            20                  25                  30

Val Ser Tyr Gln Val Ile Thr Ser Leu
        35                  40


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

<220>
<221> source
<223> /note="Payload ID: 62; "

<220>
<221> source
<223> /note="Gene Symbol: HTR1B; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 1B,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P28222; "

<220>
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<400> 390

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

```
Asp Ile Thr Cys Cys Thr Ala Ser Ile Leu His Leu Cys Val Ile Ala
    130                 135                 140

Leu Asp Arg Tyr Trp Ala Ile Thr Asp Ala Val Glu Tyr Ser Ala Lys
145                 150                 155                 160

Arg Thr Pro Lys Arg Ala Ala Val Met Ile Ala Leu Val Trp Val Phe
                165                 170                 175

Ser Ile Ser Ile Ser Leu Pro Pro Phe Phe Trp Arg Gln Ala Lys Ala
            180                 185                 190

Glu Glu Glu Val Ser Glu Cys Val Val Asn Thr Asp His Ile Leu Tyr
        195                 200                 205

Thr Val Tyr Ser Thr Val Gly Ala Phe Tyr Phe Pro Thr Leu Leu Leu
    210                 215                 220

Ile Ala Leu Tyr Gly Arg Ile Tyr Val Glu Ala Arg Ser Arg Ile Leu
225                 230                 235                 240

Lys Gln Thr Pro Asn Arg Thr Gly Lys Arg Leu Thr Arg Ala Gln Leu
                245                 250                 255

Ile Thr Asp Ser Pro Gly Ser Thr Ser Ser Val Thr Ser Ile Asn Ser
            260                 265                 270

Arg Val Pro Asp Val Pro Ser Glu Ser Gly Ser Pro Val Tyr Val Asn
        275                 280                 285

Gln Val Lys Val Arg Val Ser Asp Ala Leu Leu Glu Lys Lys Lys Leu
    290                 295                 300

Met Ala Ala Arg Glu Arg Lys Ala Thr Lys Thr Leu Gly Ile Ile Leu
305                 310                 315                 320

Gly Ala Phe Ile Val Cys Trp Leu Pro Phe Phe Ile Ile Ser Leu Val
                325                 330                 335

Met Pro Ile Cys Lys Asp Ala Cys Trp Phe His Leu Ala Ile Phe Asp
            340                 345                 350
```

```
Phe Phe Thr Trp Leu Gly Tyr Leu Asn Ser Leu Ile Asn Pro Ile Ile
        355                 360                 365


Tyr Thr Met Ser Asn Glu Asp Phe Lys Gln Ala Phe His Lys Leu Ile
    370                 375                 380


Arg Phe Lys Cys Thr Ser
385                 390


<210> 391
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 63; "

<220>
<221> source
<223> /note="Gene Symbol: HTR1D; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 1D,
      G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  P28221; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000363748"

<400> 391
Met Ser Pro Leu Asn Gln Ser Ala Glu Gly Leu Pro Gln Glu Ala Ser
1               5                   10                  15


Asn Arg Ser Leu Asn Ala Thr Glu Thr Ser Glu Ala Trp Asp Pro Arg
            20                  25                  30


Thr Leu Gln Ala Leu Lys Ile Ser Leu Ala Val Val Leu Ser Val Ile
        35                  40                  45


Thr Leu Ala Thr Val Leu Ser Asn Ala Phe Val Leu Thr Thr Ile Leu
    50                  55                  60


Leu Thr Arg Lys Leu His Thr Pro Ala Asn Tyr Leu Ile Gly Ser Leu
```

65 70 75 80

Ala Thr Thr Asp Leu Leu Val Ser Ile Leu Val Met Pro Ile Ser Ile
85 90 95

Ala Tyr Thr Ile Thr His Thr Trp Asn Phe Gly Gln Ile Leu Cys Asp
100 105 110

Ile Trp Leu Ser Ser Asp Ile Thr Cys Cys Thr Ala Ser Ile Leu His
115 120 125

Leu Cys Val Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Ala Leu
130 135 140

Glu Tyr Ser Lys Arg Arg Thr Ala Gly His Ala Ala Thr Met Ile Ala
145 150 155 160

Ile Val Trp Ala Ile Ser Ile Cys Ile Ser Ile Pro Pro Leu Phe Trp
165 170 175

Arg Gln Ala Lys Ala Gln Glu Glu Met Ser Asp Cys Leu Val Asn Thr
180 185 190

Ser Gln Ile Ser Tyr Thr Ile Tyr Ser Thr Cys Gly Ala Phe Tyr Ile
195 200 205

Pro Ser Val Leu Leu Ile Ile Leu Tyr Gly Arg Ile Tyr Arg Ala Ala
210 215 220

Arg Asn Arg Ile Leu Asn Pro Pro Ser Leu Tyr Gly Lys Arg Phe Thr
225 230 235 240

Thr Ala His Leu Ile Thr Gly Ser Ala Gly Ser Ser Leu Cys Ser Leu
245 250 255

Asn Ser Ser Leu His Glu Gly His Ser His Ser Ala Gly Ser Pro Leu
260 265 270

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

Lys Arg Ile Ser Ala Ala Arg Glu Arg Lys Ala Thr Lys Ile Leu Gly
290 295 300

```
Ile Ile Leu Gly Ala Phe Ile Ile Cys Trp Leu Pro Phe Phe Val Val
305                 310                 315                 320


Ser Leu Val Leu Pro Ile Cys Arg Asp Ser Cys Trp Ile His Pro Ala
                325                 330                 335


Leu Phe Asp Phe Phe Thr Trp Leu Gly Tyr Leu Asn Ser Leu Ile Asn
            340                 345                 350


Pro Ile Ile Tyr Thr Val Phe Asn Glu Glu Phe Arg Gln Ala Phe Gln
        355                 360                 365


Lys Ile Val Pro Phe Arg Lys Ala Ser
    370                 375


<210> 392
<211> 365
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 64; "

<220>
<221> source
<223> /note="Gene Symbol: HTR1E; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 1E,
      G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  P28566; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000307766"

<400> 392
Met Asn Ile Thr Asn Cys Thr Thr Glu Ala Ser Met Ala Ile Arg Pro
1               5                   10                  15


Lys Thr Ile Thr Glu Lys Met Leu Ile Cys Met Thr Leu Val Val Ile
            20                  25                  30
```

```
Thr Thr Leu Thr Thr Leu Leu Asn Leu Ala Val Ile Met Ala Ile Gly
        35                  40                  45

Thr Thr Lys Lys Leu His Gln Pro Ala Asn Tyr Leu Ile Cys Ser Leu
    50                  55                  60

Ala Val Thr Asp Leu Leu Val Ala Val Leu Val Met Pro Leu Ser Ile
65                  70                  75                  80

Ile Tyr Ile Val Met Asp Arg Trp Lys Leu Gly Tyr Phe Leu Cys Glu
                85                  90                  95

Val Trp Leu Ser Val Asp Met Thr Cys Cys Thr Cys Ser Ile Leu His
            100                 105                 110

Leu Cys Val Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asn Ala Ile
        115                 120                 125

Glu Tyr Ala Arg Lys Arg Thr Ala Lys Arg Ala Ala Leu Met Ile Leu
    130                 135                 140

Thr Val Trp Thr Ile Ser Ile Phe Ile Ser Met Pro Pro Leu Phe Trp
145                 150                 155                 160

Arg Ser His Arg Arg Leu Ser Pro Pro Pro Ser Gln Cys Thr Ile Gln
                165                 170                 175

His Asp His Val Ile Tyr Thr Ile Tyr Ser Thr Leu Gly Ala Phe Tyr
            180                 185                 190

Ile Pro Leu Thr Leu Ile Leu Ile Leu Tyr Tyr Arg Ile Tyr His Ala
        195                 200                 205

Ala Lys Ser Leu Tyr Gln Lys Arg Gly Ser Ser Arg His Leu Ser Asn
    210                 215                 220

Arg Ser Thr Asp Ser Gln Asn Ser Phe Ala Ser Cys Lys Leu Thr Gln
225                 230                 235                 240

Thr Phe Cys Val Ser Asp Phe Ser Thr Ser Asp Pro Thr Thr Glu Phe
                245                 250                 255
```

```
Glu Lys Phe His Ala Ser Ile Arg Ile Pro Pro Phe Asp Asn Asp Leu
            260                 265                 270

Asp His Pro Gly Glu Arg Gln Gln Ile Ser Ser Thr Arg Glu Arg Lys
        275                 280                 285

Ala Ala Arg Ile Leu Gly Leu Ile Leu Gly Ala Phe Ile Leu Ser Trp
    290                 295                 300

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

Val Ser Ser Glu Val Ala Asp Phe Leu Thr Trp Leu Gly Tyr Val Asn
                325                 330                 335

Ser Leu Ile Asn Pro Leu Leu Tyr Thr Ser Phe Asn Glu Asp Phe Lys
            340                 345                 350

Leu Ala Phe Lys Lys Leu Ile Arg Cys Arg Glu His Thr
        355                 360                 365


<210> 393
<211> 366
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 65; "

<220>
<221> source
<223> /note="Gene Symbol: HTR1F; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 1F,
      G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  P30939; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000322924"

<400> 393
Met Asp Phe Leu Asn Ser Ser Asp Gln Asn Leu Thr Ser Glu Glu Leu
```

```
1               5                   10                  15

Leu Asn Arg Met Pro Ser Lys Ile Leu Val Ser Leu Thr Leu Ser Gly
            20                  25                  30

Leu Ala Leu Met Thr Thr Thr Ile Asn Ser Leu Val Ile Ala Ala Ile
        35                  40                  45

Ile Val Thr Arg Lys Leu His His Pro Ala Asn Tyr Leu Ile Cys Ser
    50                  55                  60

Leu Ala Val Thr Asp Phe Leu Val Ala Val Leu Val Met Pro Phe Ser
65                  70                  75                  80

Ile Val Tyr Ile Val Arg Glu Ser Trp Ile Met Gly Gln Val Val Cys
                85                  90                  95

Asp Ile Trp Leu Ser Val Asp Ile Thr Cys Cys Thr Cys Ser Ile Leu
            100                 105                 110

His Leu Ser Ala Ile Ala Leu Asp Arg Tyr Arg Ala Ile Thr Asp Ala
        115                 120                 125

Val Glu Tyr Ala Arg Lys Arg Thr Pro Lys His Ala Gly Ile Met Ile
    130                 135                 140

Thr Ile Val Trp Ile Ile Ser Val Phe Ile Ser Met Pro Pro Leu Phe
145                 150                 155                 160

Trp Arg His Gln Gly Thr Ser Arg Asp Asp Glu Cys Ile Ile Lys His
                165                 170                 175

Asp His Ile Val Ser Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile
            180                 185                 190

Pro Leu Ala Leu Ile Leu Ile Leu Tyr Tyr Lys Ile Tyr Arg Ala Ala
        195                 200                 205

Lys Thr Leu Tyr His Lys Arg Gln Ala Ser Arg Ile Ala Lys Glu Glu
    210                 215                 220

Val Asn Gly Gln Val Leu Leu Glu Ser Gly Glu Lys Ser Thr Lys Ser
225                 230                 235                 240
```

```
Val Ser Thr Ser Tyr Val Leu Glu Lys Ser Leu Ser Asp Pro Ser Thr
                245                 250                 255

Asp Phe Asp Lys Ile His Ser Thr Val Arg Ser Leu Arg Ser Glu Phe
            260                 265                 270

Lys His Glu Lys Ser Trp Arg Arg Gln Lys Ile Ser Gly Thr Arg Glu
        275                 280                 285

Arg Lys Ala Ala Thr Thr Leu Gly Leu Ile Leu Gly Ala Phe Val Ile
    290                 295                 300

Cys Trp Leu Pro Phe Phe Val Lys Glu Leu Val Val Asn Val Cys Asp
305                 310                 315                 320

Lys Cys Lys Ile Ser Glu Glu Met Ser Asn Phe Leu Ala Trp Leu Gly
                325                 330                 335

Tyr Leu Asn Ser Leu Ile Asn Pro Leu Ile Tyr Thr Ile Phe Asn Glu
            340                 345                 350

Asp Phe Lys Lys Ala Phe Gln Lys Leu Val Arg Cys Arg Cys
        355                 360                 365


<210> 394
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 66; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2A; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 2A,
      G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  P28223; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000367959"

<400> 394
Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn
1   5   10   15

Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe
            20   25   30

Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
        35   40   45

Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
    50   55   60

Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
65   70   75   80

Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
                85   90   95

Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
            100   105   110

Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
        115   120   125

Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
    130   135   140

Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
145   150   155   160

Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
                165   170   175

Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
            180   185   190

Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
        195   200   205

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

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

Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
                245                 250                 255

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

Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
        275                 280                 285

Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
    290                 295                 300

Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
305                 310                 315                 320

Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
                325                 330                 335

Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
            340                 345                 350

Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
        355                 360                 365

Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
    370                 375                 380

Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
385                 390                 395                 400

Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
                405                 410                 415

Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
            420                 425                 430

Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
```

435 440 445

Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
450 455 460

Asn Glu Lys Val Ser Cys Val
465 470

<210> 395
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 66; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2A; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2A,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P28223; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437737"

<400> 395
Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn
1 5 10 15

Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe
20 25 30

Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
35 40 45

Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
50 55 60

Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
65 70 75 80

```
Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
                85                  90                  95

Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
            100                 105                 110

Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
        115                 120                 125

Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
    130                 135                 140

Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
145                 150                 155                 160

Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
                165                 170                 175

Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
            180                 185                 190

Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
        195                 200                 205

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

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

Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
                245                 250                 255

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

Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
        275                 280                 285

Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
    290                 295                 300
```

```
Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
305                 310                 315                 320

Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
                325                 330                 335

Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
            340                 345                 350

Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
        355                 360                 365

Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
    370                 375                 380

Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
385                 390                 395                 400

Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
                405                 410                 415

Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
            420                 425                 430

Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
        435                 440                 445

Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
    450                 455                 460

Asn Glu Lys Val Ser Cys Val
465                 470


<210> 396
<211> 387
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 66; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2A; "
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<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2A,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P28223; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000441861"

<400> 396
Met Gln Phe Leu Lys Ser Ala Lys Gln Lys Pro Asn Tyr Tyr His Ile
1   5   10   15

Met Leu Val Glu Asp Gln Glu Glu Gly Thr Leu His Gln Phe Asn Tyr
            20   25   30

Cys Glu Arg Cys Ser Glu Ser Gln Asn Asn Lys Cys Ile Ser Cys Val
        35   40   45

Asp Pro Glu Asp Lys Trp Tyr Arg Trp Pro Leu Pro Ser Lys Leu Cys
    50   55   60

Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met
65   70   75   80

His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Gln Asn Pro
                85   90   95

Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala Phe Leu Lys Ile
            100   105   110

Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met Pro Ile Pro Val
        115   120   125

Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu Gly Ser Cys Leu
    130   135   140

Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe Val Ser Phe Phe
145   150   155   160

Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu Thr Ile Lys Ser

```
                165                 170                 175

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

Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser Leu Ser Ser Glu
        195                 200                 205

Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly Ser Tyr Thr Gly
    210                 215                 220

Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys Ala Cys Lys Val
225                 230                 235                 240

Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp Cys Pro Phe Phe
                245                 250                 255

Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser Cys Asn Glu Asp
            260                 265                 270

Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile Gly Tyr Leu Ser
        275                 280                 285

Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn Lys Thr Tyr Arg
    290                 295                 300

Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys Glu Asn Lys Lys
305                 310                 315                 320

Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala Leu Ala Tyr Lys
                325                 330                 335

Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser Lys Gln Asp Ala
            340                 345                 350

Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu Gly Lys Gln His
        355                 360                 365

Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val Asn Glu Lys Val
    370                 375                 380

Ser Cys Val
385
```

<210> 397
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 66; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2A; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2A,
G prt-coupled; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482708"

<400> 397
Phe Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val
1 5 10 15

Asp Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro
20 25 30

Ser Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu
35 40 45

Leu Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val
50 55 60

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

Phe Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val
85 90 95

Met Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Glu Trp His
100 105 110

<210> 398
<211> 481
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 67; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2B; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2B,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P41595; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000258400"

<400> 398

```
Met Ala Leu Ser Tyr Arg Val Ser Glu Leu Gln Ser Thr Ile Pro Glu
1               5                  10                  15


His Ile Leu Gln Ser Thr Phe Val His Val Ile Ser Ser Asn Trp Ser
            20                  25                  30


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


Glu Gln Gly Asn Lys Leu His Trp Ala Ala Leu Leu Ile Leu Met Val
    50                  55                  60


Ile Ile Pro Thr Ile Gly Gly Asn Thr Leu Val Ile Leu Ala Val Ser
65                  70                  75                  80


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


Ala Val Ala Asp Leu Leu Val Gly Leu Phe Val Met Pro Ile Ala Leu
            100                 105                 110


Leu Thr Ile Met Phe Glu Ala Met Trp Pro Leu Pro Leu Val Leu Cys
        115                 120                 125
```

```
Pro Ala Trp Leu Phe Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met
    130                 135                 140

His Leu Cys Ala Ile Ser Val Asp Arg Tyr Ile Ala Ile Lys Lys Pro
145                 150                 155                 160

Ile Gln Ala Asn Gln Tyr Asn Ser Arg Ala Thr Ala Phe Ile Lys Ile
                165                 170                 175

Thr Val Val Trp Leu Ile Ser Ile Gly Ile Ala Ile Pro Val Pro Ile
            180                 185                 190

Lys Gly Ile Glu Thr Asp Val Asp Asn Pro Asn Asn Ile Thr Cys Val
        195                 200                 205

Leu Thr Lys Glu Arg Phe Gly Asp Phe Met Leu Phe Gly Ser Leu Ala
    210                 215                 220

Ala Phe Phe Thr Pro Leu Ala Ile Met Ile Val Thr Tyr Phe Leu Thr
225                 230                 235                 240

Ile His Ala Leu Gln Lys Lys Ala Tyr Leu Val Lys Asn Lys Pro Pro
                245                 250                 255

Gln Arg Leu Thr Trp Leu Thr Val Ser Thr Val Phe Gln Arg Asp Glu
            260                 265                 270

Thr Pro Cys Ser Ser Pro Glu Lys Val Ala Met Leu Asp Gly Ser Arg
        275                 280                 285

Lys Asp Lys Ala Leu Pro Asn Ser Gly Asp Glu Thr Leu Met Arg Arg
    290                 295                 300

Thr Ser Thr Ile Gly Lys Lys Ser Val Gln Thr Ile Ser Asn Glu Gln
305                 310                 315                 320

Arg Ala Ser Lys Val Leu Gly Ile Val Phe Phe Leu Phe Leu Leu Met
                325                 330                 335

Trp Cys Pro Phe Phe Ile Thr Asn Ile Thr Leu Val Leu Cys Asp Ser
            340                 345                 350

Cys Asn Gln Thr Thr Leu Gln Met Leu Leu Glu Ile Phe Val Trp Ile
```

```
        355                 360                 365

Gly Tyr Val Ser Ser Gly Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
    370                 375                 380

Lys Thr Phe Arg Asp Ala Phe Gly Arg Tyr Ile Thr Cys Asn Tyr Arg
385                 390                 395                 400

Ala Thr Lys Ser Val Lys Thr Leu Arg Lys Arg Ser Ser Lys Ile Tyr
                405                 410                 415

Phe Arg Asn Pro Met Ala Glu Asn Ser Lys Phe Phe Lys Lys His Gly
            420                 425                 430

Ile Arg Asn Gly Ile Asn Pro Ala Met Tyr Gln Ser Pro Met Arg Leu
        435                 440                 445

Arg Ser Ser Thr Ile Gln Ser Ser Ser Ile Ile Leu Leu Asp Thr Leu
    450                 455                 460

Leu Leu Thr Glu Asn Glu Gly Asp Lys Thr Glu Glu Gln Val Ser Tyr
465                 470                 475                 480

Val
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<210> 399
<211> 458
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 68; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2C; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2C,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P28335; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000276198"

<400> 399
Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile
1   5   10   15

Gly Leu Leu Val Trp Gln Ser Asp Ile Ser Val Ser Pro Val Ala Ala
            20   25   30

Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe
        35   40   45

Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile
    50   55   60

Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met
65   70   75   80

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

Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu
            100   105   110

Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro
        115   120   125

Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His
    130   135   140

Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Arg Asn Pro Ile
145   150   155   160

Glu His Ser Arg Phe Asn Ser Arg Thr Lys Ala Ile Met Lys Ile Ala
                165   170   175

Ile Val Trp Ala Ile Ser Ile Gly Val Ser Val Pro Ile Pro Val Ile
            180   185   190

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

```
Leu Asn Asp Pro Asn Phe Val Leu Ile Gly Ser Phe Val Ala Phe Phe
    210                 215                 220

Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu Thr Ile Tyr Val
225                 230                 235                 240

Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His Thr Glu Glu Pro
                245                 250                 255

Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys Arg Asn Thr Ala
            260                 265                 270

Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln Asn Ala Arg Arg
        275                 280                 285

Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met Gln Ala Ile Asn
    290                 295                 300

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

Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Leu Ser Val Leu
                325                 330                 335

Cys Glu Lys Ser Cys Asn Gln Lys Leu Met Glu Lys Leu Leu Asn Val
            340                 345                 350

Phe Val Trp Ile Gly Tyr Val Cys Ser Gly Ile Asn Pro Leu Val Tyr
        355                 360                 365

Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser Asn Tyr Leu Arg
    370                 375                 380

Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg Gln Ile Pro Arg
385                 390                 395                 400

Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn Val Asn Ile Tyr
                405                 410                 415

Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser Asp Asn Glu Pro
            420                 425                 430
```

Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro Val Asn Pro Ser
435 440 445

Ser Val Val Ser Glu Arg Ile Ser Ser Val
450 455

<210> 400
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 68; "

<220>
<221> source
<223> /note="Gene Symbol: HTR2C; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2C,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P28335; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000361018"

<400> 400
Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile
1 5 10 15

Gly Leu Leu Val Trp Gln Ser Asp Ile Ser Val Ser Pro Val Ala Ala
20 25 30

Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe
35 40 45

Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile
50 55 60

Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met
65 70 75 80

Glu Lys Lys Leu His Asn Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala

```
                85                  90                  95

Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu
            100                 105                 110

Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro
        115                 120                 125

Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His
    130                 135                 140

Leu Cys Ala Ile Ser Leu Asp Arg Cys Ile Ser Ser Tyr Pro Cys Asp
145                 150                 155                 160

Trp Thr Glu Gly Arg Arg Lys Gly Val Arg Glu Gln His Asp Val Arg
                165                 170                 175

Ala Gln Arg Pro Lys Phe Arg Ser Tyr Trp Val Leu Arg Ser Phe Leu
            180                 185                 190

His Thr Ala Asp Asp Tyr Gly Asp Tyr Val Leu Pro Asp His Leu Arg
        195                 200                 205

Ser Ala Pro Thr Ser Phe Asp Val Thr Ala Arg Pro His Arg Gly Thr
    210                 215                 220

Ala Trp Thr Lys Ser Gly Phe Pro Glu Val Leu Gln Glu Glu Tyr Gly
225                 230                 235                 240

Arg Gly Arg Glu Leu Cys Lys Pro
                245
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<210> 401
<211> 458
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 68; "

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<223> /note="Gene Symbol: HTR2C; "

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<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 2C,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P28335; "

<220>
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<223> /note="ENSP ID: ENSP00000361019"

<400> 401

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Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile
1               5                  10                  15

Gly Leu Leu Val Trp Gln Ser Asp Ile Ser Val Ser Pro Val Ala Ala
            20                  25                  30

Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe
        35                  40                  45

Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile
    50                  55                  60

Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met
65                  70                  75                  80

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

Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu
            100                 105                 110

Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro
        115                 120                 125

Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His
    130                 135                 140

Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Arg Asn Pro Ile
145                 150                 155                 160

Glu His Ser Arg Phe Asn Ser Arg Thr Lys Ala Ile Met Lys Ile Ala
                165                 170                 175
```

```
Ile Val Trp Ala Ile Ser Ile Gly Val Ser Val Pro Ile Pro Val Ile
            180                 185                 190

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

Leu Asn Asp Pro Asn Phe Val Leu Ile Gly Ser Phe Val Ala Phe Phe
    210                 215                 220

Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu Thr Ile Tyr Val
225                 230                 235                 240

Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His Thr Glu Glu Pro
                245                 250                 255

Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys Arg Asn Thr Ala
            260                 265                 270

Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln Asn Ala Arg Arg
        275                 280                 285

Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met Gln Ala Ile Asn
    290                 295                 300

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

Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Leu Ser Val Leu
                325                 330                 335

Cys Glu Lys Ser Cys Asn Gln Lys Leu Met Glu Lys Leu Leu Asn Val
            340                 345                 350

Phe Val Trp Ile Gly Tyr Val Cys Ser Gly Ile Asn Pro Leu Val Tyr
        355                 360                 365

Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser Asn Tyr Leu Arg
    370                 375                 380

Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg Gln Ile Pro Arg
385                 390                 395                 400
```

```
Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn Val Asn Ile Tyr
                405                 410                 415

Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser Asp Asn Glu Pro
            420                 425                 430

Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro Val Asn Pro Ser
        435                 440                 445

Ser Val Val Ser Glu Arg Ile Ser Ser Val
    450                 455


<210> 402
<211> 463
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 69; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3A; "

<220>
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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3A, ionotropic;
"

<220>
<221> source
<223> /note="Uniprot ID:  P46098; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000299961"

<400> 402
Met His Arg Ser Phe Leu Gln Ala Arg Arg Ser Arg Asn Thr Thr Arg
1               5                   10                  15

Pro Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu Thr Asn Tyr Arg Lys
            20                  25                  30

Gly Val Arg Pro Val Arg Asp Trp Arg Lys Pro Thr Thr Val Ser Ile
        35                  40                  45

Asp Val Ile Val Tyr Ala Ile Leu Asn Val Asp Glu Lys Asn Gln Val
```

```
    50                  55                  60

Leu Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu
65                  70                  75                  80

Gln Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro
                85                  90                  95

Thr Asp Ser Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp
            100                 105                 110

Val Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln Gly
        115                 120                 125

Glu Val Gln Asn Tyr Lys Pro Leu Gln Val Val Thr Ala Cys Ser Leu
    130                 135                 140

Asp Ile Tyr Asn Phe Pro Phe Asp Val Gln Asn Cys Ser Leu Thr Phe
145                 150                 155                 160

Thr Ser Trp Leu His Thr Ile Gln Asp Ile Asn Ile Ser Leu Trp Arg
                165                 170                 175

Leu Pro Glu Lys Val Lys Ser Asp Arg Ser Val Phe Met Asn Gln Gly
            180                 185                 190

Glu Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe Arg Glu Phe Ser Met
        195                 200                 205

Glu Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe Tyr Val Val Ile Arg
    210                 215                 220

Arg Arg Pro Leu Phe Tyr Val Val Ser Leu Leu Leu Pro Ser Ile Phe
225                 230                 235                 240

Leu Met Val Met Asp Ile Val Gly Phe Tyr Leu Pro Pro Asn Ser Gly
                245                 250                 255

Glu Arg Val Ser Phe Lys Ile Thr Leu Leu Leu Gly Tyr Ser Val Phe
            260                 265                 270

Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr Ala Ile Gly Thr Pro
        275                 280                 285
```

```
Leu Ile Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu Val Ile Ser
    290                 295                 300

Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val His Lys Gln Asp Leu
305                 310                 315                 320

Gln Gln Pro Val Pro Ala Trp Leu Arg His Leu Val Leu Glu Arg Ile
                325                 330                 335

Ala Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr Ser Gln Arg Pro Pro
            340                 345                 350

Ala Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys Ser Ala Met Gly Asn
        355                 360                 365

His Cys Ser His Met Gly Gly Pro Gln Asp Phe Glu Lys Ser Pro Arg
    370                 375                 380

Asp Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu Ala Ser Leu Ala Val
385                 390                 395                 400

Cys Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg Gln Phe Leu Glu Lys
                405                 410                 415

Arg Asp Glu Ile Arg Glu Val Ala Arg Asp Trp Leu Arg Val Gly Ser
            420                 425                 430

Val Leu Asp Lys Leu Leu Phe His Ile Tyr Leu Leu Ala Val Leu Ala
        435                 440                 445

Tyr Ser Ile Thr Leu Val Met Leu Trp Ser Ile Trp Gln Tyr Ala
    450                 455                 460


<210> 403
<211> 516
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 69; "

<220>
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<223> /note="Gene Symbol: HTR3A; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3A, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID: P46098; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000347754"

<400> 403

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

```
Thr Ala Cys Ser Leu Asp Ile Tyr Asn Phe Pro Phe Asp Val Gln Asn
                165                 170                 175

Cys Ser Leu Thr Phe Thr Ser Trp Leu His Thr Ile Gln Asp Ile Asn
            180                 185                 190

Ile Ser Leu Trp Arg Leu Pro Glu Lys Val Lys Ser Asp Arg Ser Val
        195                 200                 205

Phe Met Asn Gln Gly Glu Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe
    210                 215                 220

Arg Glu Phe Ser Met Glu Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe
225                 230                 235                 240

Tyr Val Val Ile Arg Arg Arg Pro Leu Phe Tyr Val Val Ser Leu Leu
                245                 250                 255

Leu Pro Ser Ile Phe Leu Met Val Met Asp Ile Val Gly Phe Tyr Leu
            260                 265                 270

Pro Pro Asn Ser Gly Glu Arg Val Ser Phe Lys Ile Thr Leu Leu Leu
        275                 280                 285

Gly Tyr Ser Val Phe Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr
    290                 295                 300

Ala Ile Gly Thr Pro Leu Ile Gly Lys Ala Pro Pro Gly Ser Arg Ala
305                 310                 315                 320

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

Ala Ser Ala Leu Gly Cys Thr Gly Val Tyr Phe Val Val Cys Met Ala
            340                 345                 350

Leu Leu Val Ile Ser Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val
        355                 360                 365

His Lys Gln Asp Leu Gln Gln Pro Val Pro Ala Trp Leu Arg His Leu
    370                 375                 380

Val Leu Glu Arg Ile Ala Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr
```

```
385                 390                 395                 400

Ser Gln Arg Pro Pro Ala Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys
                405                 410                 415

Ser Ala Met Gly Asn His Cys Ser His Met Gly Gly Pro Gln Asp Phe
            420                 425                 430

Glu Lys Ser Pro Arg Asp Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu
        435                 440                 445

Ala Ser Leu Ala Val Cys Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg
    450                 455                 460

Gln Phe Leu Glu Lys Arg Asp Glu Ile Arg Glu Val Ala Arg Asp Trp
465                 470                 475                 480

Leu Arg Val Gly Ser Val Leu Asp Lys Leu Leu Phe His Ile Tyr Leu
                485                 490                 495

Leu Ala Val Leu Ala Tyr Ser Ile Thr Leu Val Met Leu Trp Ser Ile
            500                 505                 510

Trp Gln Tyr Ala
        515


<210> 404
<211> 484
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 69; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3A; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3A, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID:  P46098; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000364648"

<400> 404
Met Leu Gly Lys Leu Ala Met Leu Leu Trp Val Gln Gln Ala Leu Leu
1   5   10   15

Ala Leu Leu Leu Pro Thr Leu Leu Ala Gln Gly Glu Ala Arg Arg Ser
            20   25   30

Arg Asn Thr Thr Arg Pro Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu
        35   40   45

Thr Asn Tyr Arg Lys Gly Val Arg Pro Val Arg Asp Trp Arg Lys Pro
    50   55   60

Thr Thr Val Ser Ile Asp Val Ile Val Tyr Ala Ile Leu Asn Val Asp
65   70   75   80

Glu Lys Asn Gln Val Leu Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp
                85   90   95

Thr Asp Glu Phe Leu Gln Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr
            100   105   110

Lys Leu Ser Ile Pro Thr Asp Ser Ile Trp Val Pro Asp Ile Leu Ile
        115   120   125

Asn Glu Phe Val Asp Val Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr
    130   135   140

Ile Arg His Gln Gly Glu Val Gln Asn Tyr Lys Pro Leu Gln Val Val
145   150   155   160

Thr Ala Cys Ser Leu Asp Ile Tyr Asn Phe Pro Phe Asp Val Gln Asn
                165   170   175

Cys Ser Leu Thr Phe Thr Ser Trp Leu His Thr Ile Gln Asp Ile Asn
            180   185   190

Ile Ser Leu Trp Arg Leu Pro Glu Lys Val Lys Ser Asp Arg Ser Val
        195   200   205

```
Phe Met Asn Gln Gly Glu Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe
    210                 215                 220

Arg Glu Phe Ser Met Glu Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe
225                 230                 235                 240

Tyr Val Val Ile Arg Arg Arg Pro Leu Phe Tyr Val Val Ser Leu Leu
                245                 250                 255

Leu Pro Ser Ile Phe Leu Met Val Met Asp Ile Val Gly Phe Tyr Leu
            260                 265                 270

Pro Pro Asn Ser Gly Glu Arg Val Ser Phe Lys Ile Thr Leu Leu Leu
        275                 280                 285

Gly Tyr Ser Val Phe Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr
    290                 295                 300

Ala Ile Gly Thr Pro Leu Ile Gly Val Tyr Phe Val Val Cys Met Ala
305                 310                 315                 320

Leu Leu Val Ile Ser Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val
                325                 330                 335

His Lys Gln Asp Leu Gln Gln Pro Val Pro Ala Trp Leu Arg His Leu
            340                 345                 350

Val Leu Glu Arg Ile Ala Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr
        355                 360                 365

Ser Gln Arg Pro Pro Ala Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys
    370                 375                 380

Ser Ala Met Gly Asn His Cys Ser His Met Gly Gly Pro Gln Asp Phe
385                 390                 395                 400

Glu Lys Ser Pro Arg Asp Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu
                405                 410                 415

Ala Ser Leu Ala Val Cys Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg
            420                 425                 430
```

```
Gln Phe Leu Glu Lys Arg Asp Glu Ile Arg Glu Val Ala Arg Asp Trp
        435                 440                 445


Leu Arg Val Gly Ser Val Leu Asp Lys Leu Leu Phe His Ile Tyr Leu
    450                 455                 460


Leu Ala Val Leu Ala Tyr Ser Ile Thr Leu Val Met Leu Trp Ser Ile
465                 470                 475                 480


Trp Gln Tyr Ala



<210> 405
<211> 238
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 69; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3A; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3A, ionotropic;
"

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423653"

<400> 405
Met Leu Leu Trp Val Gln Gln Ala Leu Leu Ala Leu Leu Leu Pro Thr
1               5                   10                  15


Leu Leu Ala Gln Gly Glu Ala Arg Arg Ser Arg Asn Thr Thr Arg Pro
            20                  25                  30


Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu Thr Asn Tyr Arg Lys Gly
        35                  40                  45


Val Arg Pro Val Arg Asp Trp Arg Lys Pro Thr Thr Val Ser Ile Asp
    50                  55                  60


Val Ile Val Tyr Ala Ile Leu Asn Val Asp Glu Lys Asn Gln Val Leu
```

```
65                  70                  75                  80

Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu Gln
                85                  90                  95

Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro Thr
            100                 105                 110

Asp Ser Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp Val
        115                 120                 125

Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln Gly Glu
    130                 135                 140

Val Gln Asn Tyr Lys Pro Leu Gln Val Val Thr Ala Cys Ser Leu Asp
145                 150                 155                 160

Ile Tyr Asn Phe Pro Phe Asp Val Gln Asn Cys Ser Leu Thr Phe Thr
                165                 170                 175

Ser Trp Leu His Thr Ser Gly His Pro Pro Ala Ala Pro Leu Leu Cys
            180                 185                 190

Gly Gln Pro Ala Thr Ala Gln His Leu Pro His Gly His Gly His Arg
        195                 200                 205

Gly Leu Leu Pro Ala Pro Gln Gln Trp Arg Glu Gly Leu Phe Gln Asp
    210                 215                 220

Tyr Thr Pro Pro Gly Leu Leu Gly Leu Pro Asp His Arg Phe
225                 230                 235


<210> 406
<211> 478
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 69; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3A; "

<220>
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<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3A, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID: P46098; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424189"

<400> 406

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Met Leu Leu Trp Val Gln Gln Ala Leu Leu Ala Leu Leu Leu Pro Thr
1               5                  10                  15

Leu Leu Ala Gln Gly Glu Ala Arg Arg Ser Arg Asn Thr Thr Arg Pro
            20                  25                  30

Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu Thr Asn Tyr Arg Lys Gly
        35                  40                  45

Val Arg Pro Val Arg Asp Trp Arg Lys Pro Thr Thr Val Ser Ile Asp
    50                  55                  60

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

Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu Gln
                85                  90                  95

Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro Thr
            100                 105                 110

Asp Ser Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp Val
        115                 120                 125

Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln Gly Glu
    130                 135                 140

Val Gln Asn Tyr Lys Pro Leu Gln Val Val Thr Ala Cys Ser Leu Asp
145                 150                 155                 160

Ile Tyr Asn Phe Pro Phe Asp Val Gln Asn Cys Ser Leu Thr Phe Thr
                165                 170                 175
```

```
Ser Trp Leu His Thr Ile Gln Asp Ile Asn Ile Ser Leu Trp Arg Leu
            180                 185                 190

Pro Glu Lys Val Lys Ser Asp Arg Ser Val Phe Met Asn Gln Gly Glu
        195                 200                 205

Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe Arg Glu Phe Ser Met Glu
    210                 215                 220

Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe Tyr Val Val Ile Arg Arg
225                 230                 235                 240

Arg Pro Leu Phe Tyr Val Val Ser Leu Leu Leu Pro Ser Ile Phe Leu
                245                 250                 255

Met Val Met Asp Ile Val Gly Phe Tyr Leu Pro Pro Asn Ser Gly Glu
            260                 265                 270

Arg Val Ser Phe Lys Ile Thr Leu Leu Leu Gly Tyr Ser Val Phe Leu
        275                 280                 285

Ile Ile Val Ser Asp Thr Leu Pro Ala Thr Ala Ile Gly Thr Pro Leu
    290                 295                 300

Ile Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu Val Ile Ser Leu
305                 310                 315                 320

Ala Glu Thr Ile Phe Ile Val Arg Leu Val His Lys Gln Asp Leu Gln
                325                 330                 335

Gln Pro Val Pro Ala Trp Leu Arg His Leu Val Leu Glu Arg Ile Ala
            340                 345                 350

Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr Ser Gln Arg Pro Pro Ala
        355                 360                 365

Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys Ser Ala Met Gly Asn His
    370                 375                 380

Cys Ser His Met Gly Gly Pro Gln Asp Phe Glu Lys Ser Pro Arg Asp
385                 390                 395                 400
```

```
Arg Cys Ser Pro Pro Pro Pro Arg Glu Ala Ser Leu Ala Val Cys
                405                 410                 415

Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg Gln Phe Leu Glu Lys Arg
            420                 425                 430

Asp Glu Ile Arg Glu Val Ala Arg Asp Trp Leu Arg Val Gly Ser Val
        435                 440                 445

Leu Asp Lys Leu Leu Phe His Ile Tyr Leu Leu Ala Val Leu Ala Tyr
    450                 455                 460

Ser Ile Thr Leu Val Met Leu Trp Ser Ile Trp Gln Tyr Ala
465                 470                 475


<210> 407
<211> 510
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 69; "

<220>
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<223> /note="Gene Symbol: HTR3A; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3A, ionotropic;
"

<220>
<221> source
<223> /note="Uniprot ID:  P46098; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424776"

<400> 407
Met Leu Leu Trp Val Gln Gln Ala Leu Leu Ala Leu Leu Leu Pro Thr
1               5                   10                  15

Leu Leu Ala Gln Gly Glu Ala Arg Arg Ser Arg Asn Thr Thr Arg Pro
            20                  25                  30

Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu Thr Asn Tyr Arg Lys Gly
```

```
        35                  40                  45

Val Arg Pro Val Arg Asp Trp Arg Lys Pro Thr Thr Val Ser Ile Asp
    50                  55                  60

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

Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu Gln
                85                  90                  95

Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro Thr
            100                 105                 110

Asp Ser Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp Val
        115                 120                 125

Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln Gly Glu
    130                 135                 140

Val Gln Asn Tyr Lys Pro Leu Gln Val Val Thr Ala Cys Ser Leu Asp
145                 150                 155                 160

Ile Tyr Asn Phe Pro Phe Asp Val Gln Asn Cys Ser Leu Thr Phe Thr
                165                 170                 175

Ser Trp Leu His Thr Ile Gln Asp Ile Asn Ile Ser Leu Trp Arg Leu
            180                 185                 190

Pro Glu Lys Val Lys Ser Asp Arg Ser Val Phe Met Asn Gln Gly Glu
        195                 200                 205

Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe Arg Glu Phe Ser Met Glu
    210                 215                 220

Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe Tyr Val Val Ile Arg Arg
225                 230                 235                 240

Arg Pro Leu Phe Tyr Val Val Ser Leu Leu Leu Pro Ser Ile Phe Leu
                245                 250                 255

Met Val Met Asp Ile Val Gly Phe Tyr Leu Pro Pro Asn Ser Gly Glu
            260                 265                 270
```

```
Arg Val Ser Phe Lys Ile Thr Leu Leu Leu Gly Tyr Ser Val Phe Leu
        275                 280                 285

Ile Ile Val Ser Asp Thr Leu Pro Ala Thr Ala Ile Gly Thr Pro Leu
    290                 295                 300

Ile Gly Lys Ala Pro Pro Gly Ser Arg Ala Gln Ser Gly Glu Lys Pro
305                 310                 315                 320

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

Thr Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu Val Ile Ser Leu
            340                 345                 350

Ala Glu Thr Ile Phe Ile Val Arg Leu Val His Lys Gln Asp Leu Gln
        355                 360                 365

Gln Pro Val Pro Ala Trp Leu Arg His Leu Val Leu Glu Arg Ile Ala
    370                 375                 380

Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr Ser Gln Arg Pro Pro Ala
385                 390                 395                 400

Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys Ser Ala Met Gly Asn His
                405                 410                 415

Cys Ser His Met Gly Gly Pro Gln Asp Phe Glu Lys Ser Pro Arg Asp
            420                 425                 430

Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu Ala Ser Leu Ala Val Cys
        435                 440                 445

Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg Gln Phe Leu Glu Lys Arg
    450                 455                 460

Asp Glu Ile Arg Glu Val Ala Arg Asp Trp Leu Arg Val Gly Ser Val
465                 470                 475                 480

Leu Asp Lys Leu Leu Phe His Ile Tyr Leu Leu Ala Val Leu Ala Tyr
                485                 490                 495
```

```
Ser Ile Thr Leu Val Met Leu Trp Ser Ile Trp Gln Tyr Ala
            500                 505                 510


<210> 408
<211> 441
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 70; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3B; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3B, ionotropic;
"

<220>
<221> source
<223> /note="Uniprot ID:  O95264; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000260191"

<400> 408
Met Leu Ser Ser Val Met Ala Pro Leu Trp Ala Cys Ile Leu Val Ala
1               5                   10                  15


Ala Gly Ile Leu Ala Thr Asp Thr His His Pro Gln Asp Ser Ala Leu
            20                  25                  30


Tyr His Leu Ser Lys Gln Leu Leu Gln Lys Tyr His Lys Glu Val Arg
        35                  40                  45


Pro Val Tyr Asn Trp Thr Lys Ala Thr Thr Val Tyr Leu Asp Leu Phe
    50                  55                  60


Val His Ala Ile Leu Asp Val Asp Ala Glu Asn Gln Ile Leu Lys Thr
65                  70                  75                  80


Ser Val Trp Tyr Gln Glu Val Trp Asn Asp Glu Phe Leu Ser Trp Asn
                85                  90                  95
```

```
Ser Ser Met Phe Asp Glu Ile Arg Glu Ile Ser Leu Pro Leu Ser Ala
            100                 105                 110

Ile Trp Ala Pro Asp Ile Ile Ile Asn Glu Phe Val Asp Ile Glu Arg
        115                 120                 125

Tyr Pro Asp Leu Pro Tyr Val Tyr Val Asn Ser Ser Gly Thr Ile Glu
    130                 135                 140

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

Ala Phe Pro Phe Asp Val Gln Asn Cys Ser Leu Thr Phe Lys Ser Ile
                165                 170                 175

Leu His Thr Val Glu Asp Val Asp Leu Ala Phe Leu Arg Ser Pro Glu
            180                 185                 190

Asp Ile Gln His Asp Lys Lys Ala Phe Leu Asn Asp Ser Glu Trp Glu
        195                 200                 205

Leu Leu Ser Val Ser Ser Thr Tyr Ser Ile Leu Gln Ser Ser Ala Gly
    210                 215                 220

Gly Phe Ala Gln Ile Gln Phe Asn Val Val Met Arg Arg His Pro Leu
225                 230                 235                 240

Val Tyr Val Val Ser Leu Leu Ile Pro Ser Ile Phe Leu Met Leu Val
                245                 250                 255

Asp Leu Gly Ser Phe Tyr Leu Pro Pro Asn Cys Arg Ala Arg Ile Val
            260                 265                 270

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

Ser Asn Gln Val Pro Arg Ser Val Gly Ser Thr Pro Leu Ile Gly His
    290                 295                 300

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

Ile Val Leu Val Lys Phe Leu His Asp Glu Gln Arg Gly Gly Gln Glu
```

```
                325                 330                 335

Gln Pro Phe Leu Cys Leu Arg Gly Asp Thr Asp Ala Asp Arg Pro Arg
            340                 345                 350

Val Glu Pro Arg Ala Gln Arg Ala Val Val Thr Glu Ser Ser Leu Tyr
        355                 360                 365

Gly Glu His Leu Ala Gln Pro Gly Thr Leu Lys Glu Val Trp Ser Gln
    370                 375                 380

Leu Gln Ser Ile Ser Asn Tyr Leu Gln Thr Gln Asp Gln Thr Asp Gln
385                 390                 395                 400

Gln Glu Ala Glu Trp Leu Val Leu Leu Ser Arg Phe Asp Arg Leu Leu
                405                 410                 415

Phe Gln Ser Tyr Leu Phe Met Leu Gly Ile Tyr Thr Ile Thr Leu Cys
            420                 425                 430

Ser Leu Trp Ala Leu Trp Gly Gly Val
        435                 440


<210> 409
<211> 175
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 70; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3B; "

<220>
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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3B, ionotropic;
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000440894"


<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 409
Xaa Ala Glu Asn Gln Ile Leu Lys Thr Ser Val Trp Tyr Gln Glu Val
1 5 10 15

Trp Asn Asp Glu Phe Leu Ser Trp Asn Ser Ser Met Phe Asp Glu Ile
20 25 30

Arg Glu Ile Ser Leu Pro Leu Ser Ala Ile Trp Ala Pro Asp Ile Ile
35 40 45

Ile Asn Glu Phe Val Asp Ile Glu Arg Tyr Pro Asp Leu Pro Tyr Val
50 55 60

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

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

Asn Cys Ser Leu Thr Phe Lys Ser Ile Leu His Thr Val Glu Asp Val
100 105 110

Asp Leu Ala Phe Leu Arg Ser Pro Glu Asp Ile Gln His Asp Lys Lys
115 120 125

Ala Phe Leu Asn Asp Ser Glu Trp Glu Leu Leu Ser Val Ser Ser Thr
130 135 140

Tyr Ser Ile Leu Gln Ser Ser Ala Gly Gly Phe Ala Gln Ile Gln Phe
145 150 155 160

Asn Gly Thr Ser Ser Pro Ser Ala Trp Pro Ser Trp Phe Ser Ala
165 170 175

<210> 410
<211> 430
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<213> Homo sapiens

<220>
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<223> /note="Payload ID: 70; "

<220>
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<223> /note="Gene Symbol: HTR3B; "

<220>
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<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3B, ionotropic;
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<220>
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<223> /note="Uniprot ID: O95264; "

<220>
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<400> 410
Met Ile Val Tyr Phe Pro Gly Ile Leu Ala Thr Asp Thr His His Pro
1   5   10   15

Gln Asp Ser Ala Leu Tyr His Leu Ser Lys Gln Leu Leu Gln Lys Tyr
            20   25   30

His Lys Glu Val Arg Pro Val Tyr Asn Trp Thr Lys Ala Thr Thr Val
        35   40   45

Tyr Leu Asp Leu Phe Val His Ala Ile Leu Asp Val Asp Ala Glu Asn
    50   55   60

Gln Ile Leu Lys Thr Ser Val Trp Tyr Gln Glu Val Trp Asn Asp Glu
65   70   75   80

Phe Leu Ser Trp Asn Ser Ser Met Phe Asp Glu Ile Arg Glu Ile Ser
                85   90   95

Leu Pro Leu Ser Ala Ile Trp Ala Pro Asp Ile Ile Ile Asn Glu Phe
            100   105   110

Val Asp Ile Glu Arg Tyr Pro Asp Leu Pro Tyr Val Tyr Val Asn Ser
        115   120   125

Ser Gly Thr Ile Glu Asn Tyr Lys Pro Ile Gln Val Val Ser Ala Cys
    130   135   140

Ser Leu Glu Thr Tyr Ala Phe Pro Phe Asp Val Gln Asn Cys Ser Leu
145   150   155   160

```
Thr Phe Lys Ser Ile Leu His Thr Val Glu Asp Val Asp Leu Ala Phe
                165                 170                 175

Leu Arg Ser Pro Glu Asp Ile Gln His Asp Lys Lys Ala Phe Leu Asn
            180                 185                 190

Asp Ser Glu Trp Glu Leu Leu Ser Val Ser Ser Thr Tyr Ser Ile Leu
        195                 200                 205

Gln Ser Ser Ala Gly Gly Phe Ala Gln Ile Gln Phe Asn Val Val Met
    210                 215                 220

Arg Arg His Pro Leu Val Tyr Val Val Ser Leu Leu Ile Pro Ser Ile
225                 230                 235                 240

Phe Leu Met Leu Val Asp Leu Gly Ser Phe Tyr Leu Pro Pro Asn Cys
                245                 250                 255

Arg Ala Arg Ile Val Phe Lys Thr Ser Val Leu Val Gly Tyr Thr Val
            260                 265                 270

Phe Arg Val Asn Met Ser Asn Gln Val Pro Arg Ser Val Gly Ser Thr
        275                 280                 285

Pro Leu Ile Gly His Phe Phe Thr Ile Cys Met Ala Phe Leu Val Leu
    290                 295                 300

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

Arg Gly Gly Gln Glu Gln Pro Phe Leu Cys Leu Arg Gly Asp Thr Asp
                325                 330                 335

Ala Asp Arg Pro Arg Val Glu Pro Arg Ala Gln Arg Ala Val Val Thr
            340                 345                 350

Glu Ser Ser Leu Tyr Gly Glu His Leu Ala Gln Pro Gly Thr Leu Lys
        355                 360                 365

Glu Val Trp Ser Gln Leu Gln Ser Ile Ser Asn Tyr Leu Gln Thr Gln
    370                 375                 380
```

```
Asp Gln Thr Asp Gln Gln Glu Ala Glu Trp Leu Val Leu Leu Ser Arg
385                 390                 395                 400


Phe Asp Arg Leu Leu Phe Gln Ser Tyr Leu Phe Met Leu Gly Ile Tyr
                405                 410                 415


Thr Ile Thr Leu Cys Ser Leu Trp Ala Leu Trp Gly Gly Val
            420                 425                 430


<210> 411
<211> 447
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 71; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3C; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3C, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID:  Q8WXA8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000322617"

<400> 411
Met Glu Gly Gly Trp Pro Ala Arg Gln Ser Ala Leu Leu Cys Leu Thr
1               5                   10                  15


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


Ser Gly Phe Asp Gln His Gly Val Asp Pro Ala Val Phe Gln Ala Val
        35                  40                  45


Phe Asp Arg Lys Ala Phe Arg Pro Phe Thr Asn Tyr Ser Ile Pro Thr
    50                  55                  60
```

```
Arg Val Asn Ile Ser Phe Thr Leu Ser Ala Ile Leu Gly Val Asp Ala
65                  70                  75                  80

Gln Leu Gln Leu Leu Thr Ser Phe Leu Trp Met Asp Leu Val Trp Asp
                85                  90                  95

Asn Pro Phe Ile Asn Trp Asn Pro Lys Glu Cys Val Gly Ile Asn Lys
            100                 105                 110

Leu Thr Val Leu Ala Glu Asn Leu Trp Leu Pro Asp Ile Phe Ile Val
        115                 120                 125

Glu Ser Met Asp Val Asp Gln Thr Pro Ser Gly Leu Thr Ala Tyr Ile
    130                 135                 140

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

Ile Cys Asn Leu Asp Ile Phe Tyr Phe Pro Phe Asp Gln Gln Asn Cys
                165                 170                 175

Thr Phe Thr Phe Ser Ser Phe Leu Tyr Thr Val Asp Ser Met Leu Leu
            180                 185                 190

Gly Met Asp Lys Glu Val Trp Glu Ile Thr Asp Thr Ser Arg Lys Val
        195                 200                 205

Ile Gln Thr Gln Gly Glu Trp Glu Leu Leu Gly Ile Asn Lys Ala Thr
    210                 215                 220

Pro Lys Met Ser Met Gly Asn Asn Leu Tyr Asp Gln Ile Met Phe Tyr
225                 230                 235                 240

Val Ala Ile Arg Arg Arg Pro Ser Leu Tyr Ile Ile Asn Leu Leu Val
                245                 250                 255

Pro Ser Ser Phe Leu Val Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro
            260                 265                 270

Ala Glu Ser Glu Asn Arg Ala Pro Phe Lys Ile Thr Leu Leu Leu Gly
        275                 280                 285

Tyr Asn Val Phe Leu Leu Met Met Asn Asp Leu Leu Pro Ala Ser Gly
```

```
    290                 295                 300

Thr Pro Leu Ile Ser Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val
305                 310                 315                 320

Val Ser Leu Leu Glu Thr Val Phe Ile Thr Tyr Leu Leu His Val Ala
                325                 330                 335

Thr Thr Gln Pro Pro Pro Met Pro Arg Trp Leu His Ser Leu Leu Leu
            340                 345                 350

His Cys Thr Ser Pro Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Gly
        355                 360                 365

Asn Lys Gly Leu Gly Leu Thr Leu Thr His Leu Pro Gly Pro Lys Glu
    370                 375                 380

Pro Gly Glu Leu Ala Gly Lys Lys Leu Gly Pro Arg Glu Thr Glu Pro
385                 390                 395                 400

Asp Gly Gly Ser Gly Trp Thr Lys Thr Gln Leu Met Glu Leu Trp Val
                405                 410                 415

Gln Phe Ser His Ala Met Asp Thr Leu Leu Phe Arg Leu Tyr Leu Leu
            420                 425                 430

Phe Met Ala Ser Ser Ile Leu Thr Val Ile Val Leu Trp Asn Thr
        435                 440                 445


<210> 412
<211> 279
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<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 72; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3D; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3D, ionotropic;
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000334315"

<400> 412
Met Ala Ser Met Ser Ile Val Lys Ala Thr Ser Asn Thr Ile Ser Gln
1   5   10   15

Cys Gly Trp Ser Ala Ser Ala Asn Trp Thr Pro Ser Ile Ser Pro Ser
            20   25   30

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

Ala Ile Arg Arg Arg Cys Arg Pro Ser Pro Tyr Val Val Asn Phe Leu
    50   55   60

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

Pro Leu Glu Ser Gly Asn Cys Ala Pro Phe Lys Met Thr Val Leu Leu
                85   90   95

Gly Tyr Ser Val Phe Leu Leu Met Met Asn Asp Leu Leu Pro Ala Thr
            100   105   110

Ser Thr Ser Ser His Ala Ser Leu Val Arg Pro His Pro Ser Arg Asp
        115   120   125

Gln Lys Arg Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val Gly
    130   135   140

Ser Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val Ala Thr
145   150   155   160

Thr Gln Pro Leu Pro Leu Pro Arg Trp Leu His Ser Leu Leu Leu His
                165   170   175

Cys Thr Gly Gln Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Gly Asn
            180   185   190

Lys Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys Glu Pro
        195   200   205

```
Glu Val Ser Ala Gly Gln Met Pro Gly Pro Gly Glu Ala Glu Leu Thr
    210                 215                 220

Gly Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala Gln Lys
225                 230                 235                 240

Gln His Ser Val Glu Leu Trp Val Gln Phe Ser His Ala Met Asp Ala
                245                 250                 255

Leu Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile Ile Thr
            260                 265                 270

Val Ile Cys Leu Trp Asn Thr
        275


<210> 413
<211> 454
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 72; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3D; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3D, ionotropic;
"

<220>
<221> source
<223> /note="Uniprot ID:  Q70Z44; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000371929"

<400> 413
Met Gln Lys His Ser Pro Gly Pro Pro Ala Leu Ala Leu Leu Ser Gln
1               5                   10                  15

Ser Leu Leu Thr Thr Gly Asn Gly Asp Thr Leu Ile Ile Asn Cys Pro
            20                  25                  30
```

```
Gly Phe Gly Gln His Arg Val Asp Pro Ala Ala Phe Gln Ala Val Phe
        35                  40                  45

Asp Arg Lys Ala Ile Gly Pro Val Thr Asn Tyr Ser Val Ala Thr His
    50                  55                  60

Val Asn Ile Ser Phe Thr Leu Ser Ala Ile Trp Asn Cys Tyr Ser Arg
65                  70                  75                  80

Ile His Thr Phe Asn Cys His His Ala Arg Pro Trp His Asn Gln Phe
                85                  90                  95

Val Gln Trp Asn Pro Asp Glu Cys Gly Gly Ile Lys Lys Ser Gly Met
            100                 105                 110

Ala Thr Glu Asn Leu Trp Leu Ser Asp Val Phe Ile Glu Glu Ser Val
        115                 120                 125

Asp Gln Thr Pro Ala Gly Leu Met Ala Ser Met Ser Ile Val Lys Ala
    130                 135                 140

Thr Ser Asn Thr Ile Ser Gln Cys Gly Trp Ser Ala Ser Ala Asn Trp
145                 150                 155                 160

Thr Pro Ser Ile Ser Pro Ser Met Asp Arg Ala Arg Ala Trp Arg Arg
                165                 170                 175

Met Ser Arg Ser Phe Gln Ile His His Arg Thr Ser Phe Arg Thr Arg
            180                 185                 190

Arg Glu Trp Val Leu Leu Gly Ile Gln Lys Arg Thr Ile Lys Val Thr
        195                 200                 205

Val Ala Thr Asn Gln Tyr Glu Gln Ala Ile Phe His Val Ala Ile Arg
    210                 215                 220

Arg Arg Cys Arg Pro Ser Pro Tyr Val Val Asn Phe Leu Val Pro Ser
225                 230                 235                 240

Gly Ile Leu Ile Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro Leu Glu
                245                 250                 255

Ser Gly Asn Cys Ala Pro Phe Lys Met Thr Val Leu Leu Gly Tyr Ser
```

```
            260                 265                 270

Val Phe Leu Leu Met Met Asn Asp Leu Leu Pro Ala Thr Ser Thr Ser
        275                 280                 285

Ser His Ala Ser Leu Val Ala Pro Leu Ala Leu Met Gln Thr Pro Leu
    290                 295                 300

Pro Ala Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val Gly Ser
305                 310                 315                 320

Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val Ala Thr Thr
                325                 330                 335

Gln Pro Leu Pro Leu Pro Arg Trp Leu His Ser Leu Leu Leu His Cys
            340                 345                 350

Thr Gly Gln Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Gly Asn Lys
        355                 360                 365

Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys Glu Pro Glu
    370                 375                 380

Val Ser Ala Gly Gln Met Pro Gly Pro Gly Glu Ala Glu Leu Thr Gly
385                 390                 395                 400

Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala Gln Lys Gln
                405                 410                 415

His Ser Val Glu Leu Trp Val Gln Phe Ser His Ala Met Asp Ala Leu
            420                 425                 430

Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile Ile Thr Val
        435                 440                 445

Ile Cys Leu Trp Asn Thr
    450
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<210> 414
<211> 233
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 72; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3D; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3D, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID: Q70Z44; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389268"

<400> 414

```
Met Val Ala Ile Arg Arg Arg Cys Arg Pro Ser Pro Tyr Val Val Asn
1               5                  10                  15

Phe Leu Val Pro Ser Gly Ile Leu Ile Ala Ile Asp Ala Leu Ser Phe
            20                  25                  30

Tyr Leu Pro Leu Glu Ser Gly Asn Cys Ala Pro Phe Lys Met Thr Val
        35                  40                  45

Leu Leu Gly Tyr Ser Val Phe Leu Leu Met Met Asn Asp Leu Leu Pro
    50                  55                  60

Ala Thr Ser Thr Ser Ser His Ala Ser Leu Val Arg Pro His Pro Ser
65                  70                  75                  80

Arg Asp Gln Lys Arg Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met
                85                  90                  95

Val Gly Ser Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val
            100                 105                 110

Ala Thr Thr Gln Pro Leu Pro Leu Pro Arg Trp Leu His Ser Leu Leu
        115                 120                 125

Leu His Cys Thr Gly Gln Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys
    130                 135                 140
```

```
Gly Asn Lys Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys
145                 150                 155                 160

Glu Pro Glu Val Ser Ala Gly Gln Met Pro Gly Pro Gly Glu Ala Glu
                165                 170                 175

Leu Thr Gly Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala
            180                 185                 190

Gln Lys Gln His Ser Val Glu Leu Trp Val Gln Phe Ser His Ala Met
        195                 200                 205

Asp Ala Leu Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile
    210                 215                 220

Ile Thr Val Ile Cys Leu Trp Asn Thr
225                 230


<210> 415
<211> 404
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 72; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3D; "

<220>
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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3D, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID:  Q70Z44; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405409"

<400> 415
Met Glu Arg Gly Trp Phe His Gly Lys Gly Phe Leu Leu Gly Phe Ile
1               5                   10                  15
```

```
Leu His Leu Leu Leu Gln Asp Ser His Leu Gln Leu Val Thr Ser Phe
            20                  25                  30

Leu Trp Leu Asn Met Trp Asn Pro Asp Glu Cys Gly Gly Ile Lys Lys
        35                  40                  45

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

Glu Ser Val Asp Gln Thr Pro Ala Gly Leu Met Ala Ser Met Ser Ile
65                  70                  75                  80

Val Lys Ala Thr Ser Asn Thr Ile Ser Gln Cys Gly Trp Ser Ala Ser
                85                  90                  95

Ala Asn Trp Thr Pro Ser Ile Ser Pro Ser Met Asp Arg Gly Glu Arg
            100                 105                 110

Ser Pro Ser Ala Leu Ser Pro Thr Gln Val Thr Arg Ala Trp Arg Arg
        115                 120                 125

Met Ser Arg Ser Phe Gln Ile His His Arg Thr Ser Phe Arg Thr Arg
    130                 135                 140

Arg Glu Trp Val Leu Leu Gly Ile Gln Lys Arg Thr Ile Lys Val Thr
145                 150                 155                 160

Val Ala Thr Asn Gln Tyr Glu Gln Ala Ile Phe His Val Ala Ile Arg
                165                 170                 175

Arg Arg Cys Arg Pro Ser Pro Tyr Val Val Asn Phe Leu Val Pro Ser
            180                 185                 190

Gly Ile Leu Ile Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro Leu Glu
        195                 200                 205

Ser Gly Asn Cys Ala Pro Phe Lys Met Thr Val Leu Leu Gly Tyr Ser
    210                 215                 220

Val Phe Leu Leu Met Met Asn Asp Leu Leu Pro Ala Thr Ser Thr Ser
225                 230                 235                 240

Ser His Ala Ser Leu Val Arg Pro His Pro Ser Arg Asp Gln Lys Arg
```

```
                245                 250                 255

Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val Gly Ser Leu Leu
            260                 265                 270

Glu Thr Ile Phe Ile Thr His Leu Leu His Val Ala Thr Thr Gln Pro
        275                 280                 285

Leu Pro Leu Pro Arg Trp Leu His Ser Leu Leu Leu His Cys Thr Gly
    290                 295                 300

Gln Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Gly Asn Lys Gly Pro
305                 310                 315                 320

Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys Glu Pro Glu Val Ser
                325                 330                 335

Ala Gly Gln Met Pro Gly Pro Gly Glu Ala Glu Leu Thr Gly Gly Ser
            340                 345                 350

Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala Gln Lys Gln His Ser
        355                 360                 365

Val Glu Leu Trp Val Gln Phe Ser His Ala Met Asp Ala Leu Leu Phe
    370                 375                 380

Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile Ile Thr Val Ile Cys
385                 390                 395                 400

Leu Trp Asn Thr
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<210> 416
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 73; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3E; "

<220>

<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3E, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID: A5X5Y0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000335511"

<400> 416
Met Leu Ala Phe Ile Leu Ser Arg Ala Thr Pro Arg Pro Ala Leu Gly
1   5   10   15

Pro Leu Ser Tyr Arg Glu His Arg Val Ala Leu Leu His Leu Thr His
            20   25   30

Ser Met Ser Thr Thr Gly Arg Gly Val Thr Phe Thr Ile Asn Cys Ser
        35   40   45

Gly Phe Gly Gln His Gly Ala Asp Pro Thr Ala Leu Asn Ser Val Phe
    50   55   60

Asn Arg Lys Pro Phe Arg Pro Val Thr Asn Ile Ser Val Pro Thr Gln
65   70   75   80

Val Asn Ile Ser Phe Ala Met Ser Ala Ile Leu Asp Val Asn Glu Gln
                85   90   95

Leu His Leu Leu Ser Ser Phe Leu Trp Leu Glu Met Val Trp Asp Asn
            100   105   110

Pro Phe Ile Ser Trp Asn Pro Glu Glu Cys Glu Gly Ile Thr Lys Met
        115   120   125

Ser Met Ala Ala Lys Asn Leu Trp Leu Pro Asp Ile Phe Ile Ile Glu
    130   135   140

Leu Met Asp Val Asp Lys Thr Pro Lys Gly Leu Thr Ala Tyr Val Ser
145   150   155   160

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

```
Cys Asn Leu Asp Ile Phe Tyr Phe Pro Phe Asp Gln Gln Asn Cys Thr
            180                 185                 190

Leu Thr Phe Ser Ser Phe Leu Tyr Thr Val Asp Ser Met Leu Leu Asp
        195                 200                 205

Met Glu Lys Glu Val Trp Glu Ile Thr Asp Ala Ser Arg Asn Ile Leu
    210                 215                 220

Gln Thr His Gly Glu Trp Glu Leu Leu Gly Leu Ser Lys Ala Thr Ala
225                 230                 235                 240

Lys Leu Ser Arg Gly Gly Asn Leu Tyr Asp Gln Ile Val Phe Tyr Val
                245                 250                 255

Ala Ile Arg Arg Arg Pro Ser Leu Tyr Val Ile Asn Leu Leu Val Pro
            260                 265                 270

Ser Gly Phe Leu Val Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro Val
        275                 280                 285

Lys Ser Gly Asn Arg Val Pro Phe Lys Ile Thr Leu Leu Leu Gly Tyr
    290                 295                 300

Asn Val Phe Leu Leu Met Met Ser Asp Leu Leu Pro Thr Ser Gly Thr
305                 310                 315                 320

Pro Leu Ile Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val Gly
                325                 330                 335

Ser Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val Ala Thr
            340                 345                 350

Thr Gln Pro Pro Pro Leu Pro Arg Trp Leu His Ser Leu Leu Leu His
        355                 360                 365

Cys Asn Ser Pro Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Glu Asn
    370                 375                 380

Lys Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys Glu Pro
385                 390                 395                 400
```

```
Glu Val Ser Ala Gly Gln Met Pro Gly Pro Ala Glu Ala Glu Leu Thr
                405                 410                 415

Gly Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala Gln Lys
            420                 425                 430

Gln His Ser Val Glu Leu Trp Leu Gln Phe Ser His Ala Met Asp Ala
        435                 440                 445

Met Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile Ile Thr
    450                 455                 460

Val Ile Cys Leu Trp Asn Thr
465                 470


<210> 417
<211> 158
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 73; "

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<223> /note="Gene Symbol: HTR3E; "

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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3E, ionotropic;
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<220>
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<223> /note="ENSP ID: ENSP00000391254"

<400> 417
Met Ser Ala Ile Leu Asp Val Asn Glu Gln Leu His Leu Leu Ser Ser
1               5                   10                  15

Phe Leu Trp Leu Glu Met Val Trp Asp Asn Pro Phe Ile Ser Trp Asn
            20                  25                  30

Pro Glu Glu Cys Glu Gly Ile Thr Lys Met Ser Met Ala Ala Lys Asn
        35                  40                  45

Leu Trp Leu Pro Asp Ile Phe Ile Ile Glu Leu Met Asp Val Asp Lys
```

```
    50                  55                  60

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

Tyr Lys Lys Pro Met Lys Val Asp Ser Ile Cys Asn Leu Asp Ile Phe
                85                  90                  95

Tyr Phe Pro Phe Asp Gln Gln Asn Cys Thr Leu Thr Phe Ser Ser Phe
            100                 105                 110

Leu Tyr Thr Val Asp Ser Met Leu Leu Asp Met Glu Lys Glu Val Trp
        115                 120                 125

Glu Ile Thr Asp Ala Ser Arg Asn Ile Leu Gln Thr His Gly Glu Trp
    130                 135                 140

Glu Leu Leu Gly Leu Ser Lys Ala Thr Ala Lys Leu Ser Arg
145                 150                 155


<210> 418
<211> 456
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<213> Homo sapiens

<220>
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<223> /note="Payload ID: 73; "

<220>
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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3E, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID:  A5X5Y0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000395833"

<400> 418
Met Leu Ala Phe Ile Leu Ser Arg Ala Thr Pro Arg Pro Ala Leu Gly
1               5                   10                  15
```

```
Pro Leu Ser Tyr Arg Glu His Arg Val Ala Leu Leu His Leu Thr His
            20                  25                  30

Ser Met Ser Thr Thr Gly Arg Gly Val Thr Phe Thr Ile Asn Cys Ser
        35                  40                  45

Gly Phe Gly Gln His Gly Ala Asp Pro Thr Ala Leu Asn Ser Val Phe
    50                  55                  60

Asn Arg Lys Pro Phe Arg Pro Val Thr Asn Ile Ser Val Pro Thr Gln
65                  70                  75                  80

Val Asn Ile Ser Phe Ala Met Ser Ala Ile Leu Asp Val Val Trp Asp
                85                  90                  95

Asn Pro Phe Ile Ser Trp Asn Pro Glu Glu Cys Glu Gly Ile Thr Lys
            100                 105                 110

Met Ser Met Ala Ala Lys Asn Leu Trp Leu Pro Asp Ile Phe Ile Ile
        115                 120                 125

Glu Leu Met Asp Val Asp Lys Thr Pro Lys Gly Leu Thr Ala Tyr Val
    130                 135                 140

Ser Asn Glu Gly Arg Ile Arg Tyr Lys Lys Pro Met Lys Val Asp Ser
145                 150                 155                 160

Ile Cys Asn Leu Asp Ile Phe Tyr Phe Pro Phe Asp Gln Gln Asn Cys
                165                 170                 175

Thr Leu Thr Phe Ser Ser Phe Leu Tyr Thr Val Asp Ser Met Leu Leu
            180                 185                 190

Asp Met Glu Lys Glu Val Trp Glu Ile Thr Asp Ala Ser Arg Asn Ile
        195                 200                 205

Leu Gln Thr His Gly Glu Trp Glu Leu Leu Gly Leu Ser Lys Ala Thr
    210                 215                 220

Ala Lys Leu Ser Arg Gly Gly Asn Leu Tyr Asp Gln Ile Val Phe Tyr
225                 230                 235                 240
```

```
Val Ala Ile Arg Arg Arg Pro Ser Leu Tyr Val Ile Asn Leu Leu Val
                245                 250                 255

Pro Ser Gly Phe Leu Val Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro
            260                 265                 270

Val Lys Ser Gly Asn Arg Val Pro Phe Lys Ile Thr Leu Leu Leu Gly
        275                 280                 285

Tyr Asn Val Phe Leu Leu Met Met Ser Asp Leu Leu Pro Thr Ser Gly
    290                 295                 300

Thr Pro Leu Ile Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val
305                 310                 315                 320

Gly Ser Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val Ala
                325                 330                 335

Thr Thr Gln Pro Pro Pro Leu Pro Arg Trp Leu His Ser Leu Leu Leu
            340                 345                 350

His Cys Asn Ser Pro Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Glu
        355                 360                 365

Asn Lys Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys Glu
    370                 375                 380

Pro Glu Val Ser Ala Gly Gln Met Pro Gly Pro Ala Glu Ala Glu Leu
385                 390                 395                 400

Thr Gly Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala Gln
                405                 410                 415

Lys Gln His Ser Val Glu Leu Trp Leu Gln Phe Ser His Ala Met Asp
            420                 425                 430

Ala Met Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile Ile
        435                 440                 445

Thr Val Ile Cys Leu Trp Asn Thr
    450                 455
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<210> 419
<211> 456
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 73; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3E; "

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<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3E, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID: A5X5Y0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401444"

<400> 419
Met Glu Gly Ser Trp Phe His Arg Lys Arg Phe Ser Phe Tyr Leu Leu
1   5   10   15

Leu Gly Phe Leu Leu Gln Gly Arg Gly Val Thr Phe Thr Ile Asn Cys
            20   25   30

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

Phe Asn Arg Lys Pro Phe Arg Pro Val Thr Asn Ile Ser Val Pro Thr
    50   55   60

Gln Val Asn Ile Ser Phe Ala Met Ser Ala Ile Leu Asp Val Asn Glu
65   70   75   80

Gln Leu His Leu Leu Ser Ser Phe Leu Trp Leu Glu Met Val Trp Asp
                85   90   95

Asn Pro Phe Ile Ser Trp Asn Pro Glu Glu Cys Glu Gly Ile Thr Lys
            100   105   110

Met Ser Met Ala Ala Lys Asn Leu Trp Leu Pro Asp Ile Phe Ile Ile

```
        115                 120                 125

Glu Leu Met Asp Val Asp Lys Thr Pro Lys Gly Leu Thr Ala Tyr Val
    130                 135                 140

Ser Asn Glu Gly Arg Ile Arg Tyr Lys Lys Pro Met Lys Val Asp Ser
145                 150                 155                 160

Ile Cys Asn Leu Asp Ile Phe Tyr Phe Pro Phe Asp Gln Gln Asn Cys
                165                 170                 175

Thr Leu Thr Phe Ser Ser Phe Leu Tyr Thr Val Asp Ser Met Leu Leu
            180                 185                 190

Asp Met Glu Lys Glu Val Trp Glu Ile Thr Asp Ala Ser Arg Asn Ile
        195                 200                 205

Leu Gln Thr His Gly Glu Trp Glu Leu Leu Gly Leu Ser Lys Ala Thr
    210                 215                 220

Ala Lys Leu Ser Arg Gly Gly Asn Leu Tyr Asp Gln Ile Val Phe Tyr
225                 230                 235                 240

Val Ala Ile Arg Arg Arg Pro Ser Leu Tyr Val Ile Asn Leu Leu Val
                245                 250                 255

Pro Ser Gly Phe Leu Val Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro
            260                 265                 270

Val Lys Ser Gly Asn Arg Val Pro Phe Lys Ile Thr Leu Leu Leu Gly
        275                 280                 285

Tyr Asn Val Phe Leu Leu Met Met Ser Asp Leu Leu Pro Thr Ser Gly
    290                 295                 300

Thr Pro Leu Ile Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met Val
305                 310                 315                 320

Gly Ser Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val Ala
                325                 330                 335

Thr Thr Gln Pro Pro Pro Leu Pro Arg Trp Leu His Ser Leu Leu Leu
            340                 345                 350
```

```
His Cys Asn Ser Pro Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys Glu
        355                 360                 365

Asn Lys Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys Glu
    370                 375                 380

Pro Glu Val Ser Ala Gly Gln Met Pro Gly Pro Ala Glu Ala Glu Leu
385                 390                 395                 400

Thr Gly Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala Gln
                405                 410                 415

Lys Gln His Ser Val Glu Leu Trp Leu Gln Phe Ser His Ala Met Asp
            420                 425                 430

Ala Met Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile Ile
        435                 440                 445

Thr Val Ile Cys Leu Trp Asn Thr
    450                 455


<210> 420
<211> 441
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Symbol: HTR3E; "

<220>
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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 3E, ionotropic;
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<220>
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<223> /note="Uniprot ID:  A5X5Y0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401900"
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<400> 420
Met Glu Gly Ser Trp Phe His Arg Lys Arg Phe Ser Phe Tyr Leu Leu
1 5 10 15

Leu Gly Phe Leu Leu Gln Gly Arg Gly Val Thr Phe Thr Ile Asn Cys
20 25 30

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

Phe Asn Arg Lys Pro Phe Arg Pro Val Thr Asn Ile Ser Val Pro Thr
50 55 60

Gln Val Asn Ile Ser Phe Ala Met Ser Ala Ile Leu Asp Val Val Trp
65 70 75 80

Asp Asn Pro Phe Ile Ser Trp Asn Pro Glu Glu Cys Glu Gly Ile Thr
85 90 95

Lys Met Ser Met Ala Ala Lys Asn Leu Trp Leu Pro Asp Ile Phe Ile
100 105 110

Ile Glu Leu Met Asp Val Asp Lys Thr Pro Lys Gly Leu Thr Ala Tyr
115 120 125

Val Ser Asn Glu Gly Arg Ile Arg Tyr Lys Lys Pro Met Lys Val Asp
130 135 140

Ser Ile Cys Asn Leu Asp Ile Phe Tyr Phe Pro Phe Asp Gln Gln Asn
145 150 155 160

Cys Thr Leu Thr Phe Ser Ser Phe Leu Tyr Thr Val Asp Ser Met Leu
165 170 175

Leu Asp Met Glu Lys Glu Val Trp Glu Ile Thr Asp Ala Ser Arg Asn
180 185 190

Ile Leu Gln Thr His Gly Glu Trp Glu Leu Leu Gly Leu Ser Lys Ala
195 200 205

Thr Ala Lys Leu Ser Arg Gly Gly Asn Leu Tyr Asp Gln Ile Val Phe
210 215 220

Tyr Val Ala Ile Arg Arg Arg Pro Ser Leu Tyr Val Ile Asn Leu Leu
225 230 235 240

Val Pro Ser Gly Phe Leu Val Ala Ile Asp Ala Leu Ser Phe Tyr Leu
245 250 255

Pro Val Lys Ser Gly Asn Arg Val Pro Phe Lys Ile Thr Leu Leu Leu
260 265 270

Gly Tyr Asn Val Phe Leu Leu Met Met Ser Asp Leu Leu Pro Thr Ser
275 280 285

Gly Thr Pro Leu Ile Gly Val Tyr Phe Ala Leu Cys Leu Ser Leu Met
290 295 300

Val Gly Ser Leu Leu Glu Thr Ile Phe Ile Thr His Leu Leu His Val
305 310 315 320

Ala Thr Thr Gln Pro Pro Pro Leu Pro Arg Trp Leu His Ser Leu Leu
325 330 335

Leu His Cys Asn Ser Pro Gly Arg Cys Cys Pro Thr Ala Pro Gln Lys
340 345 350

Glu Asn Lys Gly Pro Gly Leu Thr Pro Thr His Leu Pro Gly Val Lys
355 360 365

Glu Pro Glu Val Ser Ala Gly Gln Met Pro Gly Pro Ala Glu Ala Glu
370 375 380

Leu Thr Gly Gly Ser Glu Trp Thr Arg Ala Gln Arg Glu His Glu Ala
385 390 395 400

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

Asp Ala Met Leu Phe Arg Leu Tyr Leu Leu Phe Met Ala Ser Ser Ile
420 425 430

Ile Thr Val Ile Cys Leu Trp Asn Thr
435 440

<210> 421

<211> 482
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 73; "

<220>
<221> source
<223> /note="Gene Symbol: HTR3E; "

<220>
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<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 3E, ionotropic;
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<220>
<221> source
<223> /note="Uniprot ID: A5X5Y0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000406050"

<400> 421
Met Leu Ala Phe Ile Leu Ser Arg Ala Thr Pro Arg Pro Ala Leu Gly
1   5   10   15

Pro Leu Ser Tyr Arg Glu His Arg Val Ala Leu Leu His Leu Thr His
            20   25   30

Ser Met Ser Thr Thr Gly Arg Gly Val Thr Phe Thr Ile Asn Cys Ser
        35   40   45

Gly Phe Gly Gln His Gly Ala Asp Pro Thr Ala Leu Asn Ser Val Phe
    50   55   60

Asn Arg Lys Pro Phe Arg Pro Val Thr Asn Ile Ser Val Pro Thr Gln
65   70   75   80

Val Asn Ile Ser Phe Ala Met Ser Ala Ile Leu Asp Val Val Trp Asp
                85   90   95

Asn Pro Phe Ile Ser Trp Asn Pro Glu Glu Cys Glu Gly Ile Thr Lys
            100   105   110

Met Ser Met Ala Ala Lys Asn Leu Trp Leu Pro Asp Ile Phe Ile Ile
        115   120   125

```
Glu Leu Cys Val Ser Arg Ala Gly Gln Arg Glu Val Pro Ser Pro Gly
    130                 135                 140

Ser His Arg Asp His Ser Leu Pro Leu Gly Pro Leu Met Asp Val Asp
145                 150                 155                 160

Lys Thr Pro Lys Gly Leu Thr Ala Tyr Val Ser Asn Glu Gly Arg Ile
                165                 170                 175

Arg Tyr Lys Lys Pro Met Lys Val Asp Ser Ile Cys Asn Leu Asp Ile
            180                 185                 190

Phe Tyr Phe Pro Phe Asp Gln Gln Asn Cys Thr Leu Thr Phe Ser Ser
        195                 200                 205

Phe Leu Tyr Thr Val Asp Ser Met Leu Leu Asp Met Glu Lys Glu Val
    210                 215                 220

Trp Glu Ile Thr Asp Ala Ser Arg Asn Ile Leu Gln Thr His Gly Glu
225                 230                 235                 240

Trp Glu Leu Leu Gly Leu Ser Lys Ala Thr Ala Lys Leu Ser Arg Gly
                245                 250                 255

Gly Asn Leu Tyr Asp Gln Ile Val Phe Tyr Val Ala Ile Arg Arg Arg
            260                 265                 270

Pro Ser Leu Tyr Val Ile Asn Leu Leu Val Pro Ser Gly Phe Leu Val
        275                 280                 285

Ala Ile Asp Ala Leu Ser Phe Tyr Leu Pro Val Lys Ser Gly Asn Arg
    290                 295                 300

Val Pro Phe Lys Ile Thr Leu Leu Leu Gly Tyr Asn Val Phe Leu Leu
305                 310                 315                 320

Met Met Ser Asp Leu Leu Pro Thr Ser Gly Thr Pro Leu Ile Gly Val
                325                 330                 335

Tyr Phe Ala Leu Cys Leu Ser Leu Met Val Gly Ser Leu Leu Glu Thr
            340                 345                 350
```

```
Ile Phe Ile Thr His Leu Leu His Val Ala Thr Thr Gln Pro Pro Pro
        355                 360                 365

Leu Pro Arg Trp Leu His Ser Leu Leu Leu His Cys Asn Ser Pro Gly
    370                 375                 380

Arg Cys Cys Pro Thr Ala Pro Gln Lys Glu Asn Lys Gly Pro Gly Leu
385                 390                 395                 400

Thr Pro Thr His Leu Pro Gly Val Lys Glu Pro Glu Val Ser Ala Gly
                405                 410                 415

Gln Met Pro Gly Pro Ala Glu Ala Glu Leu Thr Gly Gly Ser Glu Trp
            420                 425                 430

Thr Arg Ala Gln Arg Glu His Glu Ala Gln Lys Gln His Ser Val Glu
        435                 440                 445

Leu Trp Leu Gln Phe Ser His Ala Met Asp Ala Met Leu Phe Arg Leu
    450                 455                 460

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

Asn Thr
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<210> 422
<211> 428
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>

<221> source
<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000353915"

<400> 422

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

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
            20                  25                  30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
        35                  40                  45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
    50                  55                  60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65                  70                  75                  80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
                85                  90                  95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115                 120                 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
```

195 200 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
210 215 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225 230 235 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
245 250 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
260 265 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
275 280 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
290 295 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305 310 315 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
325 330 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
340 345 350

Gly Ser Thr His Val Leu Arg Thr Asp Phe Leu Phe Asp Arg Asp Ile
355 360 365

Leu Ala Arg Tyr Trp Thr Lys Pro Ala Arg Ala Gly Pro Phe Ser Gly
370 375 380

Thr Leu Ser Ile Arg Cys Leu Thr Ala Arg Lys Pro Val Leu Gly Asp
385 390 395 400

Ala Val Glu Cys Gly Gly Gln Trp Glu Ser Gln Cys His Pro Pro Ala
405 410 415

Thr Ser Pro Leu Val Ala Ala Gln Pro Ser Asp Thr
420 425

<210> 423
<211> 428
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355037"

<400> 423

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

Val	Glu	Lys	Val	Val	Leu	Leu	Thr	Phe	Leu	Ser	Thr	Val	Ile	Leu	Met
		20						25					30		

Ala	Ile	Leu	Gly	Asn	Leu	Leu	Val	Met	Val	Ala	Val	Cys	Trp	Asp	Arg
	35						40					45			

Gln	Leu	Arg	Lys	Ile	Lys	Thr	Asn	Tyr	Phe	Ile	Val	Ser	Leu	Ala	Phe
	50					55					60				

Ala	Asp	Leu	Leu	Val	Ser	Val	Leu	Val	Met	Pro	Phe	Gly	Ala	Ile	Glu
65					70					75					80

Leu	Val	Gln	Asp	Ile	Trp	Ile	Tyr	Gly	Glu	Val	Phe	Cys	Leu	Val	Arg
				85					90					95	

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

```
Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115                 120                 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335
```

```
Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350

Gly Ser Thr His Val Leu Arg Thr Asp Phe Leu Phe Asp Arg Asp Ile
        355                 360                 365

Leu Ala Arg Tyr Trp Thr Lys Pro Ala Arg Ala Gly Pro Phe Ser Gly
    370                 375                 380

Thr Leu Ser Ile Arg Cys Leu Thr Ala Arg Lys Pro Val Leu Gly Asp
385                 390                 395                 400

Ala Val Glu Cys Gly Gly Gln Trp Glu Ser Gln Cys His Pro Pro Ala
                405                 410                 415

Thr Ser Pro Leu Val Ala Ala Gln Pro Ser Asp Thr
            420                 425


<210> 424
<211> 388
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 4,
      G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000367120"

<400> 424
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1               5                   10                  15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
```

```
            20                  25                  30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
        35                  40                  45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
    50                  55                  60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65                  70                  75                  80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
                85                  90                  95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115                 120                 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255
```

```
Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350

Gly Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp
        355                 360                 365

Glu Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln
    370                 375                 380

Pro Ser Asp Thr
385
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<210> 425
<211> 411
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427913"

<400> 425
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1   5   10   15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
            20   25   30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
        35   40   45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
    50   55   60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65   70   75   80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
                85   90   95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115   120   125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130   135   140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145   150   155   160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165   170   175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180   185   190

```
Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350

Gly Ser Thr His Val Leu Ser Ser Gly Thr Glu Thr Asp Arg Lys Lys
        355                 360                 365

Leu Trp Asn Lys Glu Glu Lys Ile Asp Gln Thr Ile Gln Met Pro Lys
    370                 375                 380

Arg Lys Arg Lys Lys Lys Ala Ser Leu Ser Tyr Glu Asp Leu Ile Leu
385                 390                 395                 400

Leu Gly Arg Lys Ser Cys Phe Arg Glu Gly Lys
                405                 410
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<210> 426

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

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428320"

<400> 426

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

```
Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350
```

```
Gly Ser Thr His Val Leu Arg Tyr Thr Val Leu His Arg Gly His His
        355                 360                 365

Gln Glu Leu Glu Lys Leu Pro Ile His Asn Asp Pro Glu Ser Leu Glu
    370                 375                 380

Ser Cys Phe
385
```

<210> 427
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429634"

<400> 427

```
Met Cys His Leu Val Arg Leu Ser His Ala Ser Pro Phe Ser Leu Leu
1               5                   10                  15

His Phe Pro Gly Phe Ile Pro Arg Arg Arg Met Glu Glu Thr Arg Ala
            20                  25                  30

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

Ser Met Ile Ile Gln Gly Glu Leu Asp Gln Val Leu Leu Arg Pro Ala
    50                  55                  60

Ala Trp Met Leu Tyr Ile Gln Lys Asp Pro Val Gly Ile Glu Ile Gln
65                  70                  75                  80
```

Leu Thr His Ala Tyr Phe Leu
85

<210> 428
<211> 371
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430451"

<400> 428
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1 5 10 15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
20 25 30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65 70 75 80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
85 90 95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val

```
        115                 120                 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350
```

Gly Ser Thr His Val Leu Arg Ala Val Arg Gly Asn Arg Asn Ser Thr
355 360 365

Ser Ser Ala
370

<210> 429
<211> 378
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430874"

<400> 429
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1 5 10 15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
20 25 30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65 70 75 80

```
Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
                85                  90                  95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115                 120                 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300
```

```
Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320


Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335


Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350


Gly Ser Thr His Val Leu Ser Gly Cys Ser Pro Val Ser Ser Phe Leu
        355                 360                 365


Leu Leu Phe Cys Asn Arg Pro Val Pro Val
    370                 375


<210> 430
<211> 378
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 4,
      G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430979"

<400> 430
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1               5                   10                  15


Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
            20                  25                  30


Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
```

```
        35                  40                  45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
    50                  55                  60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65                  70                  75                  80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
                85                  90                  95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115                 120                 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130                 135                 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145                 150                 155                 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165                 170                 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180                 185                 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195                 200                 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270
```

```
Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350

Gly Ser Thr His Val Leu Ser Gly Cys Ser Pro Val Ser Ser Phe Leu
        355                 360                 365

Leu Leu Phe Cys Asn Arg Pro Val Pro Val
    370                 375
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<210> 431
<211> 360
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 4,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435904"

<400> 431
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1 5 10 15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
20 25 30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65 70 75 80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
85 90 95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
115 120 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
130 135 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145 150 155 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
165 170 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
180 185 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
195 200 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
210 215 220

```
Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350

Gly Ser Thr His Val Leu Arg Phe
        355                 360


<210> 432
<211> 388
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 74; "

<220>
<221> source
<223> /note="Gene Symbol: HTR4; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 4,
      G prt-coupled; "

<220>
<221> source
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<223> /note="Uniprot ID: Q13639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485747"

<400> 432
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1   5   10   15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
            20   25   30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
        35   40   45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
    50   55   60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65   70   75   80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
                85   90   95

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

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
        115   120   125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
    130   135   140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145   150   155   160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
                165   170   175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
            180   185   190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
        195   200   205

```
Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
    210                 215                 220

Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
225                 230                 235                 240

Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
                245                 250                 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
            260                 265                 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
        275                 280                 285

Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
    290                 295                 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305                 310                 315                 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
                325                 330                 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
            340                 345                 350

Gly Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp
        355                 360                 365

Glu Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln
    370                 375                 380

Pro Ser Asp Thr
385
```

<210> 433
<211> 357
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 75; "

<220>
<221> source
<223> /note="Gene Symbol: HTR5A; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 5A,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P47898; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000287907"

<400> 433

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Met Asp Leu Pro Val Asn Leu Thr Ser Phe Ser Leu Ser Thr Pro Ser
1               5                  10                  15


Pro Leu Glu Thr Asn His Ser Leu Gly Lys Asp Asp Leu Arg Pro Ser
            20                  25                  30


Ser Pro Leu Leu Ser Val Phe Gly Val Leu Ile Leu Thr Leu Leu Gly
        35                  40                  45


Phe Leu Val Ala Ala Thr Phe Ala Trp Asn Leu Leu Val Leu Ala Thr
    50                  55                  60


Ile Leu Arg Val Arg Thr Phe His Arg Val Pro His Asn Leu Val Ala
65                  70                  75                  80


Ser Met Ala Val Ser Asp Val Leu Val Ala Ala Leu Val Met Pro Leu
                85                  90                  95


Ser Leu Val His Glu Leu Ser Gly Arg Arg Trp Gln Leu Gly Arg Arg
            100                 105                 110


Leu Cys Gln Leu Trp Ile Ala Cys Asp Val Leu Cys Cys Thr Ala Ser
        115                 120                 125


Ile Trp Asn Val Thr Ala Ile Ala Leu Asp Arg Tyr Trp Ser Ile Thr
    130                 135                 140
```

```
Arg His Met Glu Tyr Thr Leu Arg Thr Arg Lys Cys Val Ser Asn Val
145                 150                 155                 160

Met Ile Ala Leu Thr Trp Ala Leu Ser Ala Val Ile Ser Leu Ala Pro
                165                 170                 175

Leu Leu Phe Gly Trp Gly Glu Thr Tyr Ser Glu Gly Ser Glu Glu Cys
            180                 185                 190

Gln Val Ser Arg Glu Pro Ser Tyr Ala Val Phe Ser Thr Val Gly Ala
        195                 200                 205

Phe Tyr Leu Pro Leu Cys Val Val Leu Phe Val Tyr Trp Lys Ile Tyr
    210                 215                 220

Lys Ala Ala Lys Phe Arg Val Gly Ser Arg Lys Thr Asn Ser Val Ser
225                 230                 235                 240

Pro Ile Ser Glu Ala Val Glu Val Lys Asp Ser Ala Lys Gln Pro Gln
                245                 250                 255

Met Val Phe Thr Val Arg His Ala Thr Val Thr Phe Gln Pro Glu Gly
            260                 265                 270

Asp Thr Trp Arg Glu Gln Lys Glu Gln Arg Ala Ala Leu Met Val Gly
        275                 280                 285

Ile Leu Ile Gly Val Phe Val Leu Cys Trp Ile Pro Phe Phe Leu Thr
    290                 295                 300

Glu Leu Ile Ser Pro Leu Cys Ser Cys Asp Ile Pro Ala Ile Trp Lys
305                 310                 315                 320

Ser Ile Phe Leu Trp Leu Gly Tyr Ser Asn Ser Phe Phe Asn Pro Leu
                325                 330                 335

Ile Tyr Thr Ala Phe Asn Lys Asn Tyr Asn Ser Ala Phe Lys Asn Phe
            340                 345                 350

Phe Ser Arg Gln His
        355
```

<210> 434

<211> 440
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 76; "

<220>
<221> source
<223> /note="Gene Symbol: HTR6; "

<220>
<221> source
<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 6,
G prt-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P50406; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000289753"

<400> 434

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

```
Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Pro Leu Arg Ala Leu
    130                 135                 140

Ala Leu Val Leu Gly Ala Trp Ser Leu Ala Ala Leu Ala Ser Phe Leu
145                 150                 155                 160

Pro Leu Leu Leu Gly Trp His Glu Leu Gly His Ala Arg Pro Pro Val
                165                 170                 175

Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val Leu Val Ala
            180                 185                 190

Ser Gly Leu Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys Phe Thr Tyr
        195                 200                 205

Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln Val Ala Ser
    210                 215                 220

Leu Thr Thr Gly Met Ala Ser Gln Ala Ser Glu Thr Leu Gln Val Pro
225                 230                 235                 240

Arg Thr Pro Arg Pro Gly Val Glu Ser Ala Asp Ser Arg Arg Leu Ala
                245                 250                 255

Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser Leu Thr Leu Gly Ile
            260                 265                 270

Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro Phe Phe Val Ala Asn
        275                 280                 285

Ile Val Gln Ala Val Cys Asp Cys Ile Ser Pro Gly Leu Phe Asp Val
    290                 295                 300

Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met Asn Pro Ile Ile Tyr
305                 310                 315                 320

Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu Gly Arg Phe Leu Pro
                325                 330                 335

Cys Pro Arg Cys Pro Arg Glu Arg Gln Ala Ser Leu Ala Ser Pro Ser
            340                 345                 350
```

```
Leu Arg Thr Ser His Ser Gly Pro Arg Pro Gly Leu Ser Leu Gln Gln
        355                 360                 365

Val Leu Pro Leu Pro Leu Pro Pro Asp Ser Asp Ser Asp Ser Asp Ala
    370                 375                 380

Gly Ser Gly Gly Ser Ser Gly Leu Arg Leu Thr Ala Gln Leu Leu Leu
385                 390                 395                 400

Pro Gly Glu Ala Thr Gln Asp Pro Pro Leu Pro Thr Arg Ala Ala Ala
                405                 410                 415

Ala Val Asn Phe Phe Asn Ile Asp Pro Ala Glu Pro Glu Leu Arg Pro
            420                 425                 430

His Pro Leu Gly Ile Pro Thr Asn
        435                 440


<210> 435
<211> 445
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 77; "

<220>
<221> source
<223> /note="Gene Symbol: HTR7; "

<220>
<221> source
<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 7, adenylate
      cyclase-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  P34969; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000277874"

<400> 435
Met Met Asp Val Asn Ser Ser Gly Arg Pro Asp Leu Tyr Gly His Leu
1               5                   10                  15
```

```
Arg Ser Phe Leu Leu Pro Glu Val Gly Arg Gly Leu Pro Asp Leu Ser
            20                  25                  30

Pro Asp Gly Gly Ala Asp Pro Val Ala Gly Ser Trp Ala Pro His Leu
        35                  40                  45

Leu Ser Glu Val Thr Ala Ser Pro Ala Pro Thr Trp Asp Ala Pro Pro
    50                  55                  60

Asp Asn Ala Ser Gly Cys Gly Glu Gln Ile Asn Tyr Gly Arg Val Glu
65                  70                  75                  80

Lys Val Val Ile Gly Ser Ile Leu Thr Leu Ile Thr Leu Leu Thr Ile
                85                  90                  95

Ala Gly Asn Cys Leu Val Val Ile Ser Val Cys Phe Val Lys Lys Leu
            100                 105                 110

Arg Gln Pro Ser Asn Tyr Leu Ile Val Ser Leu Ala Leu Ala Asp Leu
        115                 120                 125

Ser Val Ala Val Ala Val Met Pro Phe Val Ser Val Thr Asp Leu Ile
    130                 135                 140

Gly Gly Lys Trp Ile Phe Gly His Phe Phe Cys Asn Val Phe Ile Ala
145                 150                 155                 160

Met Asp Val Met Cys Cys Thr Ala Ser Ile Met Thr Leu Cys Val Ile
                165                 170                 175

Ser Ile Asp Arg Tyr Leu Gly Ile Thr Arg Pro Leu Thr Tyr Pro Val
            180                 185                 190

Arg Gln Asn Gly Lys Cys Met Ala Lys Met Ile Leu Ser Val Trp Leu
        195                 200                 205

Leu Ser Ala Ser Ile Thr Leu Pro Pro Leu Phe Gly Trp Ala Gln Asn
    210                 215                 220

Val Asn Asp Asp Lys Val Cys Leu Ile Ser Gln Asp Phe Gly Tyr Thr
225                 230                 235                 240

Ile Tyr Ser Thr Ala Val Ala Phe Tyr Ile Pro Met Ser Val Met Leu
```

245 250 255

Phe Met Tyr Tyr Gln Ile Tyr Lys Ala Ala Arg Lys Ser Ala Ala Lys
260 265 270

His Lys Phe Pro Gly Phe Pro Arg Val Glu Pro Asp Ser Val Ile Ala
275 280 285

Leu Asn Gly Ile Val Lys Leu Gln Lys Glu Val Glu Glu Cys Ala Asn
290 295 300

Leu Ser Arg Leu Leu Lys His Glu Arg Lys Asn Ile Ser Ile Phe Lys
305 310 315 320

Arg Glu Gln Lys Ala Ala Thr Thr Leu Gly Ile Ile Val Gly Ala Phe
325 330 335

Thr Val Cys Trp Leu Pro Phe Phe Leu Leu Ser Thr Ala Arg Pro Phe
340 345 350

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

Phe Leu Trp Leu Gly Tyr Ala Asn Ser Leu Ile Asn Pro Phe Ile Tyr
370 375 380

Ala Phe Phe Asn Arg Asp Leu Arg Thr Thr Tyr Arg Ser Leu Leu Gln
385 390 395 400

Cys Gln Tyr Arg Asn Ile Asn Arg Lys Leu Ser Ala Ala Gly Met His
405 410 415

Glu Ala Leu Lys Leu Ala Glu Arg Pro Glu Arg Pro Glu Phe Val Leu
420 425 430

Gln Asn Ala Asp Tyr Cys Arg Lys Lys Gly His Asp Ser
435 440 445

<210> 436
<211> 479
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 77; "

<220>
<221> source
<223> /note="Gene Symbol: HTR7; "

<220>
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<223> /note="Gene Name:
5-hydroxytryptamine (serotonin) receptor 7, adenylate
cyclase-coupled; "

<220>
<221> source
<223> /note="Uniprot ID: P34969; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000337949"

<400> 436

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Met Met Asp Val Asn Ser Ser Gly Arg Pro Asp Leu Tyr Gly His Leu
1               5                  10                  15

Arg Ser Phe Leu Leu Pro Glu Val Gly Arg Gly Leu Pro Asp Leu Ser
            20                  25                  30

Pro Asp Gly Gly Ala Asp Pro Val Ala Gly Ser Trp Ala Pro His Leu
        35                  40                  45

Leu Ser Glu Val Thr Ala Ser Pro Ala Pro Thr Trp Asp Ala Pro Pro
    50                  55                  60

Asp Asn Ala Ser Gly Cys Gly Glu Gln Ile Asn Tyr Gly Arg Val Glu
65                  70                  75                  80

Lys Val Val Ile Gly Ser Ile Leu Thr Leu Ile Thr Leu Leu Thr Ile
                85                  90                  95

Ala Gly Asn Cys Leu Val Val Ile Ser Val Cys Phe Val Lys Lys Leu
            100                 105                 110

Arg Gln Pro Ser Asn Tyr Leu Ile Val Ser Leu Ala Leu Ala Asp Leu
        115                 120                 125

Ser Val Ala Val Ala Val Met Pro Phe Val Ser Val Thr Asp Leu Ile
    130                 135                 140
```

```
Gly Gly Lys Trp Ile Phe Gly His Phe Phe Cys Asn Val Phe Ile Ala
145                 150                 155                 160

Met Asp Val Met Cys Cys Thr Ala Ser Ile Met Thr Leu Cys Val Ile
                165                 170                 175

Ser Ile Asp Arg Tyr Leu Gly Ile Thr Arg Pro Leu Thr Tyr Pro Val
            180                 185                 190

Arg Gln Asn Gly Lys Cys Met Ala Lys Met Ile Leu Ser Val Trp Leu
        195                 200                 205

Leu Ser Ala Ser Ile Thr Leu Pro Pro Leu Phe Gly Trp Ala Gln Asn
    210                 215                 220

Val Asn Asp Asp Lys Val Cys Leu Ile Ser Gln Asp Phe Gly Tyr Thr
225                 230                 235                 240

Ile Tyr Ser Thr Ala Val Ala Phe Tyr Ile Pro Met Ser Val Met Leu
                245                 250                 255

Phe Met Tyr Tyr Gln Ile Tyr Lys Ala Ala Arg Lys Ser Ala Ala Lys
            260                 265                 270

His Lys Phe Pro Gly Phe Pro Arg Val Glu Pro Asp Ser Val Ile Ala
        275                 280                 285

Leu Asn Gly Ile Val Lys Leu Gln Lys Glu Val Glu Glu Cys Ala Asn
    290                 295                 300

Leu Ser Arg Leu Leu Lys His Glu Arg Lys Asn Ile Ser Ile Phe Lys
305                 310                 315                 320

Arg Glu Gln Lys Ala Ala Thr Thr Leu Gly Ile Ile Val Gly Ala Phe
                325                 330                 335

Thr Val Cys Trp Leu Pro Phe Phe Leu Leu Ser Thr Ala Arg Pro Phe
            340                 345                 350

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

```
Phe Leu Trp Leu Gly Tyr Ala Asn Ser Leu Ile Asn Pro Phe Ile Tyr
    370                 375                 380

Ala Phe Phe Asn Arg Asp Leu Arg Thr Thr Tyr Arg Ser Leu Leu Gln
385                 390                 395                 400

Cys Gln Tyr Arg Asn Ile Asn Arg Lys Leu Ser Ala Ala Gly Met His
                405                 410                 415

Glu Ala Leu Lys Leu Ala Glu Arg Pro Glu Arg Pro Glu Phe Val Leu
            420                 425                 430

Arg Ala Cys Thr Arg Arg Val Leu Leu Arg Pro Glu Lys Arg Pro Pro
        435                 440                 445

Val Ser Val Trp Val Leu Gln Ser Pro Asp His His Asn Trp Leu Ala
    450                 455                 460

Asp Lys Met Leu Thr Thr Val Glu Lys Lys Val Met Ile His Asp
465                 470                 475


<210> 437
<211> 432
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 77; "

<220>
<221> source
<223> /note="Gene Symbol: HTR7; "

<220>
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<223> /note="Gene Name:
      5-hydroxytryptamine (serotonin) receptor 7, adenylate
      cyclase-coupled; "

<220>
<221> source
<223> /note="Uniprot ID:  P34969; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000360784"

<400> 437
Met Met Asp Val Asn Ser Ser Gly Arg Pro Asp Leu Tyr Gly His Leu
```

```
1               5                   10                  15

Arg Ser Phe Leu Leu Pro Glu Val Gly Arg Gly Leu Pro Asp Leu Ser
            20                  25                  30

Pro Asp Gly Gly Ala Asp Pro Val Ala Gly Ser Trp Ala Pro His Leu
        35                  40                  45

Leu Ser Glu Val Thr Ala Ser Pro Ala Pro Thr Trp Asp Ala Pro Pro
    50                  55                  60

Asp Asn Ala Ser Gly Cys Gly Glu Gln Ile Asn Tyr Gly Arg Val Glu
65                  70                  75                  80

Lys Val Val Ile Gly Ser Ile Leu Thr Leu Ile Thr Leu Leu Thr Ile
                85                  90                  95

Ala Gly Asn Cys Leu Val Val Ile Ser Val Cys Phe Val Lys Lys Leu
            100                 105                 110

Arg Gln Pro Ser Asn Tyr Leu Ile Val Ser Leu Ala Leu Ala Asp Leu
        115                 120                 125

Ser Val Ala Val Ala Val Met Pro Phe Val Ser Val Thr Asp Leu Ile
    130                 135                 140

Gly Gly Lys Trp Ile Phe Gly His Phe Phe Cys Asn Val Phe Ile Ala
145                 150                 155                 160

Met Asp Val Met Cys Cys Thr Ala Ser Ile Met Thr Leu Cys Val Ile
                165                 170                 175

Ser Ile Asp Arg Tyr Leu Gly Ile Thr Arg Pro Leu Thr Tyr Pro Val
            180                 185                 190

Arg Gln Asn Gly Lys Cys Met Ala Lys Met Ile Leu Ser Val Trp Leu
        195                 200                 205

Leu Ser Ala Ser Ile Thr Leu Pro Pro Leu Phe Gly Trp Ala Gln Asn
    210                 215                 220

Val Asn Asp Asp Lys Val Cys Leu Ile Ser Gln Asp Phe Gly Tyr Thr
225                 230                 235                 240
```

```
Ile Tyr Ser Thr Ala Val Ala Phe Tyr Ile Pro Met Ser Val Met Leu
                245                 250                 255

Phe Met Tyr Tyr Gln Ile Tyr Lys Ala Ala Arg Lys Ser Ala Ala Lys
            260                 265                 270

His Lys Phe Pro Gly Phe Pro Arg Val Glu Pro Asp Ser Val Ile Ala
        275                 280                 285

Leu Asn Gly Ile Val Lys Leu Gln Lys Glu Val Glu Glu Cys Ala Asn
    290                 295                 300

Leu Ser Arg Leu Leu Lys His Glu Arg Lys Asn Ile Ser Ile Phe Lys
305                 310                 315                 320

Arg Glu Gln Lys Ala Ala Thr Thr Leu Gly Ile Ile Val Gly Ala Phe
                325                 330                 335

Thr Val Cys Trp Leu Pro Phe Phe Leu Leu Ser Thr Ala Arg Pro Phe
            340                 345                 350

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

Phe Leu Trp Leu Gly Tyr Ala Asn Ser Leu Ile Asn Pro Phe Ile Tyr
    370                 375                 380

Ala Phe Phe Asn Arg Asp Leu Arg Thr Thr Tyr Arg Ser Leu Leu Gln
385                 390                 395                 400

Cys Gln Tyr Arg Asn Ile Asn Arg Lys Leu Ser Ala Ala Gly Met His
                405                 410                 415

Glu Ala Leu Lys Leu Ala Glu Arg Pro Glu Arg Pro Glu Phe Val Leu
            420                 425                 430
```

<210> 438
<211> 819
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 78; "

<220>
<221> source
<223> /note="Gene Symbol: MTR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine
methyltransferase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355535"

<400> 438

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

```
Met Asp Met Gly Ile Val Asn Ala Gly Asn Leu Pro Val Tyr Asp Asp
                165                 170                 175

Ile His Lys Glu Leu Leu Gln Leu Cys Glu Asp Leu Ile Trp Asn Lys
            180                 185                 190

Asp Pro Glu Ala Thr Glu Lys Leu Leu Arg Tyr Ala Gln Thr Gln Gly
        195                 200                 205

Thr Gly Gly Lys Lys Val Ile Gln Thr Asp Glu Trp Arg Asn Gly Pro
    210                 215                 220

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

Ile Ile Glu Asp Thr Glu Glu Ala Arg Leu Asn Gln Lys Lys Tyr Pro
                245                 250                 255

Arg Pro Leu Asn Ile Ile Glu Gly Pro Leu Met Asn Gly Met Lys Ile
            260                 265                 270

Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln Val Ile
        275                 280                 285

Lys Ser Ala Arg Val Met Lys Lys Ala Val Gly His Leu Ile Pro Phe
    290                 295                 300

Met Glu Lys Glu Arg Glu Glu Thr Arg Val Leu Asn Gly Thr Val Glu
305                 310                 315                 320

Glu Glu Asp Pro Tyr Gln Gly Thr Ile Val Leu Ala Thr Val Lys Gly
                325                 330                 335

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

Asn Asn Phe Arg Val Ile Asp Leu Gly Val Met Thr Pro Cys Asp Lys
        355                 360                 365

Ile Leu Lys Ala Ala Leu Asp His Lys Ala Asp Ile Ile Gly Leu Ser
    370                 375                 380

Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Ile Phe Val Ala Lys Glu
```

385 390 395 400

Met Glu Arg Leu Ala Ile Arg Ile Pro Leu Leu Ile Gly Gly Ala Thr
405 410 415

Thr Ser Lys Thr His Thr Ala Val Lys Ile Ala Pro Arg Tyr Ser Ala
420 425 430

Pro Val Ile His Val Leu Asp Ala Ser Lys Ser Val Val Val Cys Ser
435 440 445

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

Glu Glu Tyr Glu Asp Ile Arg Gln Asp His Tyr Glu Ser Leu Lys Glu
465 470 475 480

Arg Arg Tyr Leu Pro Leu Ser Gln Ala Arg Lys Ser Gly Phe Gln Met
485 490 495

Asp Trp Leu Ser Glu Pro His Pro Val Lys Pro Thr Phe Ile Gly Thr
500 505 510

Gln Val Phe Glu Asp Tyr Asp Leu Gln Lys Leu Val Asp Tyr Ile Asp
515 520 525

Trp Lys Pro Phe Phe Asp Val Trp Gln Leu Arg Gly Lys Tyr Pro Asn
530 535 540

Arg Gly Phe Pro Lys Ile Phe Asn Asp Lys Thr Val Gly Gly Glu Ala
545 550 555 560

Arg Lys Val Tyr Asp Asp Ala His Asn Met Leu Asn Thr Leu Ile Ser
565 570 575

Gln Lys Lys Leu Arg Ala Arg Gly Val Val Gly Phe Trp Pro Ala Gln
580 585 590

Ser Ile Gln Asp Asp Ile His Leu Tyr Ala Glu Ala Ala Val Pro Gln
595 600 605

Ala Ala Glu Pro Ile Ala Thr Phe Tyr Gly Leu Arg Gln Gln Ala Glu
610 615 620

Lys Asp Ser Ala Ser Thr Glu Pro Tyr Tyr Cys Leu Ser Asp Phe Ile
625 630 635 640

Ala Pro Leu His Ser Gly Ile Arg Asp Tyr Leu Gly Leu Phe Ala Val
645 650 655

Ala Cys Phe Gly Val Glu Glu Leu Ser Lys Ala Tyr Glu Asp Asp Gly
660 665 670

Asp Asp Tyr Ser Ser Ile Met Val Lys Ala Leu Gly Asp Arg Leu Ala
675 680 685

Glu Ala Phe Ala Glu Glu Leu His Glu Arg Val Arg Arg Glu Leu Trp
690 695 700

Ala Tyr Cys Gly Ser Glu Gln Leu Asp Val Ala Asp Leu Arg Arg Leu
705 710 715 720

Arg Tyr Lys Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ser Gln Pro Asp
725 730 735

His Thr Glu Lys Leu Thr Met Trp Arg Leu Ala Asp Ile Glu Gln Ser
740 745 750

Thr Gly Ile Arg Leu Thr Glu Ser Leu Ala Met Ala Pro Ala Ser Ala
755 760 765

Val Ser Gly Leu Tyr Phe Ser Asn Leu Lys Ser Lys Tyr Phe Ala Val
770 775 780

Gly Lys Ile Ser Lys Asp Gln Val Glu Asp Tyr Ala Leu Arg Lys Asn
785 790 795 800

Ile Ser Val Ala Glu Val Glu Lys Trp Leu Gly Pro Ile Leu Gly Tyr
805 810 815

Asp Thr Asp

<210> 439
<211> 1265
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 78; "

<220>
<221> source
<223> /note="Gene Symbol: MTR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine
methyltransferase; "

<220>
<221> source
<223> /note="Uniprot ID: Q99707; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355536"

<400> 439

Met	Ser	Pro	Ala	Leu	Gln	Asp	Leu	Ser	Gln	Pro	Glu	Gly	Leu	Lys	Lys
1				5					10					15	

Thr	Leu	Arg	Asp	Glu	Ile	Asn	Ala	Ile	Leu	Gln	Lys	Arg	Ile	Met	Val
		20						25					30		

Leu	Asp	Gly	Gly	Met	Gly	Thr	Met	Ile	Gln	Arg	Glu	Lys	Leu	Asn	Glu
	35						40					45			

Glu	His	Phe	Arg	Gly	Gln	Glu	Phe	Lys	Asp	His	Ala	Arg	Pro	Leu	Lys
	50					55					60				

Gly	Asn	Asn	Asp	Ile	Leu	Ser	Ile	Thr	Gln	Pro	Asp	Val	Ile	Tyr	Gln
65					70					75					80

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

Thr	Phe	Ser	Ser	Thr	Ser	Ile	Ala	Gln	Ala	Asp	Tyr	Gly	Leu	Glu	His
			100					105					110		

Leu	Ala	Tyr	Arg	Met	Asn	Met	Cys	Ser	Ala	Gly	Val	Ala	Arg	Lys	Ala
		115					120					125			

```
Ala Glu Glu Val Thr Leu Gln Thr Gly Ile Lys Arg Phe Val Ala Gly
    130                 135                 140

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

Arg Pro Asp Tyr Arg Asn Ile Thr Phe Asp Glu Leu Val Glu Ala Tyr
                165                 170                 175

Gln Glu Gln Ala Lys Gly Leu Leu Asp Gly Gly Val Asp Ile Leu Leu
            180                 185                 190

Ile Glu Thr Ile Phe Asp Thr Ala Asn Ala Lys Ala Ala Leu Phe Ala
        195                 200                 205

Leu Gln Asn Leu Phe Glu Glu Lys Tyr Ala Pro Arg Pro Ile Phe Ile
    210                 215                 220

Ser Gly Thr Ile Val Asp Lys Ser Gly Arg Thr Leu Ser Gly Gln Thr
225                 230                 235                 240

Gly Glu Gly Phe Val Ile Ser Val Ser His Gly Glu Pro Leu Cys Ile
                245                 250                 255

Gly Leu Asn Cys Ala Leu Gly Ala Ala Glu Met Arg Pro Phe Ile Glu
            260                 265                 270

Ile Ile Gly Lys Cys Thr Thr Ala Tyr Val Leu Cys Tyr Pro Asn Ala
        275                 280                 285

Gly Leu Pro Asn Thr Phe Gly Asp Tyr Asp Glu Thr Pro Ser Met Met
    290                 295                 300

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

Gly Gly Cys Cys Gly Ser Thr Pro Asp His Ile Arg Glu Ile Ala Glu
                325                 330                 335

Ala Val Lys Asn Cys Lys Pro Arg Val Pro Pro Ala Thr Ala Phe Glu
            340                 345                 350

Gly His Met Leu Leu Ser Gly Leu Glu Pro Phe Arg Ile Gly Pro Tyr
```

355 360 365

Thr Asn Phe Val Asn Ile Gly Glu Arg Cys Asn Val Ala Gly Ser Arg
370 375 380

Lys Phe Ala Lys Leu Ile Met Ala Gly Asn Tyr Glu Glu Ala Leu Cys
385 390 395 400

Val Ala Lys Val Gln Val Glu Met Gly Ala Gln Val Leu Asp Val Asn
405 410 415

Met Asp Asp Gly Met Leu Asp Gly Pro Ser Ala Met Thr Arg Phe Cys
420 425 430

Asn Leu Ile Ala Ser Glu Pro Asp Ile Ala Lys Val Pro Leu Cys Ile
435 440 445

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

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

Phe Leu Glu Lys Ala Arg Lys Ile Lys Lys Tyr Gly Ala Ala Met Val
485 490 495

Val Met Ala Phe Asp Glu Glu Gly Gln Ala Thr Glu Thr Asp Thr Lys
500 505 510

Ile Arg Val Cys Thr Arg Ala Tyr His Leu Leu Val Lys Lys Leu Gly
515 520 525

Phe Asn Pro Asn Asp Ile Ile Phe Asp Pro Asn Ile Leu Thr Ile Gly
530 535 540

Thr Gly Met Glu Glu His Asn Leu Tyr Ala Ile Asn Phe Ile His Ala
545 550 555 560

Thr Lys Val Ile Lys Glu Thr Leu Pro Gly Ala Arg Ile Ser Gly Gly
565 570 575

Leu Ser Asn Leu Ser Phe Ser Phe Arg Gly Met Glu Ala Ile Arg Glu
580 585 590

```
Ala Met His Gly Val Phe Leu Tyr His Ala Ile Lys Ser Gly Met Asp
        595                 600                 605

Met Gly Ile Val Asn Ala Gly Asn Leu Pro Val Tyr Asp Asp Ile His
    610                 615                 620

Lys Glu Leu Leu Gln Leu Cys Glu Asp Leu Ile Trp Asn Lys Asp Pro
625                 630                 635                 640

Glu Ala Thr Glu Lys Leu Leu Arg Tyr Ala Gln Thr Gln Gly Thr Gly
                645                 650                 655

Gly Lys Lys Val Ile Gln Thr Asp Glu Trp Arg Asn Gly Pro Val Glu
            660                 665                 670

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

Glu Asp Thr Glu Glu Ala Arg Leu Asn Gln Lys Lys Tyr Pro Arg Pro
    690                 695                 700

Leu Asn Ile Ile Glu Gly Pro Leu Met Asn Gly Met Lys Ile Val Gly
705                 710                 715                 720

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

Ala Arg Val Met Lys Lys Ala Val Gly His Leu Ile Pro Phe Met Glu
            740                 745                 750

Lys Glu Arg Glu Glu Thr Arg Val Leu Asn Gly Thr Val Glu Glu Glu
        755                 760                 765

Asp Pro Tyr Gln Gly Thr Ile Val Leu Ala Thr Val Lys Gly Asp Val
    770                 775                 780

His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gly Cys Asn Asn
785                 790                 795                 800

Phe Arg Val Ile Asp Leu Gly Val Met Thr Pro Cys Asp Lys Ile Leu
                805                 810                 815
```

```
Lys Ala Ala Leu Asp His Lys Ala Asp Ile Ile Gly Leu Ser Gly Leu
            820                 825                 830

Ile Thr Pro Ser Leu Asp Glu Met Ile Phe Val Ala Lys Glu Met Glu
        835                 840                 845

Arg Leu Ala Ile Arg Ile Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser
    850                 855                 860

Lys Thr His Thr Ala Val Lys Ile Ala Pro Arg Tyr Ser Ala Pro Val
865                 870                 875                 880

Ile His Val Leu Asp Ala Ser Lys Ser Val Val Val Cys Ser Gln Leu
                885                 890                 895

Leu Asp Glu Asn Leu Lys Asp Glu Tyr Phe Glu Glu Ile Met Glu Glu
            900                 905                 910

Tyr Glu Asp Ile Arg Gln Asp His Tyr Glu Ser Leu Lys Glu Arg Arg
        915                 920                 925

Tyr Leu Pro Leu Ser Gln Ala Arg Lys Ser Gly Phe Gln Met Asp Trp
    930                 935                 940

Leu Ser Glu Pro His Pro Val Lys Pro Thr Phe Ile Gly Thr Gln Val
945                 950                 955                 960

Phe Glu Asp Tyr Asp Leu Gln Lys Leu Val Asp Tyr Ile Asp Trp Lys
                965                 970                 975

Pro Phe Phe Asp Val Trp Gln Leu Arg Gly Lys Tyr Pro Asn Arg Gly
            980                 985                 990

Phe Pro Lys Ile Phe Asn Asp Lys  Thr Val Gly Gly Glu  Ala Arg
Lys
        995                 1000                1005

Val Tyr  Asp Asp Ala His Asn  Met Leu Asn Thr Leu  Ile Ser Gln
    1010                1015                1020

Lys Lys  Leu Arg Ala Arg Gly  Val Val Gly Phe Trp  Pro Ala Gln
    1025                1030                1035
```

```
Ser Ile  Gln Asp Asp Ile His  Leu Tyr Ala Glu Ala  Ala Val Pro
    1040                1045                1050

Gln Ala  Ala Glu Pro Ile Ala  Thr Phe Tyr Gly Leu  Arg Gln Gln
    1055                1060                1065

Ala Glu  Lys Asp Ser Ala Ser  Thr Glu Pro Tyr Tyr  Cys Leu Ser
    1070                1075                1080

Asp Phe  Ile Ala Pro Leu His  Ser Gly Ile Arg Asp  Tyr Leu Gly
    1085                1090                1095

Leu Phe  Ala Val Ala Cys Phe  Gly Val Glu Glu Leu  Ser Lys Ala
    1100                1105                1110

Tyr Glu  Asp Asp Gly Asp Asp  Tyr Ser Ser Ile Met  Val Lys Ala
    1115                1120                1125

Leu Gly  Asp Arg Leu Ala Glu  Ala Phe Ala Glu Glu  Leu His Glu
    1130                1135                1140

Arg Val  Arg Arg Glu Leu Trp  Ala Tyr Cys Gly Ser  Glu Gln Leu
    1145                1150                1155

Asp Val  Ala Asp Leu Arg Arg  Leu Arg Tyr Lys Gly  Ile Arg Pro
    1160                1165                1170

Ala Pro  Gly Tyr Pro Ser Gln  Pro Asp His Thr Glu  Lys Leu Thr
    1175                1180                1185

Met Trp  Arg Leu Ala Asp Ile  Glu Gln Ser Thr Gly  Ile Arg Leu
    1190                1195                1200

Thr Glu  Ser Leu Ala Met Ala  Pro Ala Ser Ala Val  Ser Gly Leu
    1205                1210                1215

Tyr Phe  Ser Asn Leu Lys Ser  Lys Tyr Phe Ala Val  Gly Lys Ile
    1220                1225                1230

Ser Lys  Asp Gln Val Glu Asp  Tyr Ala Leu Arg Lys  Asn Ile Ser
    1235                1240                1245
```

```
Val Ala  Glu Val Glu Lys Trp  Leu Gly Pro Ile Leu  Gly Tyr Asp
    1250                1255                1260


Thr Asp
    1265


<210> 440
<211> 1214
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 78; "

<220>
<221> source
<223> /note="Gene Symbol: MTR; "

<220>
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<223> /note="Gene Name:
      5-methyltetrahydrofolate-homocysteine
      methyltransferase; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99707; "

<220>
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<223> /note="ENSP ID: ENSP00000441845"

<400> 440
Met Ser Pro Ala Leu Gln Asp Leu Ser Gln Pro Glu Gly Leu Lys Lys
1               5                  10                  15


Thr Leu Arg Asp Glu Ile Asn Ala Ile Leu Gln Lys Arg Ile Met Val
            20                  25                  30


Leu Asp Gly Gly Met Gly Thr Met Ile Gln Arg Glu Lys Leu Asn Glu
        35                  40                  45


Glu His Phe Arg Gly Gln Glu Phe Lys Asp His Ala Arg Pro Leu Lys
    50                  55                  60


Gly Asn Asn Asp Ile Leu Ser Ile Thr Gln Pro Asp Val Ile Tyr Gln
65                  70                  75                  80


Ile His Lys Glu Tyr Leu Leu Ala Gly Ala Asp Ile Ile Glu Thr Asn
```

```
                85                  90                  95

Thr Phe Ser Ser Thr Ser Ile Ala Gln Ala Asp Tyr Gly Leu Glu His
            100                 105                 110

Leu Ala Tyr Arg Met Asn Met Cys Ser Ala Gly Val Ala Arg Lys Ala
        115                 120                 125

Ala Glu Glu Val Thr Leu Gln Thr Gly Ile Lys Arg Phe Val Ala Gly
    130                 135                 140

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

Arg Pro Asp Tyr Arg Asn Ile Thr Phe Asp Glu Leu Val Glu Ala Tyr
                165                 170                 175

Gln Glu Gln Ala Lys Gly Leu Leu Asp Gly Gly Val Asp Ile Leu Leu
            180                 185                 190

Ile Glu Thr Ile Phe Asp Thr Ala Asn Ala Lys Ala Ala Leu Phe Ala
        195                 200                 205

Leu Gln Asn Leu Phe Glu Glu Lys Tyr Ala Pro Arg Pro Ile Phe Ile
    210                 215                 220

Ser Gly Thr Ile Val Asp Lys Ser Gly Arg Thr Leu Ser Gly Gln Thr
225                 230                 235                 240

Gly Glu Gly Phe Val Ile Ser Val Ser His Gly Glu Pro Leu Cys Ile
                245                 250                 255

Gly Leu Asn Cys Ala Leu Gly Ala Ala Glu Met Arg Pro Phe Ile Glu
            260                 265                 270

Ile Ile Gly Lys Cys Thr Thr Ala Tyr Val Leu Cys Tyr Pro Asn Ala
        275                 280                 285

Gly Leu Pro Asn Thr Phe Gly Asp Tyr Asp Glu Thr Pro Ser Met Met
    290                 295                 300

Ala Lys His Leu Lys Asp Phe Ala Met Asp Gly Leu Val Asn Ile Val
305                 310                 315                 320
```

Gly Gly Cys Cys Gly Ser Thr Pro Asp His Ile Arg Glu Ile Ala Glu
325 330 335

Ala Val Lys Asn Cys Lys Pro Arg Val Pro Pro Ala Thr Ala Phe Glu
340 345 350

Gly His Met Leu Leu Ser Gly Leu Glu Pro Phe Arg Ile Gly Pro Tyr
355 360 365

Thr Asn Phe Val Asn Ile Gly Glu Arg Cys Asn Val Ala Gly Ser Arg
370 375 380

Lys Phe Ala Lys Leu Ile Met Ala Gly Asn Tyr Glu Glu Ala Leu Cys
385 390 395 400

Val Ala Lys Val Gln Val Glu Met Gly Ala Gln Val Leu Asp Val Asn
405 410 415

Met Asp Asp Gly Met Leu Asp Gly Pro Ser Ala Met Thr Arg Phe Cys
420 425 430

Asn Leu Ile Ala Ser Glu Pro Asp Ile Ala Lys Val Pro Leu Cys Ile
435 440 445

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

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

Phe Leu Glu Lys Ala Arg Lys Ile Lys Lys Tyr Gly Ala Ala Met Val
485 490 495

Val Met Ala Phe Asp Glu Glu Gly Gln Ala Thr Glu Thr Asp Thr Lys
500 505 510

Ile Arg Val Cys Thr Arg Ala Tyr His Leu Leu Val Lys Lys Leu Gly
515 520 525

Phe Asn Pro Asn Asp Ile Ile Phe Asp Pro Asn Ile Leu Thr Ile Gly
530 535 540

```
Thr Gly Met Glu Glu His Asn Leu Tyr Ala Ile Asn Phe Ile His Ala
545                 550                 555                 560

Thr Lys Val Ile Lys Glu Thr Leu Pro Gly Ala Arg Ile Ser Gly Gly
                565                 570                 575

Leu Ser Asn Leu Ser Phe Ser Phe Arg Gly Met Glu Ala Ile Arg Glu
            580                 585                 590

Ala Met His Gly Val Phe Leu Tyr His Ala Ile Lys Ser Gly Met Asp
        595                 600                 605

Met Gly Ile Val Asn Ala Gly Asn Leu Pro Val Tyr Asp Asp Ile His
    610                 615                 620

Lys Glu Leu Leu Gln Leu Cys Glu Asp Leu Ile Trp Asn Lys Asp Pro
625                 630                 635                 640

Glu Ala Thr Glu Lys Leu Leu Arg Tyr Ala Gln Thr Gln Gly Thr Gly
                645                 650                 655

Gly Lys Lys Val Ile Gln Thr Asp Glu Trp Arg Asn Gly Pro Val Glu
            660                 665                 670

Glu Arg Leu Glu Tyr Ala Leu Val Lys Val Ile Lys Ser Ala Arg Val
        675                 680                 685

Met Lys Lys Ala Val Gly His Leu Ile Pro Phe Met Glu Lys Glu Arg
    690                 695                 700

Glu Glu Thr Arg Val Leu Asn Gly Thr Val Glu Glu Glu Asp Pro Tyr
705                 710                 715                 720

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

Gly Lys Asn Ile Val Gly Val Val Leu Gly Cys Asn Asn Phe Arg Val
            740                 745                 750

Ile Asp Leu Gly Val Met Thr Pro Cys Asp Lys Ile Leu Lys Ala Ala
        755                 760                 765
```

```
Leu Asp His Lys Ala Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro
    770                 775                 780

Ser Leu Asp Glu Met Ile Phe Val Ala Lys Glu Met Glu Arg Leu Ala
785                 790                 795                 800

Ile Arg Ile Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Lys Thr His
                805                 810                 815

Thr Ala Val Lys Ile Ala Pro Arg Tyr Ser Ala Pro Val Ile His Val
            820                 825                 830

Leu Asp Ala Ser Lys Ser Val Val Val Cys Ser Gln Leu Leu Asp Glu
        835                 840                 845

Asn Leu Lys Asp Glu Tyr Phe Glu Glu Ile Met Glu Glu Tyr Glu Asp
    850                 855                 860

Ile Arg Gln Asp His Tyr Glu Ser Leu Lys Glu Arg Arg Tyr Leu Pro
865                 870                 875                 880

Leu Ser Gln Ala Arg Lys Ser Gly Phe Gln Met Asp Trp Leu Ser Glu
                885                 890                 895

Pro His Pro Val Lys Pro Thr Phe Ile Gly Thr Gln Val Phe Glu Asp
            900                 905                 910

Tyr Asp Leu Gln Lys Leu Val Asp Tyr Ile Asp Trp Lys Pro Phe Phe
        915                 920                 925

Asp Val Trp Gln Leu Arg Gly Lys Tyr Pro Asn Arg Gly Phe Pro Lys
    930                 935                 940

Ile Phe Asn Asp Lys Thr Val Gly Gly Glu Ala Arg Lys Val Tyr Asp
945                 950                 955                 960

Asp Ala His Asn Met Leu Asn Thr Leu Ile Ser Gln Lys Lys Leu Arg
                965                 970                 975

Ala Arg Gly Val Val Gly Phe Trp Pro Ala Gln Ser Ile Gln Asp Asp
            980                 985                 990

Ile His Leu Tyr Ala Glu Ala Ala  Val Pro Gln Ala Ala  Glu Pro
```

```
Ile
        995                 1000                1005

Ala Thr  Phe Tyr Gly Leu Arg  Gln Gln Ala Glu Lys  Asp Ser Ala
    1010                1015                1020

Ser Thr  Glu Pro Tyr Tyr Cys  Leu Ser Asp Phe Ile  Ala Pro Leu
    1025                1030                1035

His Ser  Gly Ile Arg Asp Tyr  Leu Gly Leu Phe Ala  Val Ala Cys
    1040                1045                1050

Phe Gly  Val Glu Glu Leu Ser  Lys Ala Tyr Glu Asp  Asp Gly Asp
    1055                1060                1065

Asp Tyr  Ser Ser Ile Met Val  Lys Ala Leu Gly Asp  Arg Leu Ala
    1070                1075                1080

Glu Ala  Phe Ala Glu Glu Leu  His Glu Arg Val Arg  Arg Glu Leu
    1085                1090                1095

Trp Ala  Tyr Cys Gly Ser Glu  Gln Leu Asp Val Ala  Asp Leu Arg
    1100                1105                1110

Arg Leu  Arg Tyr Lys Gly Ile  Arg Pro Ala Pro Gly  Tyr Pro Ser
    1115                1120                1125

Gln Pro  Asp His Thr Glu Lys  Leu Thr Met Trp Arg  Leu Ala Asp
    1130                1135                1140

Ile Glu  Gln Ser Thr Gly Ile  Arg Leu Thr Glu Ser  Leu Ala Met
    1145                1150                1155

Ala Pro  Ala Ser Ala Val Ser  Gly Leu Tyr Phe Ser  Asn Leu Lys
    1160                1165                1170

Ser Lys  Tyr Phe Ala Val Gly  Lys Ile Ser Lys Asp  Gln Val Glu
    1175                1180                1185

Asp Tyr  Ala Leu Arg Lys Asn  Ile Ser Val Ala Glu  Val Glu Lys
    1190                1195                1200

Trp Leu  Gly Pro Ile Leu Gly  Tyr Asp Thr Asp
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1205 1210

<210> 441
<211> 725
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<213> Homo sapiens

<220>
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<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UBK8; "

<220>
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<223> /note="ENSP ID: ENSP00000264668"

<400> 441
Met Gly Ala Ala Ser Val Arg Ala Gly Ala Arg Leu Val Glu Val Ala
1 5 10 15

Leu Cys Ser Phe Thr Val Thr Cys Leu Glu Val Met Arg Arg Phe Leu
20 25 30

Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys Ala Ile Ala Glu Glu
35 40 45

Ile Cys Glu Gln Ala Val Val His Gly Phe Ser Ala Asp Leu His Cys
50 55 60

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

Val Val Val Val Ser Thr Thr Gly Thr Gly Asp Pro Pro Asp Thr Ala
85 90 95

Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr Leu Pro Val Asp Phe
100 105 110

```
Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu Gly Asp Ser Glu Tyr
        115                 120                 125

Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp Lys Arg Leu Gln Glu
    130                 135                 140

Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His Ala Asp Asp Cys Val
145                 150                 155                 160

Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala Gly Leu Trp Pro Ala
                165                 170                 175

Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln Glu Glu Ile Ser Gly
            180                 185                 190

Ala Leu Pro Val Ala Ser Pro Ala Ser Ser Arg Thr Asp Leu Val Lys
        195                 200                 205

Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu Leu Leu Arg Phe Asp
    210                 215                 220

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

Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe Glu Ser Ser Leu Thr
                245                 250                 255

Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu Asn Ile Pro Gly Leu
            260                 265                 270

Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu Ser Leu Gly Gln Glu
        275                 280                 285

Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro Val Phe Gln Val Pro
    290                 295                 300

Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp Ala Ile Lys Thr Thr
305                 310                 315                 320

Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp Phe Ser Tyr Gln Pro
                325                 330                 335
```

```
Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser Asp Ser Glu Val Gln
            340                 345                 350

Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys Arg Glu His Cys Val
        355                 360                 365

Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys Gly Ala Thr Leu Pro
    370                 375                 380

Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe Ile Phe Thr Trp Cys
385                 390                 395                 400

Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe Leu Arg Ala Leu Val
                405                 410                 415

Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg Leu Gln Glu Leu Cys
            420                 425                 430

Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe Val Arg Asp Ala Cys
        435                 440                 445

Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro Ser Cys Gln Pro Pro
    450                 455                 460

Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu Gln Pro Arg Pro Tyr
465                 470                 475                 480

Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly Lys Leu His Phe Val
                485                 490                 495

Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr Thr Glu Val Leu Arg
            500                 505                 510

Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu Val Ala Ser Val Leu
        515                 520                 525

Gln Pro Asn Ile His Ala Ser His Glu Asp Ser Gly Lys Ala Leu Ala
    530                 535                 540

Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn Ser Phe His Leu Pro
545                 550                 555                 560
```

```
Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly Pro Gly Thr Gly Ile
                565                 570                 575

Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu Lys Leu Gln Glu Gln
            580                 585                 590

His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu Phe Phe Gly Cys Arg
        595                 600                 605

His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu Leu Arg His Phe Leu
    610                 615                 620

Lys His Gly Ile Leu Thr His Leu Lys Val Ser Phe Ser Arg Asp Ala
625                 630                 635                 640

Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr Val Gln Asp Asn Ile
                645                 650                 655

Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu Leu Gln Glu Asn Gly
            660                 665                 670

His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met Ala Lys Asp Val His
        675                 680                 685

Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val Gly Val Glu Lys Leu
    690                 695                 700

Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu Glu Lys Arg Tyr Leu
705                 710                 715                 720

Gln Asp Ile Trp Ser
                725


<210> 442
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "
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<220>
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<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UBK8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402510"

<400> 442
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1   5   10   15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
            20   25   30

Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
        35   40   45

Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
    50   55   60

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

Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
                85   90   95

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

Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
        115   120   125

Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
    130   135   140

Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
145   150   155   160

Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Ser Arg
                165   170   175

```
Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
            180                 185                 190

Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
        195                 200                 205

Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
    210                 215                 220

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

Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
                245                 250                 255

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

Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
        275                 280                 285

Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
    290                 295                 300

Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
305                 310                 315                 320

Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
                325                 330                 335

Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
            340                 345                 350

Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
        355                 360                 365

Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
    370                 375                 380

Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
385                 390                 395                 400
```

```
Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
                405                 410                 415

Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
            420                 425                 430

Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
        435                 440                 445

Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
    450                 455                 460

Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
465                 470                 475                 480

Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
                485                 490                 495

Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
            500                 505                 510

Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
        515                 520                 525

Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
    530                 535                 540

Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
545                 550                 555                 560

Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
                565                 570                 575

Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
            580                 585                 590

Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
        595                 600                 605

Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
    610                 615                 620
```

```
Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
625                 630                 635                 640

Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
                645                 650                 655

Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
            660                 665                 670

Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu
        675                 680                 685

Glu Lys Arg Tyr Leu Gln Asp Ile Trp Ser
    690                 695


<210> 443
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
      5-methyltetrahydrofolate-homocysteine methyltransferase
      reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421318"

<400> 443
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1               5                   10                  15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
            20                  25                  30

Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
        35                  40                  45

Glu Thr Ala Pro Leu Val Val Val Val Ser Thr Thr Gly Thr Gly Asp
```

```
    50                  55                  60

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

Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
                85                  90                  95

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


<210> 444
<211> 372
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
      5-methyltetrahydrofolate-homocysteine methyltransferase
      reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421991"


<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 444
Xaa Phe Thr Val Thr Cys Leu Glu Val Met Arg Arg Phe Leu Leu Leu
1               5                   10                  15

Tyr Ala Thr Gln Gln Gly Gln Ala Lys Ala Ile Ala Glu Glu Ile Cys
            20                  25                  30

Glu Gln Ala Val Val His Gly Phe Ser Ala Asp Leu His Cys Ile Ser
        35                  40                  45
```

```
Glu Ser Asp Lys Tyr Asp Leu Lys Thr Glu Thr Ala Pro Leu Val Val
    50                  55                  60

Val Val Ser Thr Thr Gly Thr Gly Asp Pro Pro Asp Thr Ala Arg Lys
65                  70                  75                  80

Phe Val Lys Glu Ile Gln Asn Gln Thr Leu Pro Val Asp Phe Phe Ala
                85                  90                  95

His Leu Arg Tyr Gly Leu Leu Gly Leu Gly Asp Ser Glu Tyr Thr Tyr
            100                 105                 110

Phe Cys Asn Gly Gly Lys Ile Ile Asp Lys Arg Leu Gln Glu Leu Gly
        115                 120                 125

Ala Arg His Phe Tyr Asp Thr Gly His Ala Asp Asp Cys Val Gly Leu
    130                 135                 140

Glu Leu Val Val Glu Pro Trp Ile Ala Gly Leu Trp Pro Ala Leu Arg
145                 150                 155                 160

Lys His Phe Arg Ser Ser Arg Gly Gln Glu Glu Ile Ser Gly Ala Leu
                165                 170                 175

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

Leu Leu His Ile Glu Ser Gln Val Glu Leu Leu Arg Phe Asp Asp Ser
        195                 200                 205

Gly Arg Lys Asp Ser Glu Val Leu Lys Gln Asn Ala Val Asn Ser Asn
    210                 215                 220

Gln Ser Asn Val Val Ile Glu Asp Phe Glu Ser Ser Leu Thr Arg Ser
225                 230                 235                 240

Val Pro Pro Leu Ser Gln Ala Ser Leu Asn Ile Pro Gly Leu Pro Pro
                245                 250                 255

Glu Tyr Leu Gln Val His Leu Gln Glu Ser Leu Gly Gln Glu Glu Ser
            260                 265                 270

Gln Val Ser Val Thr Ser Ala Asp Pro Val Phe Gln Val Pro Ile Ser
```

```
        275                 280                 285

Lys Ala Val Gln Leu Thr Thr Asn Asp Ala Ile Lys Thr Thr Leu Leu
    290                 295                 300

Val Glu Leu Asp Ile Ser Asn Thr Asp Phe Ser Tyr Gln Pro Gly Asp
305                 310                 315                 320

Ala Phe Ser Val Ile Cys Pro Asn Ser Asp Ser Glu Val Gln Ser Leu
                325                 330                 335

Leu Gln Arg Leu Gln Leu Glu Asp Lys Arg Glu His Cys Val Leu Leu
            340                 345                 350

Lys Ile Lys Ala Asp Thr Lys Lys Lys Gly Ile Phe Ala Ser Pro Cys
        355                 360                 365

Gly Leu Tyr Gln
    370


<210> 445
<211> 115
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
      5-methyltetrahydrofolate-homocysteine methyltransferase
      reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423139"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 445
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Xaa Val Arg Ala Gly Ala Arg Leu Val Glu Val Ala Leu Cys Ser Phe
1               5                  10                  15

Thr Val Thr Cys Leu Glu Val Met Arg Arg Phe Leu Leu Leu Tyr Ala
            20                  25                  30

Thr Gln Gln Gly Gln Ala Lys Ala Ile Ala Glu Glu Ile Cys Glu Gln
        35                  40                  45

Ala Val Val His Gly Phe Ser Ala Asp Leu His Cys Ile Ser Glu Ser
    50                  55                  60

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

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

Lys Glu Ile Gln Asn Gln Thr Leu Pro Val Asp Phe Phe Ala His Leu
            100                 105                 110

Arg Ser Arg
        115
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<210> 446
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423863"

<220>

<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 446
Xaa Val Arg Ala Gly Ala Arg Leu Val Glu Val Ala Leu Cys Arg Phe
1   5   10   15

Val Pro Gly Trp Arg Gly Val Gly Leu Gly Asp Ser Glu Tyr Thr Tyr
            20   25   30

Phe Cys Asn Gly Gly Lys Ile Ile Asp Lys Arg Leu Gln Glu Leu Gly
        35   40   45

Ala Arg His Phe Tyr Asp Thr Gly His Ala Asp Asp Cys Val Gly Leu
    50   55   60

Glu Leu Val Val Glu Pro Trp Ile Ala Gly Leu Trp Pro Ala Leu Arg
65   70   75   80

Lys His Phe Arg Ser Ser Arg Gly Gln Glu Glu Ile Ser Gly Ala Leu
                85   90   95

Pro Val Ala Ser Pro Ala Ser Ser Arg Thr Asp Leu Val Lys Ser Glu
            100   105   110

Leu Leu His Ile Glu Ser Gln Val Glu Leu Leu Arg Phe Asp Asp Ser
        115   120   125

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

Gln Ser Asn Val Val Ile Glu Asp Phe Glu Ser Ser Leu Thr Arg Ser
145   150   155   160

<210> 447
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424599"

<400> 447
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1 5 10 15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
20 25 30

Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
35 40 45

Glu Thr Ala Pro Leu Val Val Val Val Ser Thr Thr Gly Thr Gly Asp
50 55 60

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

Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
85 90 95

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

Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
115 120 125

Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
130 135 140

Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser
145 150 155

<210> 448
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424644"

<400> 448
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1 5 10 15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
20 25 30

Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Cys Glu Lys
35 40 45

<210> 449
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424719"

<220>
<221> MOD_RES

<222> (1)..(1)
<223> Any amino acid

<400> 449
Xaa Val Arg Ala Gly Ala Arg Leu Val Glu Val Ala Leu Cys Ser Phe
1   5   10   15

Thr Val Thr Cys Leu Glu Val Met Arg Arg Phe Leu Leu Leu Tyr Ala
            20   25   30

Thr Gln Gln Gly Gln Ala Lys Ala Ile Ala Glu Glu Ile Cys Glu Gln
        35   40   45

Ala Val Val His Gly Phe Ser Ala Asp Leu His Cys Ile Ser Glu Ser
    50   55   60

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

Arg

<210> 450
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
      5-methyltetrahydrofolate-homocysteine methyltransferase
      reductase; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UBK8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426132"

<400> 450
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys

```
1               5                   10                  15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
            20                  25                  30

Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val Ile Gln
        35                  40                  45

Asn Thr Pro Thr Phe Ala Met Gly Gly Arg
    50                  55
```

<210> 451
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426710"

<400> 451

```
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1               5                   10                  15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
            20                  25                  30

Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
        35                  40                  45

Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
    50                  55                  60

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

```
Leu Pro Val Asp Phe Phe Ala His Leu Arg Ser Arg
                85                  90


<210> 452
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
      5-methyltetrahydrofolate-homocysteine methyltransferase
      reductase; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UBK8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427200"

<400> 452
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1               5                   10                  15


Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
            20                  25                  30


Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val Ile Gln
        35                  40                  45


Asn Thr Pro Thr Phe Ala Met Gly Gly Arg
    50                  55


<210> 453
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 79; "

<220>
<221> source
<223> /note="Gene Symbol: MTRR; "

<220>
<221> source
<223> /note="Gene Name:
5-methyltetrahydrofolate-homocysteine methyltransferase
reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427416"

<400> 453
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1 5 10 15

Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
20 25 30

Ala Asp Leu His Cys Ile Ser Glu Ser
35 40

<210> 454
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 80; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC1; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q5TFE4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000326858"

<400> 454

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Met Ala Gln His Phe Ser Leu Ala Ala Cys Asp Val Val Gly Phe Asp
1               5                  10                  15

Leu Asp His Thr Leu Cys Arg Tyr Asn Leu Pro Glu Ser Ala Pro Leu
            20                  25                  30

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

Lys Glu Leu Leu Asn Val Thr Pro Glu Asp Trp Asp Phe Cys Cys Lys
    50                  55                  60

Gly Leu Ala Leu Asp Leu Glu Asp Gly Asn Phe Leu Lys Leu Ala Asn
65                  70                  75                  80

Asn Gly Thr Val Leu Arg Ala Ser His Gly Thr Lys Met Met Thr Pro
                85                  90                  95

Glu Val Leu Ala Glu Ala Tyr Gly Lys Lys Glu Trp Lys His Phe Leu
            100                 105                 110

Ser Asp Thr Gly Met Ala Cys Arg Ser Gly Lys Tyr Tyr Phe Tyr Asp
        115                 120                 125

Asn Tyr Phe Asp Leu Pro Gly Ala Leu Leu Cys Ala Arg Val Val Asp
    130                 135                 140

Tyr Leu Thr Lys Leu Asn Asn Gly Gln Lys Thr Phe Asp Phe Trp Lys
145                 150                 155                 160

Asp Ile Val Ala Ala Ile Gln His Asn Tyr Lys Met Ser Ala Phe Lys
                165                 170                 175

Glu Asn Cys Gly Ile Tyr Phe Pro Glu Ile Lys Arg Asp Pro Gly Arg
            180                 185                 190

Tyr Leu His Ser Cys Pro Glu Ser Val Lys Lys Trp Leu Arg Gln Leu
        195                 200                 205

Lys Asn Ala Gly Lys Ile Leu Leu Leu Ile Thr Ser Ser His Ser Asp
    210                 215                 220

Tyr Cys Arg Leu Leu Cys Glu Tyr Ile Leu Gly Asn Asp Phe Thr Asp
```

225 230 235 240

Leu Phe Asp Ile Val Ile Thr Asn Ala Leu Lys Pro Gly Phe Phe Ser
245 250 255

His Leu Pro Ser Gln Arg Pro Phe Arg Thr Leu Glu Asn Asp Glu Glu
260 265 270

Gln Glu Ala Leu Pro Ser Leu Asp Lys Pro Gly Trp Tyr Ser Gln Gly
275 280 285

Asn Ala Val His Leu Tyr Glu Leu Leu Lys Lys Met Thr Gly Lys Pro
290 295 300

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

Pro Ala Arg His Tyr Ser Asn Trp Glu Thr Val Leu Ile Leu Glu Glu
325 330 335

Leu Arg Gly Asp Glu Gly Thr Arg Ser Gln Arg Pro Glu Glu Ser Glu
340 345 350

Pro Leu Glu Lys Lys Gly Lys Tyr Glu Gly Pro Lys Ala Lys Pro Leu
355 360 365

Asn Thr Ser Ser Lys Lys Trp Gly Ser Phe Phe Ile Asp Ser Val Leu
370 375 380

Gly Leu Glu Asn Thr Glu Asp Ser Leu Val Tyr Thr Trp Ser Cys Lys
385 390 395 400

Arg Ile Ser Thr Tyr Ser Thr Ile Ala Ile Pro Ser Ile Glu Ala Ile
405 410 415

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

Ser Lys Thr Ala Gly Tyr Tyr Pro Asn Pro Pro Leu Val Leu Ser Ser
435 440 445

Asp Glu Thr Leu Ile Ser Lys
450 455

<210> 455
<211> 195
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 80; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC1; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393578"

<400> 455
Met Ala Gln His Phe Ser Leu Ala Ala Cys Asp Val Val Gly Phe Asp
1 5 10 15

Leu Asp His Thr Leu Cys Arg Tyr Asn Leu Pro Glu Ser Ala Pro Leu
20 25 30

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

Lys Glu Leu Leu Asn Val Thr Pro Glu Asp Trp Asp Phe Cys Cys Lys
50 55 60

Gly Leu Ala Leu Asp Leu Glu Asp Gly Asn Phe Leu Lys Leu Ala Asn
65 70 75 80

Asn Gly Thr Val Leu Arg Ala Ser His Gly Thr Lys Met Met Thr Pro
85 90 95

Glu Val Leu Ala Glu Ala Tyr Gly Lys Lys Glu Trp Lys His Phe Leu
100 105 110

Ser Asp Thr Gly Met Ala Cys Arg Ser Gly Lys Tyr Tyr Phe Tyr Asp
115 120 125

```
Asn Tyr Phe Asp Leu Pro Gly Ala Leu Leu Cys Ala Arg Val Val Asp
    130                 135                 140

Tyr Leu Thr Lys Leu Asn Asn Gly Gln Lys Thr Phe Asp Phe Trp Lys
145                 150                 155                 160

Asp Ile Val Ala Ala Ile Gln His Asn Tyr Lys Met Ser Ala Phe Lys
                165                 170                 175

Val Arg Arg Leu Ala Thr Ser Leu Leu Gln Asp Ile Ser Thr Ser Phe
            180                 185                 190

Ile Leu Ile
        195


<210> 456
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 80; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC1; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase
      domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433238"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 456
Xaa Asn Tyr Lys Met Ser Ala Phe Lys Glu Ile Lys Arg Asp Pro Gly
1               5                   10                  15

Arg Tyr Leu His Ser Cys Pro Glu Ser Val Lys Lys Trp Leu Arg Gln
            20                  25                  30
```

```
Leu Lys Asn Ala Gly Lys Ile Leu Leu Leu Ile Thr Ser Ser His Ser
        35                  40                  45

Asp Tyr Cys Arg Leu Leu Cys Glu Tyr Ile Leu Gly Asn Asp Phe Thr
    50                  55                  60

Asp Leu Phe Asp Ile Val Ile Thr Asn Ala Leu Lys Pro Gly Phe Phe
65                  70                  75                  80

Ser His Leu Pro Ser Gln Arg Pro Phe Arg Thr Leu Glu Asn Asp Glu
                85                  90                  95

Glu Gln Glu Ala Leu Pro Ser Leu Asp Lys Pro Gly Trp Tyr Ser Gln
            100                 105                 110

Gly Asn Ala Val His Leu Tyr Glu Leu Leu Lys Lys Met Thr Gly Lys
        115                 120                 125

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


<210> 457
<211> 520
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 81; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC2; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase
      domain containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H857; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000302468"
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<400> 457
Met Arg Val Glu Ser Gly Ser Ala Gln Glu Arg Gly Ile Leu Leu Glu
1 5 10 15

Ser Leu Ser Thr Leu Leu Glu Lys Thr Thr Ala Ser His Glu Gly Arg
20 25 30

Ala Pro Gly Asn Arg Glu Leu Thr Asp Leu Leu Pro Pro Glu Val Cys
35 40 45

Ser Leu Leu Asn Pro Ala Ala Ile Tyr Ala Asn Asn Glu Ile Ser Leu
50 55 60

Arg Asp Val Glu Val Tyr Gly Phe Asp Tyr Asp Tyr Thr Leu Ala Gln
65 70 75 80

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

Leu Ile Glu His Tyr Lys Tyr Pro Glu Gly Ile Arg Lys Tyr Asp Tyr
100 105 110

Asn Pro Ser Phe Ala Ile Arg Gly Leu His Tyr Asp Ile Gln Lys Ser
115 120 125

Leu Leu Met Lys Ile Asp Ala Phe His Tyr Val Gln Leu Gly Thr Ala
130 135 140

Tyr Arg Gly Leu Gln Pro Val Pro Asp Glu Glu Val Ile Glu Leu Tyr
145 150 155 160

Gly Gly Thr Gln His Ile Pro Leu Tyr Gln Met Ser Gly Phe Tyr Gly
165 170 175

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

Met Ala Leu Leu Ser Cys Val Val Asp Tyr Phe Leu Gly His Ser Leu
195 200 205

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

```
Asp Val His Val Lys Gly Leu Met Tyr Gln Trp Ile Glu Gln Asp Met
225                 230                 235                 240

Glu Lys Tyr Ile Leu Arg Gly Asp Glu Thr Phe Ala Val Leu Ser Arg
                245                 250                 255

Leu Val Ala His Gly Lys Gln Leu Phe Leu Ile Thr Asn Ser Pro Phe
            260                 265                 270

Ser Phe Val Asp Lys Gly Met Arg His Met Val Gly Pro Asp Trp Arg
        275                 280                 285

Gln Leu Phe Asp Val Val Ile Val Gln Ala Asp Lys Pro Ser Phe Phe
    290                 295                 300

Thr Asp Arg Arg Lys Pro Phe Arg Lys Leu Asp Glu Lys Gly Ser Leu
305                 310                 315                 320

Gln Trp Asp Arg Ile Thr Arg Leu Glu Lys Gly Lys Ile Tyr Arg Gln
                325                 330                 335

Gly Asn Leu Phe Asp Phe Leu Arg Leu Thr Glu Trp Arg Gly Pro Arg
            340                 345                 350

Val Leu Tyr Phe Gly Asp His Leu Tyr Ser Asp Leu Ala Asp Leu Met
        355                 360                 365

Leu Arg His Gly Trp Arg Thr Gly Ala Ile Ile Pro Glu Leu Glu Arg
    370                 375                 380

Glu Ile Arg Ile Ile Asn Thr Glu Gln Tyr Met His Ser Leu Thr Trp
385                 390                 395                 400

Gln Gln Ala Leu Thr Gly Leu Leu Glu Arg Met Gln Thr Tyr Gln Asp
                405                 410                 415

Ala Glu Ser Arg Gln Val Leu Ala Ala Trp Met Lys Glu Arg Gln Glu
            420                 425                 430

Leu Arg Cys Ile Thr Lys Ala Leu Phe Asn Ala Gln Phe Gly Ser Ile
        435                 440                 445

Phe Arg Thr Phe His Asn Pro Thr Tyr Phe Ser Arg Arg Leu Val Arg
```

```
    450                 455                 460

Phe Ser Asp Leu Tyr Met Ala Ser Leu Ser Cys Leu Leu Asn Tyr Arg
465                 470                 475                 480

Val Asp Phe Thr Phe Tyr Pro Arg Arg Thr Pro Leu Gln His Glu Ala
                485                 490                 495

Pro Leu Trp Met Asp Gln Leu Cys Thr Gly Cys Met Lys Thr Pro Phe
            500                 505                 510

Leu Gly Asp Met Ala His Ile Arg
        515                 520


<210> 458
<211> 557
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 81; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC2; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase
      domain containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H857; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000406933"

<400> 458
Met Ala Gly Ala Gly Leu Arg Ala Ala Ala Arg Arg Trp Leu Leu Cys
1               5                   10                  15

Gly Gly His Gly Gly Pro Arg Ala Ala Ser Ser Ser Pro Ser Cys Pro
            20                  25                  30

Gly Cys Gly Pro Pro Gly Pro Gly Ala His Cys Pro Gly Val Pro Arg
        35                  40                  45
```

```
Ser Ala Pro Ala Gln Ala Pro Thr Ser Gly Ala Asp Leu Ser Ala His
    50                  55                  60

Leu Trp Ala Arg Tyr Gln Asp Met Arg Arg Leu Val His Asp Leu Leu
65                  70                  75                  80

Pro Pro Glu Val Cys Ser Leu Leu Asn Pro Ala Ala Ile Tyr Ala Asn
                85                  90                  95

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

Tyr Thr Leu Ala Gln Tyr Ala Asp Ala Leu His Pro Glu Ile Phe Ser
        115                 120                 125

Thr Ala Arg Asp Ile Leu Ile Glu His Tyr Lys Tyr Pro Glu Gly Ile
    130                 135                 140

Arg Lys Tyr Asp Tyr Asn Pro Ser Phe Ala Ile Arg Gly Leu His Tyr
145                 150                 155                 160

Asp Ile Gln Lys Ser Leu Leu Met Lys Ile Asp Ala Phe His Tyr Val
                165                 170                 175

Gln Leu Gly Thr Ala Tyr Arg Gly Leu Gln Pro Val Pro Asp Glu Glu
            180                 185                 190

Val Ile Glu Leu Tyr Gly Gly Thr Gln His Ile Pro Leu Tyr Gln Met
        195                 200                 205

Ser Gly Phe Tyr Gly Lys Gly Pro Ser Ile Lys Gln Phe Met Asp Ile
    210                 215                 220

Phe Ser Leu Pro Glu Met Ala Leu Leu Ser Cys Val Val Asp Tyr Phe
225                 230                 235                 240

Leu Gly His Ser Leu Glu Phe Asp Gln Ala His Leu Tyr Lys Asp Val
                245                 250                 255

Thr Asp Ala Ile Arg Asp Val His Val Lys Gly Leu Met Tyr Gln Trp
            260                 265                 270
```

```
Ile Glu Gln Asp Met Glu Lys Tyr Ile Leu Arg Gly Asp Glu Thr Phe
        275                 280                 285

Ala Val Leu Ser Arg Leu Val Ala His Gly Lys Gln Leu Phe Leu Ile
    290                 295                 300

Thr Asn Ser Pro Phe Ser Phe Val Asp Lys Gly Met Arg His Met Val
305                 310                 315                 320

Gly Pro Asp Trp Arg Gln Leu Phe Asp Val Val Ile Val Gln Ala Asp
                325                 330                 335

Lys Pro Ser Phe Phe Thr Asp Arg Arg Lys Pro Phe Arg Lys Leu Asp
            340                 345                 350

Glu Lys Gly Ser Leu Gln Trp Asp Arg Ile Thr Arg Leu Glu Lys Gly
        355                 360                 365

Lys Ile Tyr Arg Gln Gly Asn Leu Phe Asp Phe Leu Arg Leu Thr Glu
    370                 375                 380

Trp Arg Gly Pro Arg Val Leu Tyr Phe Gly Asp His Leu Tyr Ser Asp
385                 390                 395                 400

Leu Ala Asp Leu Met Leu Arg His Gly Trp Arg Thr Gly Ala Ile Ile
                405                 410                 415

Pro Glu Leu Glu Arg Glu Ile Arg Ile Ile Asn Thr Glu Gln Tyr Met
            420                 425                 430

His Ser Leu Thr Trp Gln Gln Ala Leu Thr Gly Leu Leu Glu Arg Met
        435                 440                 445

Gln Thr Tyr Gln Asp Ala Glu Ser Arg Gln Val Leu Ala Ala Trp Met
    450                 455                 460

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

Gln Phe Gly Ser Ile Phe Arg Thr Phe His Asn Pro Thr Tyr Phe Ser
                485                 490                 495
```

```
Arg Arg Leu Val Arg Phe Ser Asp Leu Tyr Met Ala Ser Leu Ser Cys
            500                 505                 510

Leu Leu Asn Tyr Arg Val Asp Phe Thr Phe Tyr Pro Arg Arg Thr Pro
        515                 520                 525

Leu Gln His Glu Ala Pro Leu Trp Met Asp Gln Leu Cys Thr Gly Cys
    530                 535                 540

Met Lys Thr Pro Phe Leu Gly Asp Met Ala His Ile Arg
545                 550                 555


<210> 459
<211> 258
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 81; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC2; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase
      domain containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417269"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 459
Xaa Gln Asp Met Arg Arg Leu Val His Asp Leu Leu Pro Pro Glu Val
1               5                   10                  15

Cys Ser Leu Leu Asn Pro Ala Ala Ile Tyr Ala Asn Asn Glu Ile Ser
            20                  25                  30

Leu Arg Asp Val Glu Val Tyr Gly Phe Asp Tyr Asp Tyr Thr Leu Ala
        35                  40                  45
```

```
Gln Tyr Ala Asp Ala Leu His Pro Glu Ile Phe Ser Thr Ala Arg Asp
    50                  55                  60

Ile Leu Ile Glu His Tyr Lys Ser Leu Leu Met Lys Ile Asp Ala Phe
65                  70                  75                  80

His Tyr Val Gln Leu Gly Thr Ala Tyr Arg Gly Leu Gln Pro Val Pro
                85                  90                  95

Asp Glu Glu Gly Pro Ser Ile Lys Gln Phe Met Asp Ile Phe Ser Leu
            100                 105                 110

Pro Glu Met Ala Leu Leu Ser Cys Val Val Asp Tyr Phe Leu Gly His
        115                 120                 125

Ser Leu Glu Phe Asp Gln Ala His Leu Tyr Lys Asp Val Thr Asp Ala
    130                 135                 140

Ile Arg Asp Val His Val Lys Gly Leu Met Tyr Gln Trp Ile Glu Gln
145                 150                 155                 160

Asp Met Glu Lys Tyr Ile Leu Arg Gly Asp Glu Thr Phe Ala Val Leu
                165                 170                 175

Ser Arg Leu Val Ala His Gly Lys Gln Leu Phe Leu Ile Thr Asn Ser
            180                 185                 190

Pro Phe Ser Phe Val Asp Lys Gly Met Arg His Met Val Gly Pro Asp
        195                 200                 205

Trp Arg Gln Leu Phe Asp Val Val Ile Val Gln Ala Asp Lys Pro Ser
    210                 215                 220

Phe Phe Thr Asp Arg Arg Lys Pro Phe Arg Lys Leu Asp Glu Lys Gly
225                 230                 235                 240

Ser Leu Gln Trp Asp Arg Ile Thr Arg Leu Glu Lys Gly Lys Ile Tyr
                245                 250                 255

Arg Gln
```

<210> 460
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 81; "

<220>
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<223> /note="Gene Symbol: NT5DC2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418583"

<400> 460
Met Lys Ile Asp Ala Phe His Tyr Val Gln Leu Gly Thr Ala Tyr Arg
1 5 10 15

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

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

Asp Tyr Phe Leu Gly His Ser Leu Glu Phe Asp Gln Ala His Leu Tyr
50 55 60

Lys Asp Val Thr Asp Ala Ile Arg Asp Val His Val Lys Gly Leu Met
65 70 75 80

Tyr Gln Trp Ile Glu
85

<210> 461
<211> 194
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 81; "

<220>
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<223> /note="Gene Symbol: NT5DC2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418780"

<400> 461
Trp Arg Gln Leu Phe Asp Val Val Ile Val Gln Ala Asp Lys Pro Ser
1 5 10 15

Phe Phe Thr Asp Arg Arg Lys Pro Phe Arg Lys Leu Asp Glu Lys Gly
20 25 30

Ser Leu Gln Trp Asp Arg Ile Thr Arg Leu Glu Lys Gly Lys Ile Tyr
35 40 45

Arg Gln Gly Asn Leu Phe Asp Phe Leu Arg Leu Thr Glu Trp Arg Gly
50 55 60

Pro Arg Val Leu Tyr Phe Gly Asp His Leu Tyr Ser Asp Leu Ala Asp
65 70 75 80

Leu Met Leu Arg His Gly Trp Arg Thr Gly Ala Ile Ile Pro Glu Leu
85 90 95

Glu Arg Glu Ile Arg Ile Ile Asn Thr Glu Gln Tyr Met His Ser Leu
100 105 110

Thr Trp Gln Gln Ala Leu Thr Gly Leu Leu Glu Arg Met Gln Thr Tyr
115 120 125

Gln Asp Ala Glu Ser Arg Gln Val Leu Ala Ala Trp Met Lys Glu Arg
130 135 140

Gln Glu Leu Ser Cys Leu Leu Asn Tyr Arg Val Asp Phe Thr Phe Tyr
145 150 155 160

Pro Arg Arg Thr Pro Leu Gln His Glu Ala Pro Leu Trp Met Asp Gln
165 170 175

Leu Cys Thr Gly Cys Met Lys Thr Pro Phe Leu Gly Asp Met Ala His
180 185 190

Ile Arg

<210> 462
<211> 532
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 81; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC2; "

<220>
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<223> /note="Gene Name:
5'-nucleotidase
domain containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H857; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419547"

<400> 462
Met Ala Gly Ala Gly Leu Arg Ala Ala Ala Arg Arg Trp Leu Leu Cys
1 5 10 15

Gly Gly His Gly Gly Pro Arg Ala Ala Ser Ser Ser Pro Ser Cys Pro
20 25 30

Gly Cys Gly Pro Pro Gly Pro Gly Ala His Cys Pro Gly Val Pro Arg
35 40 45

Ser Ala Pro Ala Gln Ala Pro Thr Ser Gly Ala Asp Leu Ser Ala His
50 55 60

Leu Trp Ala Arg Tyr Gln Asp Met Arg Arg Leu Val His Asp Leu Leu
65 70 75 80

```
Pro Pro Glu Val Cys Ser Leu Leu Asn Pro Ala Ala Ile Tyr Ala Asn
                85                  90                  95

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

Tyr Thr Leu Ala Gln Tyr Ala Asp Ala Leu His Pro Glu Ile Phe Ser
        115                 120                 125

Thr Ala Arg Asp Ile Leu Ile Glu His Tyr Lys Ser Leu Leu Met Lys
    130                 135                 140

Ile Asp Ala Phe His Tyr Val Gln Leu Gly Thr Ala Tyr Arg Gly Leu
145                 150                 155                 160

Gln Pro Val Pro Asp Glu Glu Val Ile Glu Leu Tyr Gly Gly Thr Gln
                165                 170                 175

His Ile Pro Leu Tyr Gln Met Ser Gly Phe Tyr Gly Lys Gly Pro Ser
            180                 185                 190

Ile Lys Gln Phe Met Asp Ile Phe Ser Leu Pro Glu Met Ala Leu Leu
        195                 200                 205

Ser Cys Val Val Asp Tyr Phe Leu Gly His Ser Leu Glu Phe Asp Gln
    210                 215                 220

Ala His Leu Tyr Lys Asp Val Thr Asp Ala Ile Arg Asp Val His Val
225                 230                 235                 240

Lys Gly Leu Met Tyr Gln Trp Ile Glu Gln Asp Met Glu Lys Tyr Ile
                245                 250                 255

Leu Arg Gly Asp Glu Thr Phe Ala Val Leu Ser Arg Leu Val Ala His
            260                 265                 270

Gly Lys Gln Leu Phe Leu Ile Thr Asn Ser Pro Phe Ser Phe Val Asp
        275                 280                 285

Lys Gly Met Arg His Met Val Gly Pro Asp Trp Arg Gln Leu Phe Asp
    290                 295                 300
```

```
Val Val Ile Val Gln Ala Asp Lys Pro Ser Phe Phe Thr Asp Arg Arg
305                 310                 315                 320

Lys Pro Phe Arg Lys Leu Asp Glu Lys Gly Ser Leu Gln Trp Asp Arg
                325                 330                 335

Ile Thr Arg Leu Glu Lys Gly Lys Ile Tyr Arg Gln Gly Asn Leu Phe
            340                 345                 350

Asp Phe Leu Arg Leu Thr Glu Trp Arg Gly Pro Arg Val Leu Tyr Phe
        355                 360                 365

Gly Asp His Leu Tyr Ser Asp Leu Ala Asp Leu Met Leu Arg His Gly
    370                 375                 380

Trp Arg Thr Gly Ala Ile Ile Pro Glu Leu Glu Arg Glu Ile Arg Ile
385                 390                 395                 400

Ile Asn Thr Glu Gln Tyr Met His Ser Leu Thr Trp Gln Gln Ala Leu
                405                 410                 415

Thr Gly Leu Leu Glu Arg Met Gln Thr Tyr Gln Asp Ala Glu Ser Arg
            420                 425                 430

Gln Val Leu Ala Ala Trp Met Lys Glu Arg Gln Glu Leu Arg Cys Ile
        435                 440                 445

Thr Lys Ala Leu Phe Asn Ala Gln Phe Gly Ser Ile Phe Arg Thr Phe
    450                 455                 460

His Asn Pro Thr Tyr Phe Ser Arg Arg Leu Val Arg Phe Ser Asp Leu
465                 470                 475                 480

Tyr Met Ala Ser Leu Ser Cys Leu Leu Asn Tyr Arg Val Asp Phe Thr
                485                 490                 495

Phe Tyr Pro Arg Arg Thr Pro Leu Gln His Glu Ala Pro Leu Trp Met
            500                 505                 510

Asp Gln Leu Cys Thr Gly Cys Met Lys Thr Pro Phe Leu Gly Asp Met
        515                 520                 525

Ala His Ile Arg
```

530

<210> 463
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 81; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419774"

<400> 463
Met Arg Val Glu Ser Gly Ser Ala Gln Glu Arg Gly Ile Leu Leu Glu
1 5 10 15

Ser Leu Ser Thr Leu Leu Glu Lys Thr Thr Ala Ser His Glu Gly Arg
20 25 30

Ala Pro Gly Asn Arg Glu Leu Thr Gly Gln Cys Gly Gln Leu Pro Arg
35 40 45

Ser Glu Pro Ser Gly Arg Ser Asp Arg Gly Pro Gln Pro Cys Ser Ala
50 55 60

Arg Pro Ser His Leu Val Ser Gly Arg Arg Leu Pro Cys Arg Pro Leu
65 70 75 80

Gly Leu Pro Gln Arg Gly Pro Gly Thr Gly Lys Arg Gly Lys Gly Ser
85 90 95

Leu Phe Val Arg Pro Thr Ser Cys Pro Pro Arg Ser Ala Val Ser
100 105 110

<210> 464
<211> 548

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 82; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC3; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q86UY8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376615"

<400> 464

```
Met Thr Met Ala Ala Ala Ala Val Val Ala Arg Gly Ala Gly Ala Arg
1               5                  10                  15


Ala Ala Thr Ala Ala Ala Leu Arg Gly Gly Cys Gly Thr Ala Ala Arg
            20                  25                  30


Gly Arg Pro Cys Ala Gly Pro Ala Arg Pro Leu Cys Thr Ala Pro Gly
        35                  40                  45


Thr Ala Pro Asp Met Lys Arg Tyr Leu Trp Glu Arg Tyr Arg Glu Ala
    50                  55                  60


Lys Arg Ser Thr Glu Glu Leu Val Pro Ser Ile Met Ser Asn Leu Leu
65                  70                  75                  80


Asn Pro Asp Ala Ile Phe Ser Asn Asn Glu Met Ser Leu Ser Asp Ile
                85                  90                  95


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


His Leu His Thr Leu Ile Phe Asn Ala Ala Arg Asp Leu Leu Ile Asn
        115                 120                 125
```

```
Glu His Arg Tyr Pro Ala Glu Ile Arg Lys Tyr Glu Tyr Asp Pro Asn
    130                 135                 140

Phe Ala Ile Arg Gly Leu His Tyr Asp Val Gln Arg Ala Val Leu Met
145                 150                 155                 160

Lys Ile Asp Ala Phe His Tyr Ile Gln Leu Gly Thr Val Tyr Arg Gly
                165                 170                 175

Leu Ser Val Val Pro Asp Glu Glu Val Ile Glu Met Tyr Glu Gly Ser
            180                 185                 190

His Val Pro Leu Glu Gln Met Ser Asp Phe Tyr Gly Lys Ser Ser His
        195                 200                 205

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

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

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

Val His Ile Lys Gly Ile Met Tyr Arg Ala Ile Glu Ala Asp Ile Glu
            260                 265                 270

Lys Tyr Ile Cys Tyr Ala Glu Gln Thr Arg Ala Val Leu Ala Lys Leu
        275                 280                 285

Ala Asp His Gly Lys Lys Met Phe Leu Ile Thr Asn Ser Pro Ser Ser
    290                 295                 300

Phe Val Asp Lys Gly Met Ser Tyr Ile Val Gly Lys Asp Trp Arg Asp
305                 310                 315                 320

Leu Phe Asp Val Val Ile Val Gln Ala Glu Lys Pro Asn Phe Phe Asn
                325                 330                 335

Asp Lys Arg Arg Pro Phe Arg Lys Met Asn Glu Lys Gly Val Leu Leu
            340                 345                 350
```

```
Trp Asp Lys Ile His Lys Leu Gln Lys Gly Gln Ile Tyr Lys Gln Gly
        355                 360                 365

Asn Leu Tyr Glu Phe Leu Lys Leu Thr Gly Trp Arg Gly Ser Arg Val
    370                 375                 380

Leu Tyr Phe Gly Asp His Ile Tyr Ser Asp Leu Ala Asp Leu Thr Leu
385                 390                 395                 400

Lys His Gly Trp Arg Thr Gly Ala Ile Ile Pro Glu Leu Arg Ser Glu
                405                 410                 415

Leu Lys Ile Met Asn Thr Glu Gln Tyr Ile Gln Thr Met Thr Trp Leu
            420                 425                 430

Gln Thr Leu Thr Gly Leu Leu Glu Gln Met Gln Val His Arg Asp Ala
        435                 440                 445

Glu Ser Gln Leu Val Leu Gln Glu Trp Lys Lys Glu Arg Lys Glu Met
    450                 455                 460

Arg Glu Met Thr Lys Ser Phe Phe Asn Ala Gln Phe Gly Ser Leu Phe
465                 470                 475                 480

Arg Thr Asp Gln Asn Pro Thr Tyr Phe Leu Arg Arg Leu Ser Arg Phe
                485                 490                 495

Ala Asp Ile Tyr Met Ala Ser Leu Ser Cys Leu Leu Asn Tyr Asp Val
            500                 505                 510

Ser His Thr Phe Tyr Pro Arg Arg Thr Pro Leu Gln His Glu Leu Pro
        515                 520                 525

Ala Trp Ser Glu Arg Pro Pro Thr Phe Gly Thr Pro Leu Leu Gln Glu
    530                 535                 540

Ala Gln Ala Lys
545
```

<210> 465
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 82; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC3; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase
domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399171"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 465
Xaa Ala Lys Leu Ala Asp His Gly Lys Lys Met Phe Leu Ile Thr Asn
1 5 10 15

Ser Pro Ser Ser Phe Val Asp Lys Gly Met Ser Tyr Ile Val Gly Lys
20 25 30

Asp Trp Arg Asp Leu Phe Asp Val Val Ile Val Gln Ala Glu Lys Pro
35 40 45

Asn Phe Phe Asn Asp Lys Arg Arg Pro Phe Arg Lys Met Asn Glu Lys
50 55 60

Gly Val Leu Leu Trp Asp Lys Ile His Lys Leu Gln Lys Gly Gln Ile
65 70 75 80

Tyr Lys Gln Gly Asn Leu Tyr Glu Phe Leu Lys Leu Thr Gly Trp Arg
85 90 95

Gly Ser Arg Val Leu Tyr Phe Gly Asp His Ile Tyr Ser Asp Leu Ala
100 105 110

Thr Met Val Asn Asp Ser Arg Pro Ser Val Ser Ala Gly Val Val Thr
115 120 125

```
His Gly Asn Tyr Phe Gln Asn
    130                 135


<210> 466
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 82; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC3; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase
      domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413657"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 466
Xaa Thr Met Thr Trp Leu Gln Thr Leu Thr Gly Leu Leu Glu Gln Met
1               5                  10                  15


Gln Val His Arg Asp Ala Glu Ser Gln Leu Val Leu Gln Glu Trp Lys
            20                  25                  30


Lys Glu Arg Lys Glu Met Arg Glu Met Thr Lys Ser Phe Phe Asn Ala
        35                  40                  45


Gln Phe Gly Ser Leu Phe Arg Thr Asp Gln Asn Pro Thr Tyr Phe Leu
    50                  55                  60


Arg Arg Leu Ser Arg Phe Ala Asp Ile Tyr Met Ala Ser Leu Ser Cys
65                  70                  75                  80


Leu Leu Asn Tyr Asp Val Ser His Thr Phe Tyr Pro Arg Arg Thr Pro
                85                  90                  95
```

```
Leu Gln His Glu Leu Pro Ala Trp Ser Glu Arg Pro Pro Thr Phe Gly
            100                 105                 110


Thr Pro Leu Leu Gln Glu Ala Gln Ala Lys
        115                 120


<210> 467
<211> 428
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 83; "

<220>
<221> source
<223> /note="Gene Symbol: NT5DC4; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase
      domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q86YG4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000330247"

<400> 467
Met Pro Ala Trp Ile Phe Val Asn Arg Ser Leu Ala Leu Gly Lys Ile
1               5                   10                  15


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


Pro Ala Tyr Glu Ala Leu Thr Phe Glu Leu Leu Leu Glu Arg Leu Val
        35                  40                  45


Cys Ile Gly Tyr Pro His Glu Ile Leu Arg Tyr Thr Tyr Asp Pro Thr
    50                  55                  60


Phe Pro Thr Arg Arg Leu Val Phe Asp Glu Leu Tyr Gly Asn Leu Leu
65                  70                  75                  80
```

```
Lys Val Asp Ala His Gly Asn Val Leu Leu Gly Ala Tyr Gly Phe Thr
                85                  90                  95

Phe Leu Ser Glu Ala Glu Ile Trp Ser Phe Tyr Pro Ser Lys Phe Ile
            100                 105                 110

Gln Arg Asp Asp Leu Gln Cys Phe Tyr Ile Leu Asn Met Leu Phe Asn
        115                 120                 125

Leu Pro Glu Thr Tyr Leu Tyr Ala Cys Leu Val Asp Phe Phe Ser Gly
    130                 135                 140

Cys Ser Arg Tyr Thr Asn Cys Asp Thr Gly Tyr Gln His Gly Asn Leu
145                 150                 155                 160

Phe Met Ser Phe Arg Ser Leu Phe Gln Asp Val Thr Asp Ala Met Asn
                165                 170                 175

Asn Ile His Gln Ser Gly Cys Leu Lys Lys Thr Leu Glu Asp Leu Glu
            180                 185                 190

Lys Tyr Val Lys Lys Asp Pro Arg Leu Pro Ile Leu Leu Gly Lys Met
        195                 200                 205

Lys Glu Val Gly Lys Val Phe Leu Ala Thr Asn Ser Ser Tyr Asn Tyr
    210                 215                 220

Thr Asn Ala Ile Met Thr Tyr Leu Phe Ser Ile Ser Glu Ala Glu Ala
225                 230                 235                 240

Ser Gly Arg Pro Trp Arg Ser Tyr Phe Asp Leu Ile Val Val Asp Thr
                245                 250                 255

Gln Lys Pro His Phe Phe Ala Glu Gly Leu Val Leu Arg Gln Val Asn
            260                 265                 270

Thr Asp Ser Gly Lys Leu His Val Gly Thr Tyr Thr Gly Pro His Gln
        275                 280                 285

His Cys Ala Val Tyr Ser Gly Gly Ser Ser Asp Met Val Cys Glu Leu
    290                 295                 300

Leu Gly Val Arg Gly Met Asp Ile Leu Tyr Ile Gly Asp His Ile Phe
```

```
305                 310                 315                 320

Gly Asp Ile Leu Lys Ser Lys Lys Arg Gln Gly Trp Arg Thr Cys Leu
                325                 330                 335

Val Val Pro Glu Leu Ser Trp Glu Leu Asp Ile Trp Ala Gln Glu Lys
            340                 345                 350

Glu Arg Leu Glu Glu Leu Lys Arg Leu Asp Thr His Leu Ala Asp Ile
        355                 360                 365

Tyr Gln His Met Asp Gly Ser Ser Cys Glu Leu Gln Val Ile Asn Phe
    370                 375                 380

Thr Lys Arg Glu Ile Gln Met Pro His Glu Ser Val Val Glu Gln Glu
385                 390                 395                 400

Gln Ala Asn Leu Asp Pro Ala Ser Cys Leu Leu Ser Cys Asn Gln Arg
                405                 410                 415

Ser Leu Pro Ala Lys Ser Cys Leu Ser Ser Ala Ile
            420                 425


<210> 468
<211> 368
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 84; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C1A; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic IA; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9BXI3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000235628"
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<400> 468
Met Glu Pro Gly Gln Pro Arg Glu Pro Gln Glu Pro Arg Glu Pro Gly
1 5 10 15

Pro Gly Ala Glu Thr Ala Ala Ala Pro Val Trp Glu Glu Ala Lys Ile
20 25 30

Phe Tyr Asp Asn Leu Ala Pro Lys Lys Lys Pro Lys Ser Pro Lys Pro
35 40 45

Gln Asn Ala Val Thr Ile Ala Val Ser Ser Arg Ala Leu Phe Arg Met
50 55 60

Asp Glu Glu Gln Gln Ile Tyr Thr Glu Gln Gly Val Glu Glu Tyr Val
65 70 75 80

Arg Tyr Gln Leu Glu His Glu Asn Glu Pro Phe Ser Pro Gly Pro Ala
85 90 95

Phe Pro Phe Val Lys Ala Leu Glu Ala Val Asn Arg Arg Leu Arg Glu
100 105 110

Leu Tyr Pro Asp Ser Glu Asp Val Phe Asp Ile Val Leu Met Thr Asn
115 120 125

Asn His Ala Gln Val Gly Val Arg Leu Ile Asn Ser Ile Asn His Tyr
130 135 140

Asp Leu Phe Ile Glu Arg Phe Cys Met Thr Gly Gly Asn Ser Pro Ile
145 150 155 160

Cys Tyr Leu Lys Ala Tyr His Thr Asn Leu Tyr Leu Ser Ala Asp Ala
165 170 175

Glu Lys Val Arg Glu Ala Ile Asp Glu Gly Ile Ala Ala Ala Thr Ile
180 185 190

Phe Ser Pro Ser Arg Asp Val Val Val Ser Gln Ser Gln Leu Arg Val
195 200 205

Ala Phe Asp Gly Asp Ala Val Leu Phe Ser Asp Glu Ser Glu Arg Ile
210 215 220

```
Val Lys Ala His Gly Leu Asp Arg Phe Phe Glu His Glu Lys Ala His
225                 230                 235                 240

Glu Asn Lys Pro Leu Ala Gln Gly Pro Leu Lys Gly Phe Leu Glu Ala
                245                 250                 255

Leu Gly Arg Leu Gln Lys Lys Phe Tyr Ser Lys Gly Leu Arg Leu Glu
            260                 265                 270

Cys Pro Ile Arg Thr Tyr Leu Val Thr Ala Arg Ser Ala Ala Ser Ser
        275                 280                 285

Gly Ala Arg Ala Leu Lys Thr Leu Arg Ser Trp Gly Leu Glu Thr Asp
    290                 295                 300

Glu Ala Leu Phe Leu Ala Gly Ala Pro Lys Gly Pro Leu Leu Glu Lys
305                 310                 315                 320

Ile Arg Pro His Ile Phe Phe Asp Asp Gln Met Phe His Val Ala Gly
                325                 330                 335

Ala Gln Glu Met Gly Thr Val Ala Ala His Val Pro Tyr Gly Val Ala
            340                 345                 350

Gln Thr Pro Arg Arg Thr Ala Pro Ala Lys Gln Ala Pro Ser Ala Gln
        355                 360                 365


<210> 469
<211> 550
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 85; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C1B; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic IB; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96P26; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000305979"

<400> 469
Met Ser Gln Thr Ser Leu Lys Gln Lys Lys Asn Glu Pro Gly Met Arg
1 5 10 15

Ser Ser Lys Glu Ser Leu Glu Ala Glu Lys Arg Lys Glu Ser Asp Lys
20 25 30

Thr Gly Val Arg Leu Ser Asn Gln Gly Ser Gln Glu Ser Ser Leu Arg
35 40 45

Lys Thr Asp Ser Arg Gly Tyr Leu Val Arg Ser Gln Trp Ser Arg Ile
50 55 60

Ser Arg Ser Pro Ser Thr Lys Ala Pro Ser Ile Asp Glu Pro Arg Ser
65 70 75 80

Arg Asn Thr Ser Ala Lys Leu Pro Ser Ser Ser Thr Ser Ser Arg Thr
85 90 95

Pro Ser Thr Ser Pro Ser Leu His Asp Ser Ser Pro Pro Pro Leu Ser
100 105 110

Gly Gln Pro Ser Leu Gln Pro Pro Ala Ser Pro Gln Leu Pro Arg Ser
115 120 125

Leu Asp Ser Arg Pro Pro Thr Pro Pro Glu Pro Asp Pro Gly Ser Arg
130 135 140

Arg Ser Thr Lys Met Gln Glu Asn Pro Glu Ala Trp Ala Gln Gly Ile
145 150 155 160

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

Arg Thr Ser Pro Thr Glu Trp Lys Ser Ser Ser Gln Arg Arg Gly Ile
180 185 190

Tyr Pro Ala Ser Thr Gln Leu Asp Arg Asn Ser Leu Ser Glu Gln Gln
195 200 205

```
Gln Gln Gln Arg Glu Asp Glu Asp Asp Tyr Glu Ala Ala Tyr Trp Ala
    210                 215                 220

Ser Met Arg Ser Phe Tyr Glu Lys Asn Pro Ser Cys Ser Arg Pro Trp
225                 230                 235                 240

Pro Pro Lys Pro Lys Asn Ala Ile Thr Ile Ala Leu Ser Ser Cys Ala
                245                 250                 255

Leu Phe Asn Met Val Asp Gly Arg Lys Ile Tyr Glu Gln Glu Gly Leu
            260                 265                 270

Glu Lys Tyr Met Glu Tyr Gln Leu Thr Asn Glu Asn Val Ile Leu Thr
        275                 280                 285

Pro Gly Pro Ala Phe Arg Phe Val Lys Ala Leu Gln Tyr Val Asn Ala
    290                 295                 300

Arg Leu Arg Asp Leu Tyr Pro Asp Glu Gln Asp Leu Phe Asp Ile Val
305                 310                 315                 320

Leu Met Thr Asn Asn His Ala Gln Val Gly Val Arg Leu Ile Asn Ser
                325                 330                 335

Val Asn His Tyr Gly Leu Leu Ile Asp Arg Phe Cys Leu Thr Gly Gly
            340                 345                 350

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

Ala Ala Asp Ser Glu Lys Val Gln Glu Ala Ile Gln Glu Gly Ile Ala
    370                 375                 380

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

Gln Leu Arg Val Ala Phe Asp Gly Asp Ala Val Leu Phe Ser Asp Glu
                405                 410                 415

Ser Glu His Phe Thr Lys Glu His Gly Leu Asp Lys Phe Phe Gln Tyr
            420                 425                 430
```

```
Asp Thr Leu Cys Glu Ser Lys Pro Leu Ala Gln Gly Pro Leu Lys Gly
        435                 440                 445

Phe Leu Glu Asp Leu Gly Arg Leu Gln Lys Lys Phe Tyr Ala Lys Asn
    450                 455                 460

Glu Arg Leu Leu Cys Pro Ile Arg Thr Tyr Leu Val Thr Ala Arg Ser
465                 470                 475                 480

Ala Ala Ser Ser Gly Ala Arg Val Leu Lys Thr Leu Arg Arg Trp Gly
                485                 490                 495

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

Ile Leu Val Lys Ile Arg Pro His Ile Phe Phe Asp Asp His Met Phe
        515                 520                 525

His Ile Glu Gly Ala Gln Arg Leu Gly Ser Ile Ala Ala Tyr Gly Phe
    530                 535                 540

Asn Lys Lys Phe Ser Ser
545                 550


<210> 470
<211> 610
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 85; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C1B; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic IB; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96P26; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000352904"
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<400> 470
Met Ser Gln Thr Ser Leu Lys Gln Lys Lys Asn Glu Pro Gly Met Arg
1 5 10 15

Ser Ser Lys Glu Ser Leu Glu Ala Glu Lys Arg Lys Glu Ser Asp Lys
20 25 30

Thr Gly Val Arg Leu Ser Asn Gln Met Arg Arg Ala Val Asn Pro Asn
35 40 45

His Ser Leu Arg Cys Cys Pro Phe Gln Gly His Ser Ser Cys Arg Arg
50 55 60

Cys Leu Cys Ala Ala Glu Gly Thr Ala Leu Gly Pro Cys His Thr Ile
65 70 75 80

Arg Ile Tyr Ile His Met Cys Leu Leu Trp Glu Gln Gly Gln Gln Ile
85 90 95

Thr Met Met Arg Gly Ser Gln Glu Ser Ser Leu Arg Lys Thr Asp Ser
100 105 110

Arg Gly Tyr Leu Val Arg Ser Gln Trp Ser Arg Ile Ser Arg Ser Pro
115 120 125

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

Ala Lys Leu Pro Ser Ser Ser Thr Ser Ser Arg Thr Pro Ser Thr Ser
145 150 155 160

Pro Ser Leu His Asp Ser Ser Pro Pro Pro Leu Ser Gly Gln Pro Ser
165 170 175

Leu Gln Pro Pro Ala Ser Pro Gln Leu Pro Arg Ser Leu Asp Ser Arg
180 185 190

Pro Pro Thr Pro Pro Glu Pro Asp Pro Gly Ser Arg Arg Ser Thr Lys
195 200 205

Met Gln Glu Asn Pro Glu Ala Trp Ala Gln Gly Ile Val Arg Glu Ile
210 215 220

```
Arg Gln Thr Arg Asp Ser Gln Pro Leu Glu Tyr Ser Arg Thr Ser Pro
225                 230                 235                 240

Thr Glu Trp Lys Ser Ser Ser Gln Arg Arg Gly Ile Tyr Pro Ala Ser
                245                 250                 255

Thr Gln Leu Asp Arg Asn Ser Leu Ser Glu Gln Gln Gln Gln Gln Arg
            260                 265                 270

Glu Asp Glu Asp Asp Tyr Glu Ala Ala Tyr Trp Ala Ser Met Arg Ser
        275                 280                 285

Phe Tyr Glu Lys Asn Pro Ser Cys Ser Arg Pro Trp Pro Pro Lys Pro
    290                 295                 300

Lys Asn Ala Ile Thr Ile Ala Leu Ser Ser Cys Ala Leu Phe Asn Met
305                 310                 315                 320

Val Asp Gly Arg Lys Ile Tyr Glu Gln Glu Gly Leu Glu Lys Tyr Met
                325                 330                 335

Glu Tyr Gln Leu Thr Asn Glu Asn Val Ile Leu Thr Pro Gly Pro Ala
            340                 345                 350

Phe Arg Phe Val Lys Ala Leu Gln Tyr Val Asn Ala Arg Leu Arg Asp
        355                 360                 365

Leu Tyr Pro Asp Glu Gln Asp Leu Phe Asp Ile Val Leu Met Thr Asn
    370                 375                 380

Asn His Ala Gln Val Gly Val Arg Leu Ile Asn Ser Val Asn His Tyr
385                 390                 395                 400

Gly Leu Leu Ile Asp Arg Phe Cys Leu Thr Gly Gly Lys Asp Pro Ile
                405                 410                 415

Gly Tyr Leu Lys Ala Tyr Leu Thr Asn Leu Tyr Ile Ala Ala Asp Ser
            420                 425                 430

Glu Lys Val Gln Glu Ala Ile Gln Glu Gly Ile Ala Ser Ala Thr Met
        435                 440                 445
```

```
Phe Asp Gly Ala Lys Asp Met Ala Tyr Cys Asp Thr Gln Leu Arg Val
    450                 455                 460

Ala Phe Asp Gly Asp Ala Val Leu Phe Ser Asp Glu Ser Glu His Phe
465                 470                 475                 480

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

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

Leu Gly Arg Leu Gln Lys Lys Phe Tyr Ala Lys Asn Glu Arg Leu Leu
        515                 520                 525

Cys Pro Ile Arg Thr Tyr Leu Val Thr Ala Arg Ser Ala Ala Ser Ser
    530                 535                 540

Gly Ala Arg Val Leu Lys Thr Leu Arg Arg Trp Gly Leu Glu Ile Asp
545                 550                 555                 560

Glu Ala Leu Phe Leu Ala Gly Ala Pro Lys Ser Pro Ile Leu Val Lys
                565                 570                 575

Ile Arg Pro His Ile Phe Phe Asp Asp His Met Phe His Ile Glu Gly
            580                 585                 590

Ala Gln Arg Leu Gly Ser Ile Ala Ala Tyr Gly Phe Asn Lys Lys Phe
        595                 600                 605

Ser Ser
    610


<210> 471
<211> 203
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 85; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C1B; "
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<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic IB; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000383905"

<400> 471
Met Ser Gln Thr Ser Leu Lys Gln Lys Lys Asn Glu Pro Gly Met Arg
1 5 10 15

Ser Ser Lys Glu Ser Leu Glu Ala Glu Lys Arg Lys Glu Ser Asp Lys
20 25 30

Thr Gly Val Arg Leu Ser Asn Gln Gly Ser Gln Glu Ser Ser Leu Arg
35 40 45

Lys Thr Asp Ser Arg Gly Tyr Leu Val Arg Ser Gln Trp Ser Arg Ile
50 55 60

Ser Arg Ser Pro Ser Thr Lys Ala Pro Ser Ile Asp Glu Pro Arg Ser
65 70 75 80

Arg Asn Thr Ser Ala Lys Val Glu Leu Pro Ser Ser Pro Arg Ser Ser
85 90 95

His Pro Arg Arg Pro Ser Cys Pro Gly Arg Trp Thr Arg Gly Leu Pro
100 105 110

Arg Pro Gln Ser Pro Ile Leu Ala Pro Gly Ala Ala Pro Lys Cys Lys
115 120 125

Arg Ile Arg Arg Pro Gly Pro Lys Ala Ser Cys Gly Lys Ser Ala Arg
130 135 140

Pro Gly Thr Arg Ser Arg Trp Asn Ile Arg Ala Arg Pro Pro Pro Ser
145 150 155 160

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

Trp Thr Ala Thr Leu Cys Pro Ser Ser Ser Ser Ser Ser Gly Arg Thr
180 185 190

```
Arg Thr Thr Thr Arg Leu Pro Thr Gly His Pro
        195                 200


<210> 472
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 85; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C1B; "

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000390811"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 472
Xaa Arg Lys Gly Leu Gln Pro Thr Ala Leu Asp Leu Ala Leu Gln Tyr
1               5                  10                  15


Val Asn Ala Arg Leu Arg Asp Leu Tyr Pro Asp Glu Gln Asp Leu Phe
            20                  25                  30


Asp Ile Val Leu Met Thr Asn Asn His Ala Gln Val Gly Val Arg Leu
        35                  40                  45


Ile Asn Ser Val Asn His Tyr Gly Leu Leu Ile Asp Arg Phe Cys Leu
    50                  55                  60


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


Leu Tyr Ile Ala Ala Asp Ser Glu Lys Val Gln Glu Ala Ile Gln Glu
                85                  90                  95
```

```
Gly Ile Ala Ser Ala Thr Met Phe Asp Gly Ala Lys Asp Met Ala Tyr
            100                 105                 110

Cys Asp Thr Gln Leu Arg Val Ala Phe Asp Gly Asp Ala Val Leu Phe
        115                 120                 125

Ser Asp Glu Ser Glu His Phe Thr Lys Glu His Gly Leu Asp Lys Phe
    130                 135                 140

Phe Gln Tyr Asp Thr Leu Cys Glu Ser Lys Pro Leu Ala Gln Gly Pro
145                 150                 155                 160

Leu Lys Gly Phe Leu Glu Asp Leu Gly Arg Leu Gln Lys Lys Phe Tyr
                165                 170                 175

Ala Lys Asn Glu Arg Leu Leu Cys Pro Ile Arg Thr Tyr Leu Val Thr
            180                 185                 190

Ala Arg Ser Ala Ala Ser Ser Gly Ala Arg Val Leu Lys Thr Leu Arg
        195                 200                 205

Arg Trp Gly Leu Glu Ile Asp Glu Ala Leu Phe Leu Ala Gly Ala Pro
    210                 215                 220

Lys Ser Pro Ile Leu Val Lys Ile Arg Pro His Ile Phe Phe Asp Asp
225                 230                 235                 240

His Met Phe His Ile Glu Gly Ala Gln Arg Leu Gly Ser Ile Ala Ala
                245                 250                 255

Tyr Gly Phe Asn Lys Lys Phe Ser Ser
            260                 265


<210> 473
<211> 205
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 85; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C1B; "
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<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic IB; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401656"

<400> 473

```
Met Ser Gln Thr Ser Leu Lys Gln Lys Lys Asn Glu Pro Gly Met Arg
1               5                  10                  15

Ser Ser Lys Glu Ser Leu Glu Ala Glu Lys Arg Lys Glu Ser Asp Lys
            20                  25                  30

Thr Gly Val Arg Leu Ser Asn Gln Met Arg Arg Ala Val Asn Pro Asn
        35                  40                  45

His Ser Leu Arg Cys Cys Pro Phe Gln Gly His Ser Ser Cys Arg Arg
    50                  55                  60

Cys Leu Cys Ala Ala Glu Gly Thr Ala Leu Gly Pro Cys His Thr Ile
65                  70                  75                  80

Arg Ile Tyr Ile His Met Cys Leu Leu Trp Glu Gln Gly Gln Gln Ile
                85                  90                  95

Thr Met Met Arg Val Ser Arg Asp His Thr Thr Asp Ser Gly Gly Glu
            100                 105                 110

Pro Gln Thr Thr Trp Gly Ser Gln Glu Ser Ser Leu Arg Lys Thr Asp
        115                 120                 125

Ser Arg Gly Tyr Leu Val Arg Ser Gln Trp Ser Arg Ile Ser Arg Ser
    130                 135                 140

Pro Ser Thr Lys Ala Pro Ser Ile Asp Glu Pro Arg Ser Arg Asn Thr
145                 150                 155                 160

Ser Ala Lys Leu Pro Ser Ser Ser Thr Ser Ser Arg Thr Pro Ser Thr
                165                 170                 175

Ser Pro Ser Leu His Asp Ser Ser Pro Pro Pro Leu Ser Gly Gln Pro
            180                 185                 190
```

```
Ser Leu Gln Pro Pro Ala Ser Pro Gln Leu Pro Arg Ser
        195                 200                 205


<210> 474
<211> 561
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="Uniprot ID:  P49902; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000339479"

<400> 474
Met Ser Thr Ser Trp Ser Asp Arg Leu Gln Asn Ala Ala Asp Met Pro
1               5                  10                  15


Ala Asn Met Asp Lys His Ala Leu Lys Lys Tyr Arg Arg Glu Ala Tyr
            20                  25                  30


His Arg Val Phe Val Asn Arg Ser Leu Ala Met Glu Lys Ile Lys Cys
        35                  40                  45


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


Tyr Glu Ser Leu Gly Phe Glu Leu Thr Val Glu Arg Leu Val Ser Ile
65                  70                  75                  80


Gly Tyr Pro Gln Glu Leu Leu Ser Phe Ala Tyr Asp Ser Thr Phe Pro
                85                  90                  95
```

```
Thr Arg Gly Leu Val Phe Asp Thr Leu Tyr Gly Asn Leu Leu Lys Val
            100                 105                 110

Asp Ala Tyr Gly Asn Leu Leu Val Cys Ala His Gly Phe Asn Phe Ile
        115                 120                 125

Arg Gly Pro Glu Thr Arg Glu Gln Tyr Pro Asn Lys Phe Ile Gln Arg
    130                 135                 140

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

Glu Thr Tyr Leu Leu Ala Cys Leu Val Asp Phe Phe Thr Asn Cys Pro
                165                 170                 175

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

Ser Tyr Arg Ser Met Phe Gln Asp Val Arg Asp Ala Val Asp Trp Val
        195                 200                 205

His Tyr Lys Gly Ser Leu Lys Glu Lys Thr Val Glu Asn Leu Glu Lys
    210                 215                 220

Tyr Val Val Lys Asp Gly Lys Leu Pro Leu Leu Leu Ser Arg Met Lys
225                 230                 235                 240

Glu Val Gly Lys Val Phe Leu Ala Thr Asn Ser Asp Tyr Lys Tyr Thr
                245                 250                 255

Asp Lys Ile Met Thr Tyr Leu Phe Asp Phe Pro His Gly Pro Lys Pro
            260                 265                 270

Gly Ser Ser His Arg Pro Trp Gln Ser Tyr Phe Asp Leu Ile Leu Val
        275                 280                 285

Asp Ala Arg Lys Pro Leu Phe Phe Gly Glu Gly Thr Val Leu Arg Gln
    290                 295                 300

Val Asp Thr Lys Thr Gly Lys Leu Lys Ile Gly Thr Tyr Thr Gly Pro
305                 310                 315                 320

Leu Gln His Gly Ile Val Tyr Ser Gly Gly Ser Ser Asp Thr Ile Cys
```

```
                325                 330                 335

Asp Leu Leu Gly Ala Lys Gly Lys Asp Ile Leu Tyr Ile Gly Asp His
            340                 345                 350

Ile Phe Gly Asp Ile Leu Lys Ser Lys Lys Arg Gln Gly Trp Arg Thr
        355                 360                 365

Phe Leu Val Ile Pro Glu Leu Ala Gln Glu Leu His Val Trp Thr Asp
    370                 375                 380

Lys Ser Ser Leu Phe Glu Glu Leu Gln Ser Leu Asp Ile Phe Leu Ala
385                 390                 395                 400

Glu Leu Tyr Lys His Leu Asp Ser Ser Ser Asn Glu Arg Pro Asp Ile
                405                 410                 415

Ser Ser Ile Gln Arg Arg Ile Lys Lys Val Thr His Asp Met Asp Met
            420                 425                 430

Cys Tyr Gly Met Met Gly Ser Leu Phe Arg Ser Gly Ser Arg Gln Thr
        435                 440                 445

Leu Phe Ala Ser Gln Val Met Arg Tyr Ala Asp Leu Tyr Ala Ala Ser
    450                 455                 460

Phe Ile Asn Leu Leu Tyr Tyr Pro Phe Ser Tyr Leu Phe Arg Ala Ala
465                 470                 475                 480

His Val Leu Met Pro His Glu Ser Thr Val Glu His Thr His Val Asp
                485                 490                 495

Ile Asn Glu Met Glu Ser Pro Leu Ala Thr Arg Asn Arg Thr Ser Val
            500                 505                 510

Asp Phe Lys Asp Thr Asp Tyr Lys Arg His Gln Leu Thr Arg Ser Ile
        515                 520                 525

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

Thr His Cys His Asp Glu Asp Asp Asp Glu Glu Glu Glu Glu Glu Glu
545                 550                 555                 560
```

Glu

<210> 475
<211> 561
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="Uniprot ID: P49902; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000383960"

<400> 475
Met Ser Thr Ser Trp Ser Asp Arg Leu Gln Asn Ala Ala Asp Met Pro
1 5 10 15

Ala Asn Met Asp Lys His Ala Leu Lys Lys Tyr Arg Arg Glu Ala Tyr
20 25 30

His Arg Val Phe Val Asn Arg Ser Leu Ala Met Glu Lys Ile Lys Cys
35 40 45

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

Tyr Glu Ser Leu Gly Phe Glu Leu Thr Val Glu Arg Leu Val Ser Ile
65 70 75 80

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

```
Thr Arg Gly Leu Val Phe Asp Thr Leu Tyr Gly Asn Leu Leu Lys Val
            100                 105                 110

Asp Ala Tyr Gly Asn Leu Leu Val Cys Ala His Gly Phe Asn Phe Ile
        115                 120                 125

Arg Gly Pro Glu Thr Arg Glu Gln Tyr Pro Asn Lys Phe Ile Gln Arg
    130                 135                 140

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

Glu Thr Tyr Leu Leu Ala Cys Leu Val Asp Phe Phe Thr Asn Cys Pro
                165                 170                 175

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

Ser Tyr Arg Ser Met Phe Gln Asp Val Arg Asp Ala Val Asp Trp Val
        195                 200                 205

His Tyr Lys Gly Ser Leu Lys Glu Lys Thr Val Glu Asn Leu Glu Lys
    210                 215                 220

Tyr Val Val Lys Asp Gly Lys Leu Pro Leu Leu Leu Ser Arg Met Lys
225                 230                 235                 240

Glu Val Gly Lys Val Phe Leu Ala Thr Asn Ser Asp Tyr Lys Tyr Thr
                245                 250                 255

Asp Lys Ile Met Thr Tyr Leu Phe Asp Phe Pro His Gly Pro Lys Pro
            260                 265                 270

Gly Ser Ser His Arg Pro Trp Gln Ser Tyr Phe Asp Leu Ile Leu Val
        275                 280                 285

Asp Ala Arg Lys Pro Leu Phe Phe Gly Glu Gly Thr Val Leu Arg Gln
    290                 295                 300

Val Asp Thr Lys Thr Gly Lys Leu Lys Ile Gly Thr Tyr Thr Gly Pro
305                 310                 315                 320

Leu Gln His Gly Ile Val Tyr Ser Gly Gly Ser Ser Asp Thr Ile Cys
```

```
                325                 330                 335

Asp Leu Leu Gly Ala Lys Gly Lys Asp Ile Leu Tyr Ile Gly Asp His
            340                 345                 350

Ile Phe Gly Asp Ile Leu Lys Ser Lys Lys Arg Gln Gly Trp Arg Thr
        355                 360                 365

Phe Leu Val Ile Pro Glu Leu Ala Gln Glu Leu His Val Trp Thr Asp
    370                 375                 380

Lys Ser Ser Leu Phe Glu Glu Leu Gln Ser Leu Asp Ile Phe Leu Ala
385                 390                 395                 400

Glu Leu Tyr Lys His Leu Asp Ser Ser Ser Asn Glu Arg Pro Asp Ile
                405                 410                 415

Ser Ser Ile Gln Arg Arg Ile Lys Lys Val Thr His Asp Met Asp Met
            420                 425                 430

Cys Tyr Gly Met Met Gly Ser Leu Phe Arg Ser Gly Ser Arg Gln Thr
        435                 440                 445

Leu Phe Ala Ser Gln Val Met Arg Tyr Ala Asp Leu Tyr Ala Ala Ser
    450                 455                 460

Phe Ile Asn Leu Leu Tyr Tyr Pro Phe Ser Tyr Leu Phe Arg Ala Ala
465                 470                 475                 480

His Val Leu Met Pro His Glu Ser Thr Val Glu His Thr His Val Asp
                485                 490                 495

Ile Asn Glu Met Glu Ser Pro Leu Ala Thr Arg Asn Arg Thr Ser Val
            500                 505                 510

Asp Phe Lys Asp Thr Asp Tyr Lys Arg His Gln Leu Thr Arg Ser Ile
        515                 520                 525

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

Thr His Cys His Asp Glu Asp Asp Asp Glu Glu Glu Glu Glu Glu Glu
545                 550                 555                 560
```

Glu

<210> 476
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396468"

<400> 476
Met Ser Thr Ser Trp Ser Asp Arg Leu Gln Asn Ala Ala Asp Met Pro
1 5 10 15

Ala Asn Met Asp Lys His Ala Leu Lys Lys Tyr Arg Arg Glu Ala Tyr
20 25 30

His Arg Val Phe Val Asn Arg Ser Leu Ala Met Glu Lys Ile Lys Cys
35 40 45

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

Tyr Glu Ser Leu Gly Phe Glu Leu Thr Val Glu Arg Leu Val Ser Ile
65 70 75 80

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

Thr Arg Gly Leu Val Phe Asp Thr Leu Tyr Gly Asn Leu Leu Lys Val
100 105 110

```
Asp Ala Tyr Gly Asn Leu Leu Val Cys Ala His Gly Phe Asn Phe Ile
        115                 120                 125

Arg Gly Ser Gln Val Ala Val Gln Lys Arg Pro Glu Thr Arg Glu Gln
    130                 135                 140

Tyr Pro Asn Lys Phe Ile Gln Arg Asp Asp Thr Glu Arg Phe Tyr Ile
145                 150                 155                 160

Leu Asn Thr Leu Phe Asn Leu Pro Glu Thr Tyr Leu Leu Ala Cys Leu
                165                 170                 175

Val Asp Phe Phe Thr Asn Cys Pro Arg Tyr Thr Ser Cys Glu Thr Gly
            180                 185                 190

Phe Lys Asp Gly Asp Leu Phe Met Ser Tyr Arg Ser Met Phe Gln Asp
        195                 200                 205

Val Arg Asp Ala Val Asp Trp Val His Tyr Lys Gly Ser Leu Lys Glu
    210                 215                 220

Lys Thr Val Glu Asn Leu Glu Lys Tyr Val Val Lys Asp Gly Lys Leu
225                 230                 235                 240

Pro Leu Leu Leu Ser Arg Met Lys Glu Val Gly Lys Val Phe Leu Ala
                245                 250                 255

Thr Asn Ser Asp Tyr Lys Tyr Thr Asp
            260                 265


<210> 477
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic II; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000408112"

<400> 477
Val Leu Arg Gln Val Asp Thr Lys Thr Gly Lys Leu Lys Ile Gly Thr
1   5   10   15

Tyr Thr Gly Pro Leu Gln His Gly Ile Val Tyr Ser Gly Gly Ser Ser
            20   25   30

Asp Thr Ile Cys Asp Leu Leu Gly Ala Lys Gly Lys Asp Ile Leu Tyr
        35   40   45

Ile Gly Asp His Ile Phe Gly Asp Ile Leu Lys Ser Lys Lys Arg Gln
    50   55   60

Gly Trp Arg Thr Phe Leu Val Ile Pro Glu Leu Ala Gln Glu Leu His
65   70   75   80

Val Trp Thr Asp Lys Ser Ser Leu Phe Glu Glu Leu Gln Ser Leu Asp
                85   90   95

Ile Phe Leu Ala Glu Leu Tyr Lys His Leu Asp Ser Ser Ser Asn Glu
            100   105   110

Arg Pro Asp Ile Ser Ser Ile Gln Arg Arg Ile Lys Met Pro His Glu
        115   120   125

Ser Thr Val Glu His Thr His Val Asp Ile Asn Glu Met Glu Ser Pro
    130   135   140

Leu Ala
145

<210> 478
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 86; "

<220>
<221> source

<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000411330"

<400> 478

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Val Ser Ile Gly Tyr Pro Gln Glu Leu Leu Ser Phe Ala Tyr Asp Ser
1               5                  10                  15

Thr Phe Pro Thr Arg Gly Leu Val Phe Asp Thr Leu Tyr Gly Asn Leu
            20                  25                  30

Leu Lys Val Asp Ala Tyr Gly Asn Leu Leu Val Cys Ala His Gly Phe
        35                  40                  45

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

Arg Glu Gln Tyr Pro Asn Lys Phe Ile Gln Arg Asp Asp Thr Glu Arg
65                  70                  75                  80

Phe Tyr Ile Leu Asn Thr Leu Phe Asn Leu Pro Glu Thr Tyr Leu Leu
                85                  90                  95

Ala Cys Leu Val Asp Phe Phe Thr Asn Cys Pro Arg Tyr Thr Ser Cys
            100                 105                 110

Glu Thr Gly Phe Lys Asp Gly Asp Leu Phe Met Ser Tyr Arg Ser Met
        115                 120                 125

Phe Gln Asp Val Arg Asp Ala Val Asp Trp Val His Tyr Lys Gly Ser
    130                 135                 140

Leu Lys Glu Lys Thr Val Glu Asn Leu Glu Lys Tyr Val Val Lys Asp
145                 150                 155                 160

Ser Lys Ser Ser Arg Ile Gln Tyr Phe Leu Lys Val Leu Trp
                165                 170
```

<210> 479

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

<220>
<221> source
<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000447664"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 479
Xaa Ser Leu Gly Phe Glu Leu Thr Val Glu Arg Leu Val Ser Ile Gly
1 5 10 15

Tyr Pro Gln Glu Leu Leu Ser Phe Ala Tyr Asp Ser Thr Phe Pro Thr
20 25 30

Arg Gly Leu Val Phe Asp Thr Leu Tyr Gly Asn Leu Leu Lys Val Asp
35 40 45

Ala Tyr Gly Asn Leu Leu Val Cys Ala His Gly Phe Asn Phe Ile Arg
50 55 60

Gly Pro Glu Thr Arg Glu Gln Tyr Pro Asn Lys Phe Ile Gln Arg Asp
65 70 75 80

Asp Thr Glu Arg Phe Tyr Ile Leu Asn Thr Leu Phe Asn Leu Pro Glu
85 90 95

Thr Tyr Leu Leu Ala Cys Leu Val Asp Phe Phe Thr Asn Cys Pro Arg
100 105 110

Tyr Thr Ser Glu Phe Ser Ala Ser Glu Arg Cys His Ile Ala Asn Leu

```
        115                 120                 125

Arg Asp Gly Thr Ala Pro Ala Ala Pro Cys Arg Leu Ser Pro Pro Thr
    130                 135                 140

Arg Pro Leu Ser Leu Pro Val Cys Cys Ser His His Phe
145                 150                 155


<210> 480
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000474091"

<400> 480
Met Ser Thr Ser Trp Ser Asp Arg Leu Gln Asn Ala Ala Asp Met Pro
1               5                   10                  15

Ala Asn Met Asp Lys His Ala Leu Lys Lys Tyr Arg Arg Glu Ala Tyr
            20                  25                  30

His Arg Val Phe Val Asn Arg Ser Leu Ala Met Glu Lys Ile Lys Cys
        35                  40                  45

Phe Gly Phe Asp Met Asp Tyr Thr Leu Ala Gly Glu Pro Val
    50                  55                  60


<210> 481
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 86; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C2; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic II; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000474247"

<400> 481
Met Ser Thr Ser Trp Ser Asp Arg Leu Gln Asn Ala Ala Asp Met Pro
1 5 10 15

Ala Asn Met Asp Lys His Ala Leu Lys Lys Tyr Arg Arg Glu Ala Tyr
20 25 30

His Arg Arg Ala Ser Val Thr Pro Ser Arg Leu Glu
35 40

<210> 482
<211> 336
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 87; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C3A; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, cytosolic IIIA; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H0P0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000242210"

<400> 482
Met Arg Ala Pro Ser Met Asp Arg Ala Ala Val Ala Arg Val Gly Ala
1 5 10 15

```
Val Ala Ser Ala Ser Val Cys Ala Leu Val Ala Gly Val Val Leu Ala
            20                  25                  30

Gln Tyr Ile Phe Thr Leu Lys Arg Lys Thr Gly Arg Lys Thr Lys Ile
        35                  40                  45

Ile Glu Met Met Pro Glu Phe Gln Lys Ser Ser Val Arg Ile Lys Asn
    50                  55                  60

Pro Thr Arg Val Glu Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala
65                  70                  75                  80

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

Ser Tyr Lys Gly Lys Arg Cys Pro Thr Cys His Asn Ile Ile Asp Asn
            100                 105                 110

Cys Lys Leu Val Thr Asp Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys
        115                 120                 125

Glu Lys Tyr Tyr Ala Ile Glu Val Asp Pro Val Leu Thr Val Glu Glu
    130                 135                 140

Lys Tyr Pro Tyr Met Val Glu Trp Tyr Thr Lys Ser His Gly Leu Leu
145                 150                 155                 160

Val Gln Gln Ala Leu Pro Lys Ala Lys Leu Lys Glu Ile Val Ala Glu
                165                 170                 175

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

Gln Gln His Ser Ile Pro Val Phe Ile Phe Ser Ala Gly Ile Gly Asp
        195                 200                 205

Val Leu Glu Glu Val Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val
    210                 215                 220

Lys Val Val Ser Asn Phe Met Asp Phe Asp Glu Thr Gly Val Leu Lys
225                 230                 235                 240
```

```
Gly Phe Lys Gly Glu Leu Ile His Val Phe Asn Lys His Asp Gly Ala
                245                 250                 255

Leu Arg Asn Thr Glu Tyr Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile
            260                 265                 270

Ile Leu Leu Gly Asp Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val
        275                 280                 285

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

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

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


<210> 483
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Met Pro Glu Phe Gln Lys Ser Ser Val Arg Ile Lys Asn Pro Thr Arg
1               5                   10                  15

Val Glu Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala Ala Lys Leu
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```
            20                  25                  30

Gln Ile Ile Thr Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys
        35                  40                  45

Gly Lys Arg Cys Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu
    50                  55                  60

Val Thr Asp Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr
65                  70                  75                  80

Tyr Ala Ile Glu Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro
                85                  90                  95

Tyr Met Val Glu Trp Tyr Thr Lys Ser His Gly Leu Leu Val Gln Gln
            100                 105                 110

Ala Leu Pro Lys Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val
        115                 120                 125

Met Leu Lys Glu Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His
    130                 135                 140

Ser Ile Pro Val Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu
145                 150                 155                 160

Glu Val Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val
                165                 170                 175

Ser Asn Phe Met Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys
            180                 185                 190

Gly Glu Leu Ile His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn
        195                 200                 205

Thr Glu Tyr Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile Ile Leu Leu
    210                 215                 220

Gly Asp Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val
225                 230                 235                 240

Glu His Ile Leu Lys Ile Gly Tyr Leu Asn Asp Arg Val Asp Glu Leu
                245                 250                 255
```

```
Leu Glu Lys Tyr Met Asp Ser Tyr Asp Ile Val Leu Val Gln Asp Glu
            260                 265                 270


Ser Leu Glu Val Ala Asn Ser Ile Leu Gln Lys Ile Leu
        275                 280                 285


<210> 484
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<400> 484
Met Thr Asn Gln Glu Ser Ala Val His Val Lys Met Met Pro Glu Phe
1               5                   10                  15


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


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


Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys Gly Lys Arg Cys
    50                  55                  60


Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu Val Thr Asp Glu
65                  70                  75                  80
```

Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr Tyr Ala Ile Glu
85 90 95

Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro Tyr Met Val Glu
100 105 110

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

Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val Met Leu Lys Glu
130 135 140

Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His Ser Ile Pro Val
145 150 155 160

Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu Glu Val Ile Arg
165 170 175

Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val Ser Asn Phe Met
180 185 190

Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys Gly Glu Leu Ile
195 200 205

His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn Thr Glu Tyr Phe
210 215 220

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

Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val Glu His Ile Leu
245 250 255

Lys Ile Gly Tyr Leu Asn Asp Arg Val Asp Glu Leu Leu Glu Lys Tyr
260 265 270

Met Asp Ser Tyr Asp Ile Val Leu Val Gln Asp Glu Ser Leu Glu Val
275 280 285

Ala Asn Ser Ile Leu Gln Lys Ile Leu
290 295

<210> 485

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<400> 485

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

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

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

Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys Gly Lys Arg Cys
    50                  55                  60

Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu Val Thr Asp Glu
65                  70                  75                  80

Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr Tyr Ala Ile Glu
                85                  90                  95

Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro Tyr Met Val Glu
            100                 105                 110

Trp Tyr Thr Lys Ser His Gly Leu Leu Val Gln Gln Ala Leu Pro Lys
        115                 120                 125
```

```
Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val Met Leu Lys Glu
    130                 135                 140

Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His Ser Ile Pro Val
145                 150                 155                 160

Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu Glu Val Ile Arg
                165                 170                 175

Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val Ser Asn Phe Met
            180                 185                 190

Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys Gly Glu Leu Ile
        195                 200                 205

His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn Thr Glu Tyr Phe
    210                 215                 220

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

Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val Glu His Ile Leu
                245                 250                 255

Lys Ile Gly Tyr Leu Asn Asp Arg Val Asp Glu Leu Leu Glu Lys Tyr
            260                 265                 270

Met Asp Ser Tyr Asp Ile Val Leu Val Gln Asp Glu Ser Leu Glu Val
        275                 280                 285

Ala Asn Ser Ile Leu Gln Lys Ile Leu
    290                 295
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<400> 486

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Met Pro Glu Phe Gln Lys Ser Ser Val Arg Ile Lys Asn Pro Thr Arg
1               5                  10                  15

Val Glu Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala Ala Lys Leu
            20                  25                  30

Gln Ile Ile Thr Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys
        35                  40                  45

Gly Lys Arg Cys Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu
    50                  55                  60

Val Thr Asp Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr
65                  70                  75                  80

Tyr Ala Ile Glu Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro
                85                  90                  95

Tyr Met Val Glu Trp Tyr Thr Lys Ser His Gly Leu Leu Val Gln Gln
            100                 105                 110

Ala Leu Pro Lys Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val
        115                 120                 125

Met Leu Lys Glu Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His
    130                 135                 140

Ser Ile Pro Val Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu
145                 150                 155                 160

Glu Val Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val
                165                 170                 175
```

```
Ser Asn Phe Met Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys
            180                 185                 190

Gly Glu Leu Ile His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn
        195                 200                 205

Thr Glu Tyr Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile Ile Leu Leu
    210                 215                 220

Gly Asp Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val
225                 230                 235                 240

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

Leu Glu Lys Tyr Met Asp Ser Tyr Asp Ile Val Leu Val Gln Asp Glu
            260                 265                 270

Ser Leu Glu Val Ala Asn Ser Ile Leu Gln Lys Ile Leu
        275                 280                 285


<210> 487
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<400> 487
Met Thr Asn Gln Glu Ser Ala Val His Val Lys Met Met Pro Glu Phe
1               5                   10                  15
```

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

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

Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys Gly Lys Arg Cys
    50                  55                  60

Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu Val Thr Asp Glu
65                  70                  75                  80

Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr Tyr Ala Ile Glu
                85                  90                  95

Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro Tyr Met Val Glu
            100                 105                 110

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

Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val Met Leu Lys Glu
    130                 135                 140

Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His Ser Ile Pro Val
145                 150                 155                 160

Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu Glu Val Ile Arg
                165                 170                 175

Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val Ser Asn Phe Met
            180                 185                 190

Asp Phe Asp Glu Thr Val Arg Ile Ser Asn Arg Ser Ser
        195                 200                 205


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<400> 488
Met Arg Ala Pro Ser Met Asp Arg Ala Ala Val Ala Arg Val Gly Ala
1 5 10 15

Val Ala Ser Ala Ser Val Cys Ala Leu Val Ala Gly Val Val Leu Ala
20 25 30

Gln Tyr Ile Phe Thr Leu Lys Arg Lys Thr Gly Arg Lys Thr Lys Ile
35 40 45

Ile Glu Met Lys Ile Gly
50

<210> 489
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<400> 489
Met Pro Glu Phe Gln Lys Ser Ser Val Arg Ile Lys Asn Pro Thr Arg
1 5 10 15

Val Glu Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala Ala Lys Leu
            20   25   30

Gln Ile Ile Thr Asp Phe Asp Met Thr Leu
        35   40

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<400> 490
Met Asp Arg Ala Ala Val Ala Arg Val Gly Ala Val Ala Ser Ala Ser
1   5   10   15

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

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

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

Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala Ala Lys Leu Gln Ile
65   70   75   80

Ile Thr Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys Gly Lys
                85   90   95

Arg Cys Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu Val Thr
            100   105   110

```
Asp Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr Tyr Ala
        115                 120                 125

Ile Glu Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro Tyr Met
    130                 135                 140

Val Glu Trp Tyr Thr Lys Ser His Gly Leu Leu Val Gln Gln Ala Leu
145                 150                 155                 160

Pro Lys Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val Met Leu
                165                 170                 175

Lys Glu Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His Ser Ile
            180                 185                 190

Pro Val Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu Glu Val
        195                 200                 205

Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val Ser Asn
    210                 215                 220

Phe Met Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys Gly Glu
225                 230                 235                 240

Leu Ile His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn Thr Glu
                245                 250                 255

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

Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val Glu His
        275                 280                 285

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

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

Glu Val Ala Asn Ser Ile Leu Gln Lys Ile Leu
                325                 330
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<210> 491
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<400> 491
Met Arg Ala Pro Ser Met Asp Arg Ala Ala Val Ala Arg Val Gly Ala
1   5   10   15

Val Ala Ser Ala Ser Val Cys Ala Leu Val Ala Gly Val Val Leu Ala
            20   25   30

Gln Tyr Ile Phe Thr Leu Lys Arg Lys Thr Gly Arg Lys Thr Lys Ile
        35   40   45

Ile Glu Met Met Pro Glu Phe Gln Lys Ser Ser Val Arg Ile Lys Asn
    50   55   60

Pro Thr Arg Val Glu Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala
65   70   75   80

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

Ser Tyr Lys Gly Lys Arg Cys Pro Thr Cys His Asn Ile Ile Asp Asn
            100   105   110

Cys Lys Leu Val Thr Asp Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys

```
        115                 120                 125

Glu Lys Tyr Tyr Ala Ile Glu Val Asp Pro Val Leu Thr Val Glu Glu
    130                 135                 140

Lys Tyr Pro Tyr Met Val Glu Trp Tyr Thr Lys Ser His Gly Leu Leu
145                 150                 155                 160

Val Gln Gln Ala Leu Pro Lys Ala Lys Leu Lys Glu Ile Val Ala Glu
                165                 170                 175

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

Gln Gln His Ser Ile Pro Val Phe Ile Phe Ser Ala Gly Ile Gly Asp
        195                 200                 205

Val Leu Glu Glu Val Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val
    210                 215                 220

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

Gly Phe Lys Gly Glu Leu Ile His Val Phe Asn Lys His Asp Gly Ala
                245                 250                 255

Leu Arg Asn Thr Glu Tyr Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile
            260                 265                 270

Ile Leu Leu Gly Asp Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val
        275                 280                 285

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

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

Gln Asp Glu Ser Leu Glu Val Ala Asn Ser Ile Leu Gln Lys Ile Leu
                325                 330                 335
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Met Ala Glu Glu Val Ser Thr Leu Met Lys Ala Thr Val Leu Met Arg
1   5   10   15

Gln Pro Gly Arg Val Gln Glu Ile Val Gly Ala Leu Arg Lys Gly Gly
            20   25   30

Gly Asp Arg Leu Gln Val Ile Ser Asp Phe Asp Met Thr Leu Ser Arg
        35   40   45

Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser Tyr Asn Ile Leu Asp
    50   55   60

Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys Glu Leu Thr Ala Leu
65   70   75   80

Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro His Arg Thr Val Lys
                85   90   95

Glu Lys Leu Pro His Met Val Glu Trp Trp Thr Lys Ala His Asn Leu
            100   105   110

Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile Ala Gln Val Val Arg
        115   120   125

```
Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys Thr Phe Phe Asn Thr
    130                 135                 140

Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe Ser Ala Gly Ile Gly
145                 150                 155                 160

Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys Val Phe His Pro Asn
                165                 170                 175

Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn Glu Asp Gly Phe Leu
            180                 185                 190

Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr Asn Lys Asn Ser Ser
        195                 200                 205

Ala Cys Glu Asn Ser Gly Tyr Phe Gln Gln Leu Glu Gly Lys Thr Asn
    210                 215                 220

Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu Thr Met Ala Asp Gly
225                 230                 235                 240

Val Pro Gly Val Gln Asn Ile Leu Lys Ile Gly Phe Leu Asn Asp Lys
                245                 250                 255

Val Glu Glu Arg Arg Glu Arg Tyr Met Asp Ser Tyr Asp Ile Val Leu
            260                 265                 270

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

Leu Cys Gln Gly Val Gln Leu Glu Met Gln Gly Pro
    290                 295                 300


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<400> 493
Met Ala Glu Glu Val Arg Arg Glu Glu Ala Ser Gly Val Gly Arg Ala
1 5 10 15

Arg Thr Pro Thr Pro Gly Ala Leu Arg Ala Pro Gln Leu Val Thr Glu
20 25 30

Ala Pro Pro Leu His Pro Gly Glu His Pro Asp Glu Gly His Gly Pro
35 40 45

Asp Ala Ala Ala Trp Ala Gly Ala Gly Asp Arg Gly Arg Pro Pro Gln
50 55 60

Gly Arg Arg Arg Pro Val Thr Gly Asp Phe
65 70

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<400> 494
Met Ala Glu Glu Val Ser Thr Leu Met Lys Ala Thr Val Leu Met Arg
1 5 10 15

Gln Pro Gly Arg Val Gln Glu Ile Val Gly Ala Leu Arg Lys Gly Gly
20 25 30

Gly Asp Arg Leu Gln Val Ile Ser Asp Phe Asp Met Thr Leu Ser Arg
35 40 45

Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser Tyr Asn Ile Leu Asp
50 55 60

Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys Glu Leu Thr Ala Leu
65 70 75 80

Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro His Arg Thr Val Lys
85 90 95

Glu Lys Leu Pro His Met Val Glu Trp Glu Gly Tyr Lys Thr Phe Phe
100 105 110

Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe Ser Ala Gly
115 120 125

Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys Val Phe His
130 135 140

Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn Glu Asp Gly
145 150 155 160

Phe Leu Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr Asn Lys Asn
165 170 175

Ser Ser Ala Cys Glu Asn Ser Gly Tyr Phe Gln Gln Leu Glu Gly Lys
180 185 190

Thr Asn Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu Thr Met Ala
195 200 205

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

Asp Lys Val
225

<210> 495

<211> 200
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Met Ala Glu Glu Val Ile Ser Asp Phe Asp Met Thr Leu Ser Arg Phe
1               5                  10                  15

Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser Tyr Asn Ile Leu Asp Asn
            20                  25                  30

Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys Glu Leu Thr Ala Leu Leu
        35                  40                  45

His His Tyr Tyr Pro Ile Glu Ile Asp Pro His Arg Thr Val Lys Glu
    50                  55                  60

Lys Leu Pro His Met Val Glu Trp Trp Thr Lys Ala His Asn Leu Leu
65                  70                  75                  80

Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile Ala Gln Val Val Arg Glu
                85                  90                  95

Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys Thr Phe Phe Asn Thr Leu
            100                 105                 110

Tyr His Asn Asn Ile Pro Leu Phe Ile Phe Ser Ala Gly Ile Gly Asp
        115                 120                 125

Ile Leu Glu Glu Ile Ile Arg Gln Met Lys Val Phe His Pro Asn Ile
    130                 135                 140
```

```
His Ile Val Ser Asn Tyr Met Asp Phe Asn Glu Asp Val Glu Glu Arg
145                 150                 155                 160


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


Thr Leu Asp Val Val Asn Gly Leu Leu Gln His Ile Leu Cys Gln Gly
            180                 185                 190


Val Gln Leu Glu Met Gln Gly Pro
        195                 200


<210> 496
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 88; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C3B; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, cytosolic IIIB; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431066"

<400> 496
Met Ala Glu Glu Val Ser Thr Leu Met Lys Ala Thr Val Leu Met Arg
1               5                   10                  15


Gln Pro Gly Arg Val Gln Glu Ile Val Gly Ala Leu Arg Lys Gly Gly
            20                  25                  30


Gly Asp Arg Leu Gln Ile Ser Gln Tyr Gly His Ala Ala Ser Ser Asn
        35                  40                  45


Trp Thr Glu Gly Ala His Thr Ser Thr
    50                  55


<210> 497
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<211> 105
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 88; "

<220>
<221> source
<223> /note="Gene Symbol: NT5C3B; "

<220>
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<223> /note="Gene Name:
5'-nucleotidase, cytosolic IIIB; "

<220>
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<223> /note="ENSP ID: ENSP00000475710"

<400> 497
Ala His Asn Leu Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile Ala
1 5 10 15

Gln Val Val Arg Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys Thr
20 25 30

Phe Phe Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe Ser
35 40 45

Ala Gly Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys Val
50 55 60

Phe His Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn Glu
65 70 75 80

Asp Val Ser Gln Ile Leu Phe Gly Leu Gly Lys Asp Glu Gly Trp Gly
85 90 95

Pro Pro Ala Arg Ala Val Asn Ser Ala
100 105

<210> 498
<211> 574
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 89; "

<220>
<221> source
<223> /note="Gene Symbol: NT5E; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, ecto (CD73); "

<220>
<221> source
<223> /note="Uniprot ID: P21589; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000257770"

<400> 498

```
Met Cys Pro Arg Ala Ala Arg Ala Pro Ala Thr Leu Leu Leu Ala Leu
1               5                   10                  15

Gly Ala Val Leu Trp Pro Ala Ala Gly Ala Trp Glu Leu Thr Ile Leu
            20                  25                  30

His Thr Asn Asp Val His Ser Arg Leu Glu Gln Thr Ser Glu Asp Ser
        35                  40                  45

Ser Lys Cys Val Asn Ala Ser Arg Cys Met Gly Gly Val Ala Arg Leu
    50                  55                  60

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

Leu Asp Ala Gly Asp Gln Tyr Gln Gly Thr Ile Trp Phe Thr Val Tyr
                85                  90                  95

Lys Gly Ala Glu Val Ala His Phe Met Asn Ala Leu Arg Tyr Asp Ala
            100                 105                 110

Met Ala Leu Gly Asn His Glu Phe Asp Asn Gly Val Glu Gly Leu Ile
        115                 120                 125

Glu Pro Leu Leu Lys Glu Ala Lys Phe Pro Ile Leu Ser Ala Asn Ile
    130                 135                 140

Lys Ala Lys Gly Pro Leu Ala Ser Gln Ile Ser Gly Leu Tyr Leu Pro
```

145 150 155 160

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

Thr Ser Lys Glu Thr Pro Phe Leu Ser Asn Pro Gly Thr Asn Leu Val
180 185 190

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

Thr Leu Asn Val Asn Lys Ile Ile Ala Leu Gly His Ser Gly Phe Glu
210 215 220

Met Asp Lys Leu Ile Ala Gln Lys Val Arg Gly Val Asp Val Val Val
225 230 235 240

Gly Gly His Ser Asn Thr Phe Leu Tyr Thr Gly Asn Pro Pro Ser Lys
245 250 255

Glu Val Pro Ala Gly Lys Tyr Pro Phe Ile Val Thr Ser Asp Asp Gly
260 265 270

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

Tyr Leu Lys Ile Glu Phe Asp Glu Arg Gly Asn Val Ile Ser Ser His
290 295 300

Gly Asn Pro Ile Leu Leu Asn Ser Ser Ile Pro Glu Asp Pro Ser Ile
305 310 315 320

Lys Ala Asp Ile Asn Lys Trp Arg Ile Lys Leu Asp Asn Tyr Ser Thr
325 330 335

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

Cys Arg Phe Arg Glu Cys Asn Met Gly Asn Leu Ile Cys Asp Ala Met
355 360 365

Ile Asn Asn Asn Leu Arg His Thr Asp Glu Met Phe Trp Asn His Val
370 375 380

```
Ser Met Cys Ile Leu Asn Gly Gly Gly Ile Arg Ser Pro Ile Asp Glu
385                 390                 395                 400

Arg Asn Asn Gly Thr Ile Thr Trp Glu Asn Leu Ala Ala Val Leu Pro
                405                 410                 415

Phe Gly Gly Thr Phe Asp Leu Val Gln Leu Lys Gly Ser Thr Leu Lys
            420                 425                 430

Lys Ala Phe Glu His Ser Val His Arg Tyr Gly Gln Ser Thr Gly Glu
        435                 440                 445

Phe Leu Gln Val Gly Gly Ile His Val Val Tyr Asp Leu Ser Arg Lys
    450                 455                 460

Pro Gly Asp Arg Val Val Lys Leu Asp Val Leu Cys Thr Lys Cys Arg
465                 470                 475                 480

Val Pro Ser Tyr Asp Pro Leu Lys Met Asp Glu Val Tyr Lys Val Ile
                485                 490                 495

Leu Pro Asn Phe Leu Ala Asn Gly Gly Asp Gly Phe Gln Met Ile Lys
            500                 505                 510

Asp Glu Leu Leu Arg His Asp Ser Gly Asp Gln Asp Ile Asn Val Val
        515                 520                 525

Ser Thr Tyr Ile Ser Lys Met Lys Val Ile Tyr Pro Ala Val Glu Gly
    530                 535                 540

Arg Ile Lys Phe Ser Thr Gly Ser His Cys His Gly Ser Phe Ser Leu
545                 550                 555                 560

Ile Phe Leu Ser Leu Trp Ala Val Ile Phe Val Leu Tyr Gln
                565                 570
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<210> 499
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 89; "

<220>
<221> source
<223> /note="Gene Symbol: NT5E; "

<220>
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<223> /note="Gene Name:
5'-nucleotidase, ecto (CD73); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358660"

<400> 499

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Met Cys Pro Arg Ala Ala Arg Ala Pro Ala Thr Leu Leu Leu Ala Leu
1               5                  10                  15

Gly Ala Val Leu Trp Pro Ala Ala Gly Ala Trp Glu Leu Thr Ile Leu
            20                  25                  30

His Thr Asn Asp Val His Ser Arg Leu Glu Gln Thr Ser Glu Asp Ser
        35                  40                  45

Ser Lys Cys Val Asn Ala Ser Arg Cys Met Gly Gly Val Ala Arg Leu
    50                  55                  60

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

Leu Asp Ala Gly Asp Gln Tyr Gln Gly Thr Ile Trp Phe Thr Val Tyr
                85                  90                  95

Lys Gly Ala Glu Val Ala His Phe Met Asn Ala Leu Arg Tyr Asp Ala
            100                 105                 110

Met Ala Leu Gly Asn His Glu Phe Asp Asn Gly Val Glu Gly Leu Ile
        115                 120                 125

Glu Pro Leu Leu Lys Glu Ala Lys Phe Pro Ile Leu Ser Ala Asn Ile
    130                 135                 140

Lys Ala Lys Gly Pro Leu Ala Ser Gln Ile Ser Gly Leu Tyr Leu Pro
145                 150                 155                 160

Tyr Lys Val Leu Pro Val Gly Asp Glu Val Val Gly Ile Val Gly Tyr
```

```
                165                 170                 175

Thr Ser Lys Glu Thr Pro Phe Leu Ser Asn Pro Gly Thr Asn Leu Val
            180                 185                 190

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

Thr Leu Asn Val Asn Lys Ile Ile Ala Leu Gly His Ser Gly Phe Glu
    210                 215                 220

Met Asp Lys Leu Ile Ala Gln Lys Val Arg Gly Val Asp Val Val Val
225                 230                 235                 240

Gly Gly His Ser Asn Thr Phe Leu Tyr Thr Gly Asn Cys Phe Lys Arg
                245                 250                 255

Ile Ala Trp Ala Arg Met Ser Arg
            260


<210> 500
<211> 524
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 89; "

<220>
<221> source
<223> /note="Gene Symbol: NT5E; "

<220>
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<223> /note="Gene Name:
      5'-nucleotidase, ecto (CD73); "

<220>
<221> source
<223> /note="Uniprot ID:  P21589; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358665"

<400> 500
Met Cys Pro Arg Ala Ala Arg Ala Pro Ala Thr Leu Leu Leu Ala Leu
1               5                   10                  15
```

```
Gly Ala Val Leu Trp Pro Ala Ala Gly Ala Trp Glu Leu Thr Ile Leu
            20                  25                  30

His Thr Asn Asp Val His Ser Arg Leu Glu Gln Thr Ser Glu Asp Ser
        35                  40                  45

Ser Lys Cys Val Asn Ala Ser Arg Cys Met Gly Gly Val Ala Arg Leu
    50                  55                  60

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

Leu Asp Ala Gly Asp Gln Tyr Gln Gly Thr Ile Trp Phe Thr Val Tyr
                85                  90                  95

Lys Gly Ala Glu Val Ala His Phe Met Asn Ala Leu Arg Tyr Asp Ala
            100                 105                 110

Met Ala Leu Gly Asn His Glu Phe Asp Asn Gly Val Glu Gly Leu Ile
        115                 120                 125

Glu Pro Leu Leu Lys Glu Ala Lys Phe Pro Ile Leu Ser Ala Asn Ile
    130                 135                 140

Lys Ala Lys Gly Pro Leu Ala Ser Gln Ile Ser Gly Leu Tyr Leu Pro
145                 150                 155                 160

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

Thr Ser Lys Glu Thr Pro Phe Leu Ser Asn Pro Gly Thr Asn Leu Val
            180                 185                 190

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

Thr Leu Asn Val Asn Lys Ile Ile Ala Leu Gly His Ser Gly Phe Glu
    210                 215                 220

Met Asp Lys Leu Ile Ala Gln Lys Val Arg Gly Val Asp Val Val Val
225                 230                 235                 240
```

```
Gly Gly His Ser Asn Thr Phe Leu Tyr Thr Gly Asn Pro Pro Ser Lys
                245                 250                 255

Glu Val Pro Ala Gly Lys Tyr Pro Phe Ile Val Thr Ser Asp Asp Gly
            260                 265                 270

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

Tyr Leu Lys Ile Glu Phe Asp Glu Arg Gly Asn Val Ile Ser Ser His
    290                 295                 300

Gly Asn Pro Ile Leu Leu Asn Ser Ser Ile Pro Glu Asp Pro Ser Ile
305                 310                 315                 320

Lys Ala Asp Ile Asn Lys Trp Arg Ile Lys Leu Asp Asn Tyr Ser Thr
                325                 330                 335

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

Cys Arg Phe Arg Glu Cys Asn Met Gly Asn Leu Ile Cys Asp Ala Met
        355                 360                 365

Ile Asn Asn Asn Leu Arg His Thr Asp Glu Met Phe Trp Asn His Val
    370                 375                 380

Ser Met Cys Ile Leu Asn Gly Gly Gly Ile Arg Ser Pro Ile Asp Glu
385                 390                 395                 400

Arg Asn Asn Gly Ile His Val Val Tyr Asp Leu Ser Arg Lys Pro Gly
                405                 410                 415

Asp Arg Val Val Lys Leu Asp Val Leu Cys Thr Lys Cys Arg Val Pro
            420                 425                 430

Ser Tyr Asp Pro Leu Lys Met Asp Glu Val Tyr Lys Val Ile Leu Pro
        435                 440                 445

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

Leu Leu Arg His Asp Ser Gly Asp Gln Asp Ile Asn Val Val Ser Thr
```

```
465                 470                 475                 480

Tyr Ile Ser Lys Met Lys Val Ile Tyr Pro Ala Val Glu Gly Arg Ile
                485                 490                 495

Lys Phe Ser Thr Gly Ser His Cys His Gly Ser Phe Ser Leu Ile Phe
            500                 505                 510

Leu Ser Leu Trp Ala Val Ile Phe Val Leu Tyr Gln
        515                 520


<210> 501
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 89; "

<220>
<221> source
<223> /note="Gene Symbol: NT5E; "

<220>
<221> source
<223> /note="Gene Name:
      5'-nucleotidase, ecto (CD73); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387630"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 501
Xaa Asn Pro Ile Leu Leu Asn Ser Ser Ile Pro Glu Asp Pro Ser Ile
1               5                   10                  15

Lys Ala Asp Ile Asn Lys Trp Arg Ile Lys Leu Asp Asn Tyr Ser Thr
            20                  25                  30

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

Cys Arg Phe Arg Glu Cys Asn Met Gly Asn Leu Ile Cys Asp Ala Met
```

```
    50                  55                  60

Ile Asn Asn Asn Leu Arg His Thr Asp Glu Met Phe Trp Asn His Val
65                  70                  75                  80

Ser Met Cys Ile Leu Asn Gly Gly Gly Ile Arg Ser Pro Ile Asp Glu
                85                  90                  95

Arg Asn Asn Gly Thr Ile Thr Trp Glu Asn Leu Ala Ala Val Leu Pro
            100                 105                 110

Phe Gly Gly Thr Phe Asp Leu Val Gln Leu Lys Gly Ser Thr Leu Lys
        115                 120                 125

Lys Ala Phe Glu His Ser Val His Arg Tyr Gly Gln Ser Thr Gly Glu
    130                 135                 140

Phe Leu Gln Val Gly Asp Leu Lys Glu Cys Cys Pro Ile Cys Ile Asn
145                 150                 155                 160

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

Thr Trp Phe
```

<210> 502
<211> 230
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 89; "

<220>
<221> source
<223> /note="Gene Symbol: NT5E; "

<220>
<221> source
<223> /note="Gene Name:
5'-nucleotidase, ecto (CD73); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414674"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 502
Xaa Asp Val Val Val Gly Gly His Ser Asn Thr Phe Leu Tyr Thr Gly
1 5 10 15

Asn Pro Pro Ser Lys Glu Val Pro Ala Gly Lys Tyr Pro Phe Ile Val
20 25 30

Thr Ser Asp Asp Gly Arg Lys Val Pro Val Val Gln Ala Tyr Ala Phe
35 40 45

Gly Lys Tyr Leu Gly Tyr Leu Lys Ile Glu Phe Asp Glu Arg Gly Asn
50 55 60

Val Ile Ser Ser His Gly Asn Pro Ile Leu Leu Asn Ser Ser Ile Pro
65 70 75 80

Glu Asp Pro Ser Ile Lys Ala Asp Ile Asn Lys Trp Arg Ile Lys Leu
85 90 95

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

Gly Ser Ser Gln Ser Cys Arg Phe Arg Glu Cys Asn Met Gly Asn Leu
115 120 125

Ile Cys Asp Ala Met Ile Asn Asn Asn Leu Arg His Thr Asp Glu Met
130 135 140

Phe Trp Asn His Val Ser Met Cys Ile Leu Asn Gly Gly Gly Ile Arg
145 150 155 160

Ser Pro Ile Asp Glu Arg Asn Asn Gly Ile His Val Val Tyr Asp Leu
165 170 175

Ser Arg Lys Pro Gly Asp Arg Val Val Lys Leu Asp Val Leu Cys Thr
180 185 190

Lys Cys Arg Val Pro Ser Tyr Asp Pro Leu Lys Met Asp Glu Val Tyr
195 200 205

```
Lys Val Ile Leu Pro Asn Phe Leu Ala Asn Gly Gly Asp Gly Phe Gln
    210                 215                 220


Met Ile Lys Asp Glu Leu
225                 230


<210> 503
<211> 1288
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 90; "

<220>
<221> source
<223> /note="Gene Symbol: OPLAH; "

<220>
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<223> /note="Gene Name:
      5-oxoprolinase (ATP-hydrolysing); "

<220>
<221> source
<223> /note="Uniprot ID:  O14841; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480476"

<400> 503
Met Gly Ser Pro Glu Gly Arg Phe His Phe Ala Ile Asp Arg Gly Gly
1               5                   10                  15


Thr Phe Thr Asp Val Phe Ala Gln Cys Pro Gly Gly His Val Arg Val
            20                  25                  30


Leu Lys Leu Leu Ser Glu Asp Pro Ala Asn Tyr Ala Asp Ala Pro Thr
        35                  40                  45


Glu Gly Ile Arg Arg Ile Leu Glu Gln Glu Ala Gly Met Leu Leu Pro
    50                  55                  60


Arg Asp Gln Pro Leu Asp Ser Ser His Ile Ala Ser Ile Arg Met Gly
65                  70                  75                  80
```

```
Thr Thr Val Ala Thr Asn Ala Leu Leu Glu Arg Lys Gly Glu Arg Val
                85                  90                  95

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

Gln Ala Arg Gly Asp Leu Phe Asp Leu Ala Val Pro Met Pro Glu Val
        115                 120                 125

Leu Tyr Glu Glu Val Leu Glu Val Asp Glu Arg Val Val Leu His Arg
    130                 135                 140

Gly Glu Ala Gly Thr Gly Thr Pro Val Lys Gly Arg Thr Gly Asp Leu
145                 150                 155                 160

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

Glu Gly Leu Leu Ser Arg Gly Ile Arg Ser Leu Ala Val Val Leu Met
            180                 185                 190

His Ser Tyr Thr Trp Ala Gln His Glu Gln Gln Val Gly Val Leu Ala
        195                 200                 205

Arg Glu Leu Gly Phe Thr His Val Ser Leu Ser Ser Glu Ala Met Pro
    210                 215                 220

Met Val Arg Ile Val Pro Arg Gly His Thr Ala Cys Ala Asp Ala Tyr
225                 230                 235                 240

Leu Thr Pro Ala Ile Gln Arg Tyr Val Gln Gly Phe Cys Arg Gly Phe
                245                 250                 255

Gln Gly Gln Leu Lys Asp Val Gln Val Leu Phe Met Arg Ser Asp Gly
            260                 265                 270

Gly Leu Ala Pro Met Asp Thr Phe Ser Gly Ser Ser Ala Val Leu Ser
        275                 280                 285

Gly Pro Ala Gly Gly Val Val Gly Tyr Ser Ala Thr Thr Tyr Gln Gln
    290                 295                 300

Glu Gly Gly Gln Pro Val Ile Gly Phe Asp Met Gly Gly Thr Ser Thr
```

305 310 315 320

Asp Val Ser Arg Tyr Ala Gly Glu Phe Glu His Val Phe Glu Ala Ser
325 330 335

Thr Ala Gly Val Thr Leu Gln Ala Pro Gln Leu Asp Ile Asn Thr Val
340 345 350

Ala Ala Gly Gly Gly Ser Arg Leu Phe Phe Arg Ser Gly Leu Phe Val
355 360 365

Val Gly Pro Glu Ser Ala Gly Ala His Pro Gly Pro Ala Cys Tyr Arg
370 375 380

Lys Gly Gly Pro Val Thr Val Thr Asp Ala Asn Leu Val Leu Gly Arg
385 390 395 400

Leu Leu Pro Ala Ser Phe Pro Cys Ile Phe Gly Pro Gly Glu Asn Gln
405 410 415

Pro Leu Ser Pro Glu Ala Ser Arg Lys Ala Leu Glu Ala Val Ala Thr
420 425 430

Glu Val Asn Ser Phe Leu Thr Asn Gly Pro Cys Pro Ala Ser Pro Leu
435 440 445

Ser Leu Glu Glu Val Ala Met Gly Phe Val Arg Val Ala Asn Glu Ala
450 455 460

Met Cys Arg Pro Ile Arg Ala Leu Thr Gln Ala Arg Gly His Asp Pro
465 470 475 480

Ser Ala His Val Leu Ala Cys Phe Gly Gly Ala Gly Gly Gln His Ala
485 490 495

Cys Ala Ile Ala Arg Ala Leu Gly Met Asp Thr Val His Ile His Arg
500 505 510

His Ser Gly Leu Leu Ser Ala Leu Gly Leu Ala Leu Ala Asp Val Val
515 520 525

His Glu Ala Gln Glu Pro Cys Ser Leu Leu Tyr Ala Pro Glu Thr Phe
530 535 540

Val Gln Leu Asp Gln Arg Leu Ser Arg Leu Glu Glu Gln Cys Val Asp
545 550 555 560

Ala Leu Gln Ala Gln Gly Phe Pro Arg Ser Gln Ile Ser Thr Glu Ser
565 570 575

Phe Leu His Leu Arg Tyr Gln Gly Thr Asp Cys Ala Leu Met Val Ser
580 585 590

Ala His Gln His Pro Ala Thr Ala Arg Ser Pro Arg Ala Gly Asp Phe
595 600 605

Gly Ala Ala Phe Val Glu Arg Tyr Met Arg Glu Phe Gly Phe Val Ile
610 615 620

Pro Glu Arg Pro Val Val Val Asp Asp Val Arg Val Arg Gly Thr Gly
625 630 635 640

Arg Ser Gly Leu Arg Leu Glu Asp Ala Pro Lys Ala Gln Thr Gly Pro
645 650 655

Pro Arg Val Asp Lys Met Thr Gln Cys Tyr Phe Glu Gly Gly Tyr Gln
660 665 670

Glu Thr Pro Val Tyr Leu Leu Ala Glu Leu Gly Tyr Gly His Lys Leu
675 680 685

His Gly Pro Cys Leu Ile Ile Asp Ser Asn Ser Thr Ile Leu Val Glu
690 695 700

Pro Gly Cys Gln Ala Glu Val Thr Lys Thr Gly Asp Ile Cys Ile Ser
705 710 715 720

Val Gly Ala Glu Val Pro Gly Thr Val Gly Pro Gln Leu Asp Pro Ile
725 730 735

Gln Leu Ser Ile Phe Ser His Arg Phe Met Ser Ile Ala Glu Gln Met
740 745 750

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

```
Leu Asp Phe Ser Cys Ala Leu Phe Gly Pro Asp Gly Gly Leu Val Ser
    770                 775                 780

Asn Ala Pro His Ile Pro Val His Leu Gly Ala Met Gln Glu Thr Val
785                 790                 795                 800

Gln Phe Gln Ile Gln His Leu Gly Ala Asp Leu His Pro Gly Asp Val
                805                 810                 815

Leu Leu Ser Asn His Pro Ser Ala Gly Gly Ser His Leu Pro Asp Leu
            820                 825                 830

Thr Val Ile Thr Pro Val Phe Trp Pro Gly Gln Thr Arg Pro Val Phe
        835                 840                 845

Tyr Val Ala Ser Arg Gly His His Ala Asp Ile Gly Gly Ile Thr Pro
    850                 855                 860

Gly Ser Met Pro Pro His Ser Thr Met Leu Gln Gln Glu Gly Ala Val
865                 870                 875                 880

Phe Leu Ser Phe Lys Leu Val Gln Gly Gly Val Phe Gln Glu Glu Ala
                885                 890                 895

Val Thr Glu Ala Leu Arg Ala Pro Gly Lys Val Pro Asn Cys Ser Gly
            900                 905                 910

Thr Arg Asn Leu His Asp Asn Leu Ser Asp Leu Arg Ala Gln Val Ala
        915                 920                 925

Ala Asn Gln Lys Gly Ile Gln Leu Val Gly Glu Leu Ile Gly Gln Tyr
    930                 935                 940

Gly Leu Asp Val Val Gln Ala Tyr Met Gly His Ile Gln Ala Asn Ala
945                 950                 955                 960

Glu Leu Ala Val Arg Asp Met Leu Arg Ala Phe Gly Thr Ser Arg Gln
                965                 970                 975

Ala Arg Gly Leu Pro Leu Glu Val Ser Ser Glu Asp His Met Asp Asp
            980                 985                 990
```

Gly Ser Pro Ile Arg Leu Arg Val Gln Ile Ser Leu Ser Gln Gly Ser
995 1000 1005

Ala Val Phe Asp Phe Ser Gly Thr Gly Pro Glu Val Phe Gly Asn
1010 1015 1020

Leu Asn Ala Pro Arg Ala Val Thr Leu Ser Ala Leu Ile Tyr Cys
1025 1030 1035

Leu Arg Cys Leu Val Gly Arg Asp Ile Pro Leu Asn Gln Gly Cys
1040 1045 1050

Leu Ala Pro Val Arg Val Val Ile Pro Arg Gly Ser Ile Leu Asp
1055 1060 1065

Pro Ser Pro Glu Ala Ala Val Val Gly Gly Asn Val Leu Thr Ser
1070 1075 1080

Gln Arg Val Val Asp Val Ile Leu Gly Ala Phe Gly Ala Cys Ala
1085 1090 1095

Ala Ser Gln Gly Cys Met Asn Asn Val Thr Leu Gly Asn Ala His
1100 1105 1110

Met Gly Tyr Tyr Glu Thr Val Ala Gly Gly Ala Gly Ala Gly Pro
1115 1120 1125

Ser Trp His Gly Arg Ser Gly Val His Ser His Met Thr Asn Thr
1130 1135 1140

Arg Ile Thr Asp Pro Glu Ile Leu Glu Ser Arg Tyr Pro Val Ile
1145 1150 1155

Leu Arg Arg Phe Glu Leu Arg Arg Gly Ser Gly Gly Arg Gly Arg
1160 1165 1170

Phe Arg Gly Gly Asp Gly Val Thr Arg Glu Leu Leu Phe Arg Glu
1175 1180 1185

Glu Ala Leu Leu Ser Val Leu Thr Glu Arg Arg Ala Phe Arg Pro
1190 1195 1200

```
Tyr Gly  Leu His Gly Gly Glu  Pro Gly Ala Arg Gly  Leu Asn Leu
    1205                 1210                 1215


Leu Ile  Arg Lys Asn Gly Arg  Thr Val Asn Leu Gly  Gly Lys Thr
    1220                 1225                 1230


Ser Val  Thr Val Tyr Pro Gly  Asp Val Phe Cys Leu  His Thr Pro
    1235                 1240                 1245


Gly Gly  Gly Gly Tyr Gly Asp  Pro Glu Asp Pro Ala  Pro Pro Pro
    1250                 1255                 1260


Gly Ser  Pro Pro Gln Ala Leu  Ala Phe Pro Glu His  Gly Ser Val
    1265                 1270                 1275


Tyr Glu  Tyr Arg Arg Ala Gln  Glu Ala Val
    1280                 1285


<210> 504
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 90; "

<220>
<221> source
<223> /note="Gene Symbol: OPLAH; "

<220>
<221> source
<223> /note="Gene Name:
      5-oxoprolinase (ATP-hydrolysing); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481640"

<400> 504
Met Gly Ser Pro Glu Gly Arg Phe His Phe Ala Ile Asp Arg Gly Gly
1               5                  10                  15


Thr Phe Thr Asp Val Phe Ala Gln Cys Pro Gly Gly His Val Arg Val
            20                  25                  30


Leu Lys Leu Leu Ser Glu Asp Pro Ala Asn Tyr Ala Asp Ala Pro Thr
        35                  40                  45
```

```
Glu Gly Ile Arg Arg Ile Leu Glu Gln Glu Ala Gly Met Leu Leu Pro
    50                  55                  60

Arg Asp Gln Pro Leu Asp Ser Ser His Ile Ala Ser Ile Arg Met Gly
65                  70                  75                  80

Thr Thr Val Ala Thr Asn Ala Leu Leu Glu Arg Lys Gly Glu Arg Val
                85                  90                  95

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

Gln Ala Arg Gly Asp Leu Phe Asp Leu Ala Val Pro Met Pro Glu Val
        115                 120                 125

Leu Tyr Glu Glu Val Leu Glu Val Asp Glu Arg Val Val Leu His Arg
    130                 135                 140

Gly Glu Ala Gly Thr Gly Thr Pro Val Lys Gly Arg Thr
145                 150                 155


<210> 505
<211> 450
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
      5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8IUZ5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000310978"

<400> 505
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Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr Leu Ala Leu Arg Gln
1               5                  10                  15

Arg Leu Ile Ser Ser Ser Cys Arg Leu Phe Phe Pro Glu Asp Pro Val
            20                  25                  30

Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr Asp Glu Gln Gly Ala
        35                  40                  45

Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His Val Gly His Cys His
    50                  55                  60

Pro Leu Val Val Gln Ala Ala His Glu Gln Asn Gln Val Leu Asn Thr
65                  70                  75                  80

Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp Tyr Ala Gln Arg Leu
                85                  90                  95

Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe Tyr Phe Leu Asn Ser
            100                 105                 110

Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu Ala Arg His Tyr Thr
        115                 120                 125

Gly His Gln Asp Val Val Val Leu Asp His Ala Tyr His Gly His Leu
    130                 135                 140

Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe Arg Asn Leu Asp Gly
145                 150                 155                 160

Gln Lys Glu Trp Val His Val Ala Pro Leu Pro Asp Thr Tyr Arg Gly
                165                 170                 175

Pro Tyr Arg Glu Asp His Pro Asn Pro Ala Met Ala Tyr Ala Asn Glu
            180                 185                 190

Val Lys Arg Val Val Ser Ser Ala Gln Glu Lys Gly Arg Lys Ile Ala
        195                 200                 205

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

Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu His Ile Arg Lys Ala Gly
```

225 230 235 240

Gly Val Phe Val Ala Asp Glu Ile Gln Val Gly Phe Gly Arg Val Gly
245 250 255

Lys His Phe Trp Ala Phe Gln Leu Gln Gly Lys Asp Phe Val Pro Asp
260 265 270

Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly His Pro Val Ala Cys
275 280 285

Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe Glu Ala Thr Gly Val
290 295 300

Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val Ser Cys Ala Val Gly
305 310 315 320

Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln Leu Gln Asp His Ala
325 330 335

Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu Gly Gln Gln Lys Ile
340 345 350

Lys His Pro Ile Val Gly Asp Val Arg Gly Val Gly Leu Phe Ile Gly
355 360 365

Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr Pro Ala Thr Glu Glu
370 375 380

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

Thr Asp Gly Pro Gly Arg Asn Ile Leu Lys Phe Lys Pro Pro Met Cys
405 410 415

Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala Lys Leu Asp Ala Ile
420 425 430

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

Gln Pro
450

<210> 506
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000321290"

<400> 506
Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr Leu Ala Leu Arg Gln
1 5 10 15

Arg Leu Ile Ser His Leu Phe Ser Gly Ser Gly Arg Leu Thr Arg Thr
20 25 30

His Ala Glu Met Ser Lys Glu Ala Thr Glu Ala Glu Asn Ala Phe Arg
35 40 45

Asn Asn Pro Lys Phe Gln Arg Leu Val Thr Pro Ser Ala Ser Cys Phe
50 55 60

Ala Thr Thr Cys Gly Val Glu Arg Gln Val Gly His Cys His Pro Leu
65 70 75 80

Val Val Gln Ala Ala His Glu Gln Asn Gln Val Leu Asn Thr Asn Ser
85 90 95

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

Thr Leu Pro Glu Gln Leu Cys Val Phe Tyr Phe Leu Asn Ser Gly Ser
115 120 125

```
Glu Ala Asn Asp Leu Ala Leu Arg Leu Ala Arg His Tyr Thr Gly His
    130                 135                 140

Gln Asp Val Val Val Leu Asp His Ala Tyr His Gly His Leu Ser Ser
145                 150                 155                 160

Leu Ile Asp Ile Ser Pro Tyr Lys Phe Arg Asn Leu Asp Gly Gln Lys
                165                 170                 175

Glu Trp Val His Val Ala Pro Leu Pro Asp Thr Tyr Arg Gly Pro Tyr
            180                 185                 190

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

Arg Val Val Ser Ser Ala Gln Glu Lys Gly Arg
    210                 215


<210> 507
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
      5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377128"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 507
Xaa Val Pro Asp Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly His
1               5                   10                  15
```

```
Pro Val Ala Cys Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe Glu
            20                  25                  30

Ala Thr Gly Val Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val Ser
        35                  40                  45

Cys Ala Val Gly Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln Leu
    50                  55                  60

Gln Asp His Ala Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu Gly
65                  70                  75                  80

Gln Gln Lys Ile Lys His Pro Ile Val Gly Asp Val Arg Gly Val Gly
                85                  90                  95

Leu Phe Ile Gly Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr Pro
            100                 105                 110

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

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

Pro Pro Met Cys Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala Lys
145                 150                 155                 160

Leu Asp Ala Ile Leu Thr Asp Met Glu Glu Lys Val Arg Ser Cys Glu
                165                 170                 175

Thr Leu Arg Leu Gln Pro
            180
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<210> 508
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421810"

<400> 508
Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr Leu Ala Leu Arg Gln
1 5 10 15

Arg Leu Ile Ser Ser Ser Cys Arg Leu Phe Phe Pro Glu Asp Pro Val
20 25 30

Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr Asp Glu Gln Gly Ala
35 40 45

Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His Val Gly His Cys His
50 55 60

Pro Leu Val Val Gln Ala Ala His Glu Gln Asn Gln Val Leu Asn Thr
65 70 75 80

Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp Tyr Ala Gln Arg Leu
85 90 95

Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe Tyr Phe Leu Asn Ser
100 105 110

Gly Trp Gly Asn Ser Ser Ser Lys Lys Gly Thr
115 120

<210> 509
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source

<223> /note="Gene Name:
5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423806"

<400> 509
Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr Leu Ala Leu Arg Gln
1 5 10 15

Arg Leu Ile Ser Ser Ser Cys Arg Leu Phe Phe Pro Glu Asp Pro Val
20 25 30

Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr Asp Glu Gln Gly Ala
35 40 45

Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His Val Arg Ile Thr Ala
50 55 60

Thr
65

<210> 510
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424608"

<400> 510
Gln Ala Ala His Glu Gln Asn Gln Val Leu Asn Thr Asn Ser Arg Tyr
1 5 10 15

Leu His Asp Asn Ile Val Asp Tyr Ala Gln Arg Leu Ser Glu Thr Leu
20 25 30

```
Pro Glu Gln Leu Cys Val Phe Tyr Phe Leu Asn Ser Gly Ser Glu Ala
        35                  40                  45

Asn Asp Leu Ala Leu Arg Leu Ala Arg His Tyr Thr Gly His Gln Asp
    50                  55                  60

Val Val Val Leu Asp His Ala Tyr His Gly His Leu Ser Ser Leu Ile
65                  70                  75                  80

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

Val His Val Val Cys Thr Ala Gln Leu Asn Asn Ser Asp Met Leu Ser
            100                 105                 110

Ser Leu Gly
        115


<210> 511
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
      5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425425"

<400> 511
Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr Leu Ala Leu Arg Gln
1               5                   10                  15

Arg Leu Ile Arg His Ala Ala Leu Trp Ser Pro His Gly Thr Gly Gln
            20                  25                  30
```

```
Pro Pro Phe Leu Arg Ile Arg Glu Thr Asp Ala Asp Thr Cys Arg Asn
        35                  40                  45


Glu Gln Gly Gly His Arg Gly
    50                  55


<210> 512
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 91; "

<220>
<221> source
<223> /note="Gene Symbol: PHYKPL; "

<220>
<221> source
<223> /note="Gene Name:
      5-phosphohydroxy-L-lysine phospho-lyase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427444"

<400> 512
Ile Ala Ala Phe Phe Ala Glu Ser Leu Pro Ser Val Gly Gly Gln Ile
1               5                   10                  15


Ile Pro Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu
            20                  25


<210> 513
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 92; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      60S ribosomal prt L7a
      [Source:UniProtKB/Swiss-Prot;Acc:P62424]; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000486063"

<400> 513
Met Leu Val Arg Leu Asn Val Arg Cys Ser Cys Arg Gly Val Val Leu
1   5   10   15

Gly Gly Cys Arg Lys Leu Leu Ala Ser Leu Val Gln Pro Lys Gly Lys
            20   25   30

Lys Ala Lys Gly Lys Lys Val Ala Pro Ala Pro Ala Val Val Lys Lys
        35   40   45

Gln Glu Ala Lys Lys Val Val Asn Pro Leu Phe Glu Lys Arg Pro Lys
    50   55   60

Asn Phe Gly Ile Gly Gln Asp Ile Gln Pro Lys Arg Asp Leu Thr Arg
65   70   75   80

Phe Val Lys Trp Pro Arg Tyr Ile Arg Leu Gln Arg Gln Arg Ala Ile
                85   90   95

Leu Tyr Lys Arg Leu Lys Val Pro Pro Ala Ile Asn Gln Phe Thr Gln
            100   105   110

Ala Leu Asp Arg Gln Thr Ala Thr Gln Leu Leu Lys Leu Ala His Lys
        115   120   125

Tyr Arg Pro Glu Thr Lys Gln Glu Lys Lys Gln Arg Leu Leu Ala Arg
    130   135   140

Ala Glu Lys Lys Ala Ala Gly Lys Gly Asp Val Pro Thr Lys Arg Pro
145   150   155   160

Pro Val Leu Arg Ala Gly Val Asn Thr Val Thr Thr Leu Val Glu Asn
                165   170   175

Lys Lys Ala Gln Leu Val Val Ile Ala His Asp Val Asp Pro Ile
            180   185   190

<210> 514
<211> 151
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 92; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
60S ribosomal prt L7a
[Source:UniProtKB/Swiss-Prot;Acc:P62424]; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486855"

<400> 514
Met Ala Pro Leu Tyr Gln Ala Ala Gly Lys Gly Asp Val Pro Thr Lys
1 5 10 15

Arg Pro Pro Val Leu Arg Ala Gly Val Asn Thr Val Thr Thr Leu Val
20 25 30

Glu Asn Lys Lys Ala Gln Leu Val Val Ile Ala His Asp Val Asp Pro
35 40 45

Ile Glu Leu Val Val Phe Leu Pro Ala Leu Cys Arg Lys Met Gly Val
50 55 60

Pro Tyr Cys Ile Ile Lys Gly Lys Ala Arg Leu Gly Arg Leu Val His
65 70 75 80

Arg Lys Thr Cys Thr Thr Val Ala Phe Thr Gln Val Asn Ser Glu Asp
85 90 95

Lys Gly Ala Leu Ala Lys Leu Val Glu Ala Ile Arg Thr Asn Tyr Asn
100 105 110

Asp Arg Tyr Asp Glu Ile Arg Arg His Trp Gly Gly Asn Val Leu Gly
115 120 125

Pro Lys Ser Val Ala Arg Ile Ala Lys Leu Glu Lys Ala Lys Ala Lys
130 135 140

Glu Leu Ala Thr Lys Leu Gly
145 150

<210> 515
<211> 266
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 92; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
60S ribosomal prt L7a
[Source:UniProtKB/Swiss-Prot;Acc:P62424]; "

<220>
<221> source
<223> /note="Uniprot ID: P62424; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487443"

<400> 515
Met Pro Lys Gly Lys Lys Ala Lys Gly Lys Lys Val Ala Pro Ala Pro
1 5 10 15

Ala Val Val Lys Lys Gln Glu Ala Lys Lys Val Val Asn Pro Leu Phe
20 25 30

Glu Lys Arg Pro Lys Asn Phe Gly Ile Gly Gln Asp Ile Gln Pro Lys
35 40 45

Arg Asp Leu Thr Arg Phe Val Lys Trp Pro Arg Tyr Ile Arg Leu Gln
50 55 60

Arg Gln Arg Ala Ile Leu Tyr Lys Arg Leu Lys Val Pro Pro Ala Ile
65 70 75 80

Asn Gln Phe Thr Gln Ala Leu Asp Arg Gln Thr Ala Thr Gln Leu Leu
85 90 95

Lys Leu Ala His Lys Tyr Arg Pro Glu Thr Lys Gln Glu Lys Lys Gln

```
            100                 105                 110

Arg Leu Leu Ala Arg Ala Glu Lys Lys Ala Ala Gly Lys Gly Asp Val
        115                 120                 125

Pro Thr Lys Arg Pro Pro Val Leu Arg Ala Gly Val Asn Thr Val Thr
    130                 135                 140

Thr Leu Val Glu Asn Lys Lys Ala Gln Leu Val Val Ile Ala His Asp
145                 150                 155                 160

Val Asp Pro Ile Glu Leu Val Val Phe Leu Pro Ala Leu Cys Arg Lys
                165                 170                 175

Met Gly Val Pro Tyr Cys Ile Ile Lys Gly Lys Ala Arg Leu Gly Arg
            180                 185                 190

Leu Val His Arg Lys Thr Cys Thr Thr Val Ala Phe Thr Gln Val Asn
        195                 200                 205

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

Asn Tyr Asn Asp Arg Tyr Asp Glu Ile Arg Arg His Trp Gly Gly Asn
225                 230                 235                 240

Val Leu Gly Pro Lys Ser Val Ala Arg Ile Ala Lys Leu Glu Lys Ala
                245                 250                 255

Lys Ala Lys Glu Leu Ala Thr Lys Leu Gly
            260                 265


<210> 516
<211> 271
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 93; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB1; "

<220>
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<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000364131"

<400> 516

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Met Ser Pro Glu Met Gly Glu Leu Thr Gln Thr Arg Leu Gln Lys Ile
1               5                  10                  15

Trp Ile Pro His Ser Ser Gly Ser Ser Arg Leu Gln Arg Arg Arg Gly
            20                  25                  30

Ser Ser Ile Pro Gln Phe Thr Asn Ser Pro Thr Met Val Ile Met Val
        35                  40                  45

Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Thr Lys Leu Thr Arg
    50                  55                  60

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

Gln Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu Lys Asp Val His Asn
                85                  90                  95

Tyr Leu Ser His Glu Glu Gly His Val Ala Val Phe Asp Ala Thr Asn
            100                 105                 110

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

Gly Tyr Lys Gly Val Cys Glu Glu Met Thr Tyr Glu Glu Ile Gln Glu
    130                 135                 140

His Tyr Pro Glu Glu Phe Ala Leu Arg Asp Gln Asp Lys Tyr Arg Tyr
145                 150                 155                 160

Arg Tyr Pro Lys Gly Glu Ser Tyr Glu Asp Leu Val Gln Arg Leu Glu
                165                 170                 175

Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile Cys
            180                 185                 190
```

```
His Gln Ala Val Met Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ser
        195                 200                 205

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

Leu Thr Pro Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Tyr Leu Asn
225                 230                 235                 240

Val Glu Ala Val Asn Thr His Arg Glu Lys Pro Glu Asn Val Asp Ile
                245                 250                 255

Thr Arg Glu Pro Glu Glu Ala Leu Asp Thr Val Pro Ala His Tyr
            260                 265                 270


<210> 517
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 93; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB1; "

<220>
<221> source
<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P16118; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000364145"

<400> 517
Met Ser Pro Glu Met Gly Glu Leu Thr Gln Thr Arg Leu Gln Lys Ile
1               5                   10                  15

Trp Ile Pro His Ser Ser Gly Ser Ser Arg Leu Gln Arg Arg Arg Gly
            20                  25                  30

Ser Ser Ile Pro Gln Phe Thr Asn Ser Pro Thr Met Val Ile Met Val
        35                  40                  45
```

```
Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Thr Lys Leu Thr Arg
    50                  55                  60

Tyr Leu Asn Trp Ile Gly Thr Pro Thr Lys Val Phe Asn Leu Gly Gln
65                  70                  75                  80

Tyr Arg Arg Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu Pro
                85                  90                  95

Asp Asn Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu Ala Ala
            100                 105                 110

Leu Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly His Val Ala
        115                 120                 125

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

Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe Phe Ile Glu Ser Ile
145                 150                 155                 160

Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn Ile Arg Gln Val Lys Leu
                165                 170                 175

Gly Ser Pro Asp Tyr Ile Asp Cys Asp Arg Glu Lys Val Leu Glu Asp
            180                 185                 190

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

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

Thr Arg Tyr Met Val Asn Arg Val Gln Asp His Ile Gln Ser Arg Thr
225                 230                 235                 240

Val Tyr Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu
                245                 250                 255

Cys Arg His Gly Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile Gly Gly
            260                 265                 270
```

```
Asp Ser Gly Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr Ala Leu Ala
        275                 280                 285

Asn Phe Ile Gln Ser Gln Gly Ile Ser Ser Leu Lys Val Trp Thr Ser
    290                 295                 300

His Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr
305                 310                 315                 320

Glu Gln Trp Lys Ala Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu
                325                 330                 335

Met Thr Tyr Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe Ala Leu
            340                 345                 350

Arg Asp Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly Glu Ser Tyr
        355                 360                 365

Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg
    370                 375                 380

Gln Glu Asn Val Leu Val Ile Cys His Gln Ala Val Met Arg Cys Leu
385                 390                 395                 400

Leu Ala Tyr Phe Leu Asp Lys Ser Ser Asp Glu Leu Pro Tyr Leu Lys
                405                 410                 415

Cys Pro Leu His Thr Val Leu Lys Leu Thr Pro Val Ala Tyr Gly Cys
            420                 425                 430

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

Glu Lys Pro Glu Asn Val Asp Ile Thr Arg Glu Pro Glu Glu Ala Leu
    450                 455                 460

Asp Thr Val Pro Ala His Tyr
465                 470
```

<210> 518
<211> 406
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 93; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB1; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P16118; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000444074"

<400> 518
Met Glu Glu Lys Thr Ser Arg Ile Lys Val Phe Asn Leu Gly Gln Tyr
1   5   10   15

Arg Arg Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu Pro Asp
            20   25   30

Asn Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu
        35   40   45

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

Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ser Leu Ile Leu Gln
65   70   75   80

Phe Ala Lys Glu His Gly Tyr Lys Val Phe Phe Ile Glu Ser Ile Cys
                85   90   95

Asn Asp Pro Gly Ile Ile Ala Glu Asn Ile Arg Gln Val Lys Leu Gly
            100   105   110

Ser Pro Asp Tyr Ile Asp Cys Asp Arg Glu Lys Val Leu Glu Asp Phe
        115   120   125

Leu Lys Arg Ile Glu Cys Tyr Glu Val Asn Tyr Gln Pro Leu Asp Glu
    130   135   140

```
Glu Leu Asp Ser His Leu Ser Tyr Ile Lys Ile Phe Asp Val Gly Thr
145                 150                 155                 160

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

Tyr Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys
            180                 185                 190

Arg His Gly Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile Gly Gly Asp
        195                 200                 205

Ser Gly Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr Ala Leu Ala Asn
    210                 215                 220

Phe Ile Gln Ser Gln Gly Ile Ser Ser Leu Lys Val Trp Thr Ser His
225                 230                 235                 240

Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr Glu
                245                 250                 255

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

Thr Tyr Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe Ala Leu Arg
        275                 280                 285

Asp Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly Glu Ser Tyr Glu
    290                 295                 300

Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln
305                 310                 315                 320

Glu Asn Val Leu Val Ile Cys His Gln Ala Val Met Arg Cys Leu Leu
                325                 330                 335

Ala Tyr Phe Leu Asp Lys Ser Ser Asp Glu Leu Pro Tyr Leu Lys Cys
            340                 345                 350

Pro Leu His Thr Val Leu Lys Leu Thr Pro Val Ala Tyr Gly Cys Lys
        355                 360                 365
```

```
Val Glu Ser Ile Tyr Leu Asn Val Glu Ala Val Asn Thr His Arg Glu
    370                 375                 380

Lys Pro Glu Asn Val Asp Ile Thr Arg Glu Pro Glu Glu Ala Leu Asp
385                 390                 395                 400

Thr Val Pro Ala His Tyr
                405
```

<210> 519
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 93; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB1; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480232"

<400> 519

```
Met Val Asn Arg Val Gln Asp His Ile Gln Ser Arg Thr Val Tyr Tyr
1               5                   10                  15

Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg His
            20                  25                  30

Gly Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile Gly Gly Asp Ser Gly
        35                  40                  45

Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr Ala Leu Ala Asn Phe Ile
    50                  55                  60

Gln Ser Gln Gly Ile Ser Ser Leu Lys Val Trp Thr Ser His Met Lys
65                  70                  75                  80

Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr Glu Gln Trp
```

```
                85                  90                  95

Lys Ala Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Met Thr Tyr
            100                 105                 110

Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe Ala Leu Arg Asp Gln
        115                 120                 125

Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly Glu Ser Tyr Glu Asp Leu
    130                 135                 140

Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn
145                 150                 155                 160

Val Leu Val Ile Cys His Gln Ala Val Met Arg Cys Leu Leu Ala Tyr
                165                 170                 175

Phe Leu Asp Lys Ser Ser Asp Glu Leu Pro Tyr Leu Lys Cys Pro Leu
            180                 185                 190

His Thr Val Leu Lys Leu Thr Pro Val Ala Tyr Gly Cys Lys Val Glu
        195                 200                 205

Ser Ile Tyr Leu Asn Val Glu Ala Val Asn Thr His Arg Glu Lys Pro
    210                 215                 220

Glu Asn Val Asp Ile Thr Arg Glu Pro Glu Glu Ala Leu Asp Thr Val
225                 230                 235                 240

Pro Ala His Tyr
```

<210> 520
<211> 471
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 94; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB2; "

<220>

<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; "

<220>
<221> source
<223> /note="Uniprot ID: O60825; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356046"

<400> 520

```
Met Ser Gly Ala Ser Ser Ser Glu Gln Asn Asn Asn Ser Tyr Glu Thr
1               5                  10                  15

Lys Thr Pro Asn Leu Arg Met Ser Glu Lys Lys Cys Ser Trp Ala Ser
            20                  25                  30

Tyr Met Thr Asn Ser Pro Thr Leu Ile Val Met Ile Gly Leu Pro Ala
        35                  40                  45

Arg Gly Lys Thr Tyr Val Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp
    50                  55                  60

Ile Gly Val Pro Thr Lys Val Phe Asn Leu Gly Val Tyr Arg Arg Glu
65                  70                  75                  80

Ala Val Lys Ser Tyr Lys Ser Tyr Asp Phe Phe Arg His Asp Asn Glu
                85                  90                  95

Glu Ala Met Lys Ile Arg Lys Gln Cys Ala Leu Val Ala Leu Glu Asp
            100                 105                 110

Val Lys Ala Tyr Leu Thr Glu Glu Asn Gly Gln Ile Ala Val Phe Asp
        115                 120                 125

Ala Thr Asn Thr Thr Arg Glu Arg Arg Asp Met Ile Leu Asn Phe Ala
    130                 135                 140

Glu Gln Asn Ser Phe Lys Val Phe Phe Val Glu Ser Val Cys Asp Asp
145                 150                 155                 160

Pro Asp Val Ile Ala Ala Asn Ile Leu Glu Val Lys Val Ser Ser Pro
                165                 170                 175
```

```
Asp Tyr Pro Glu Arg Asn Arg Glu Asn Val Met Glu Asp Phe Leu Lys
            180                 185                 190

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

Tyr Asp Lys Asp Leu Ser Phe Ile Lys Val Ile Asn Val Gly Gln Arg
    210                 215                 220

Phe Leu Val Asn Arg Val Gln Asp Tyr Ile Gln Ser Lys Ile Val Tyr
225                 230                 235                 240

Tyr Leu Met Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg
                245                 250                 255

His Gly Glu Ser Glu Phe Asn Leu Leu Gly Lys Ile Gly Gly Asp Ser
            260                 265                 270

Gly Leu Ser Val Arg Gly Lys Gln Phe Ala Gln Ala Leu Arg Lys Phe
        275                 280                 285

Leu Glu Glu Gln Glu Ile Thr Asp Leu Lys Val Trp Thr Ser Gln Leu
    290                 295                 300

Lys Arg Thr Ile Gln Thr Ala Glu Ser Leu Gly Val Pro Tyr Glu Gln
305                 310                 315                 320

Trp Lys Ile Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Met Thr
                325                 330                 335

Tyr Ala Glu Ile Glu Lys Arg Tyr Pro Glu Glu Phe Ala Leu Arg Asp
            340                 345                 350

Gln Glu Lys Tyr Leu Tyr Arg Tyr Pro Gly Gly Glu Ser Tyr Gln Asp
        355                 360                 365

Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Gly
    370                 375                 380

Asn Val Leu Val Ile Ser His Gln Ala Val Met Arg Cys Leu Leu Ala
385                 390                 395                 400

Tyr Phe Leu Asp Lys Gly Ala Asp Glu Leu Pro Tyr Leu Arg Cys Pro
```

405 410 415

Leu His Thr Ile Phe Lys Leu Thr Pro Val Ala Tyr Gly Cys Lys Val
420 425 430

Glu Thr Ile Lys Leu Asn Val Glu Ala Val Asn Thr His Arg Asp Lys
435 440 445

Pro Thr Ala Ala Glu Thr Thr Leu Ala Val Arg Arg Arg Pro Ser Ala
450 455 460

Ala Ser Leu Met Leu Pro Cys
465 470

<210> 521
<211> 505
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 94; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB2; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; "

<220>
<221> source
<223> /note="Uniprot ID: O60825; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356047"

<400> 521
Met Ser Gly Ala Ser Ser Ser Glu Gln Asn Asn Asn Ser Tyr Glu Thr
1 5 10 15

Lys Thr Pro Asn Leu Arg Met Ser Glu Lys Lys Cys Ser Trp Ala Ser
20 25 30

Tyr Met Thr Asn Ser Pro Thr Leu Ile Val Met Ile Gly Leu Pro Ala
35 40 45

```
Arg Gly Lys Thr Tyr Val Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp
    50                  55                  60

Ile Gly Val Pro Thr Lys Val Phe Asn Leu Gly Val Tyr Arg Arg Glu
65                  70                  75                  80

Ala Val Lys Ser Tyr Lys Ser Tyr Asp Phe Phe Arg His Asp Asn Glu
                85                  90                  95

Glu Ala Met Lys Ile Arg Lys Gln Cys Ala Leu Val Ala Leu Glu Asp
            100                 105                 110

Val Lys Ala Tyr Leu Thr Glu Glu Asn Gly Gln Ile Ala Val Phe Asp
        115                 120                 125

Ala Thr Asn Thr Thr Arg Glu Arg Arg Asp Met Ile Leu Asn Phe Ala
    130                 135                 140

Glu Gln Asn Ser Phe Lys Val Phe Phe Val Glu Ser Val Cys Asp Asp
145                 150                 155                 160

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

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

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

Tyr Asp Lys Asp Leu Ser Phe Ile Lys Val Ile Asn Val Gly Gln Arg
    210                 215                 220

Phe Leu Val Asn Arg Val Gln Asp Tyr Ile Gln Ser Lys Ile Val Tyr
225                 230                 235                 240

Tyr Leu Met Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg
                245                 250                 255

His Gly Glu Ser Glu Phe Asn Leu Leu Gly Lys Ile Gly Gly Asp Ser
            260                 265                 270
```

```
Gly Leu Ser Val Arg Gly Lys Gln Phe Ala Gln Ala Leu Arg Lys Phe
        275                 280                 285

Leu Glu Glu Gln Glu Ile Thr Asp Leu Lys Val Trp Thr Ser Gln Leu
    290                 295                 300

Lys Arg Thr Ile Gln Thr Ala Glu Ser Leu Gly Val Pro Tyr Glu Gln
305                 310                 315                 320

Trp Lys Ile Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Met Thr
                325                 330                 335

Tyr Ala Glu Ile Glu Lys Arg Tyr Pro Glu Glu Phe Ala Leu Arg Asp
            340                 345                 350

Gln Glu Lys Tyr Leu Tyr Arg Tyr Pro Gly Gly Glu Ser Tyr Gln Asp
        355                 360                 365

Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Gly
    370                 375                 380

Asn Val Leu Val Ile Ser His Gln Ala Val Met Arg Cys Leu Leu Ala
385                 390                 395                 400

Tyr Phe Leu Asp Lys Gly Ala Asp Glu Leu Pro Tyr Leu Arg Cys Pro
                405                 410                 415

Leu His Thr Ile Phe Lys Leu Thr Pro Val Ala Tyr Gly Cys Lys Val
            420                 425                 430

Glu Thr Ile Lys Leu Asn Val Glu Ala Val Asn Thr His Arg Asp Lys
        435                 440                 445

Pro Thr Asn Asn Phe Pro Lys Asn Gln Thr Pro Val Arg Met Arg Arg
    450                 455                 460

Asn Ser Phe Thr Pro Leu Ser Ser Ser Asn Thr Ile Arg Arg Pro Arg
465                 470                 475                 480

Asn Tyr Ser Val Gly Ser Arg Pro Leu Lys Pro Leu Ser Pro Leu Arg
                485                 490                 495

Ala Gln Asp Met Gln Glu Gly Ala Asp
```

500 505

<210> 522
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 94; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB2; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408717"

<400> 522
Met Ser Gly Ala Ser Ser Ser Glu Gln Asn Asn Asn Ser Tyr Glu Thr
1 5 10 15

Lys Thr Pro Asn Leu Arg Met Ser Glu Lys Lys Cys Ser Trp Ala Ser
20 25 30

Tyr Met Thr Asn Ser Pro Thr Leu Ile Val Met Ile Gly Leu Pro Ala
35 40 45

Arg Gly Lys Thr Tyr Val Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp
50 55 60

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

His His Ile Ile Leu Leu Leu Lys Asp Leu Gly Val Phe Tyr Ser Val
85 90 95

<210> 523
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 94; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB2; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439420"

<400> 523
Met Ser Gly Ala Ser Ser Ser Glu Gln Asn Asn Asn Ser Tyr Glu Thr
1 5 10 15

Lys Thr Pro Asn Leu Arg Met Ser Glu Lys Lys Cys Ser Trp Ala Ser
20 25 30

Tyr Met Thr Asn Ser Pro Thr Leu Ile Val Met Ile Gly Leu Pro Ala
35 40 45

Arg Gly Lys Thr Tyr Val Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp
50 55 60

Ile Gly Val Pro Thr Lys Val Phe Asn Leu Gly Val Tyr Arg Arg Glu
65 70 75 80

Ala Val Lys Ser Tyr Lys Ser Tyr Asp Phe Phe Arg His Asp Asn Glu
85 90 95

Glu Ala Met Lys Ile Arg Lys Gln Cys Ala Leu Val Ala Leu Glu Asp
100 105 110

Val Lys Ala Tyr Leu Thr Glu Glu Asn Gly Gln Ile Ala
115 120 125

<210> 524
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 94; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB2; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484769"

<400> 524
Met Ser Gly Ala Ser Ser Ser Glu Gln Asn Asn Asn Ser Tyr Glu Thr
1 5 10 15

Lys Thr Pro Asn Leu Arg Met Ser Glu Lys Lys Cys Cys Trp Ser Ala
20 25 30

Val Thr Gly Ser Trp Leu Thr Ala Thr Leu Asn Ser
35 40

<210> 525
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 94; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB2; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484988"

<400> 525
Met Ser Gly Ala Ser Ser Ser Glu Gln Asn Asn Asn Ser Tyr Glu Thr
1 5 10 15

Lys Thr Pro Asn Leu Arg Met Ser Glu Lys Lys Cys Ser Trp Ala Ser
20 25 30

Tyr Met Thr Asn Ser Pro Thr Leu Ile Val Met Ile Gly Leu Pro Ala
        35   40   45

Arg

<210> 526
<211> 514
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q16875; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000353712"

<400> 526
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1   5   10   15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20   25   30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35   40   45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50   55   60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65   70   75   80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85   90   95

```
Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100                 105                 110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320
```

```
Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp
        435                 440                 445

Ala Lys Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro
    450                 455                 460

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

Glu His Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro
                485                 490                 495

Glu Val Pro Thr Gln Leu Pro Gly Gln Pro Leu Leu Gly Gln Ala Cys
            500                 505                 510

Leu Thr
```

<210> 527
<211> 520
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q16875; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369100"

<400> 527
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1   5   10   15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20   25   30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35   40   45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50   55   60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65   70   75   80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85   90   95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100   105   110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115   120   125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130   135   140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365
```

```
Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp
        435                 440                 445

Ala Lys Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro
    450                 455                 460

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

Glu His Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro
                485                 490                 495

Glu Val Pro Thr Gln Leu Pro Gly Gln Asn Met Lys Gly Ser Arg Ser
            500                 505                 510

Ser Ala Asp Ser Ser Arg Lys His
        515                 520
```

<210> 528
<211> 513
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:

6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369105"

<400> 528
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1   5   10   15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20   25   30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35   40   45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50   55   60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65   70   75   80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85   90   95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100   105   110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115   120   125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130   135   140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165   170   175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180   185   190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195   200   205

```
Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

Val Leu Lys Leu Thr Pro Val Ala Tyr Gly Cys Arg Val Glu Ser Ile
            420                 425                 430
```

```
Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp
        435                 440                 445

Ala Lys Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro
    450                 455                 460

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

Glu His Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro
                485                 490                 495

Glu Val Pro Thr Gln Leu Pro Gly Gln Pro Leu Leu Gly Gln Ala Cys
            500                 505                 510

Leu
```

<210> 529
<211> 526
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369111"

<400> 529

```
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1               5                   10                  15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20                  25                  30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
```

```
        35                  40                  45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50                  55                  60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65                  70                  75                  80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85                  90                  95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100                 105                 110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270
```

```
Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp
        435                 440                 445

Ala Lys Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro
    450                 455                 460

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

Glu His Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro
                485                 490                 495
```

```
Glu Val Pro Thr Gln Leu Pro Gly Gln Pro Leu Leu Gly Gln Ala Cys
            500                 505                 510

Leu Arg Thr Val Cys His Ile Phe Ser Lys Phe Ser Pro Tyr
        515                 520                 525


<210> 530
<211> 500
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="Uniprot ID:  Q16875; "

<220>
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<223> /note="ENSP ID: ENSP00000369115"

<400> 530
Met Pro Phe Arg Lys Ala Cys Gly Pro Lys Leu Thr Asn Ser Pro Thr
1               5                  10                  15

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

Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val Pro Thr Lys Val
        35                  40                  45

Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys Gln Tyr Ser Ser
    50                  55                  60

Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met Lys Val Arg Lys
65                  70                  75                  80

Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser Tyr Leu Ala Lys
```

```
                85                  90                  95

Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn Thr Thr Arg Glu
            100                 105                 110

Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn Asp Phe Lys Ala
        115                 120                 125

Phe Phe Ile Glu Ser Val Cys Asp Asp Pro Thr Val Val Ala Ser Asn
    130                 135                 140

Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys Asp Cys Asn Ser
145                 150                 155                 160

Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser Cys Tyr Glu Ala
                165                 170                 175

Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg Asp Leu Ser Leu
            180                 185                 190

Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val Asn Arg Val Gln
        195                 200                 205

Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met Asn Ile His Val
    210                 215                 220

Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu Asn Glu His Asn
225                 230                 235                 240

Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser Ser Arg Gly Lys
                245                 250                 255

Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu Gln Asn Leu Lys
            260                 265                 270

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

Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala Leu Asn Glu Ile
    290                 295                 300

Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu Ile Arg Asp Thr
305                 310                 315                 320
```

Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys Tyr Tyr Tyr Arg
325 330 335

Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln Arg Leu Glu Pro
340 345 350

Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile Cys His
355 360 365

Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ser Ala
370 375 380

Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu
385 390 395 400

Thr Pro Val Ala Tyr Gly Cys Arg Val Glu Ser Ile Tyr Leu Asn Val
405 410 415

Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp Ala Lys Lys Gly
420 425 430

Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro Leu Ala Ser Pro
435 440 445

Glu Pro Thr Lys Lys Pro Arg Ile Asn Ser Phe Glu Glu His Val Ala
450 455 460

Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro Glu Val Pro Thr
465 470 475 480

Gln Leu Pro Gly Gln Asn Met Lys Gly Ser Arg Ser Ser Ala Asp Ser
485 490 495

Ser Arg Lys His
500

<210> 531
<211> 143
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000390285"

<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 531
Xaa Val Glu Glu Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln
1 5 10 15

Leu Lys Ser Thr Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu
20 25 30

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

Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val
50 55 60

Leu Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe
65 70 75 80

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

Thr Val Leu Lys Leu Thr Pro Val Ala Tyr Gly Cys Arg Val Glu Ser
100 105 110

Ile Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu
115 120 125

Asn Met Lys Gly Ser Arg Ser Ser Ala Asp Ser Ser Arg Lys His
130 135 140

<210> 532
<211> 31
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404995"

<400> 532
Ile Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu
1 5 10 15

Asn Met Lys Gly Ser Arg Ser Ser Ala Asp Ser Ser Arg Lys His
20 25 30

<210> 533
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416677"

<400> 533
Ile Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu
1 5 10 15

```
Asp Ala Lys Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr
            20                  25                  30

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

Glu Glu His Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro
    50                  55                  60

Pro Glu Val Pro Thr Gln Leu Pro Gly Gln Pro Leu Leu Gly Gln Ala
65                  70                  75                  80

Cys Leu Asn Trp Lys Gly Val Met Arg Asn Ala Ala
                85                  90


<210> 534
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432356"

<400> 534
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1               5                   10                  15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20                  25                  30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35                  40                  45
```

```
Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50                  55                  60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65                  70                  75                  80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85                  90                  95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100                 105                 110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
```

```
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Ala
        435                 440                 445

Ala Lys Ser Thr Thr Leu Cys
    450                 455


<210> 535
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
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<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433771"

<400> 535

```
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1               5                  10                  15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20                  25                  30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35                  40                  45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50                  55                  60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65                  70                  75                  80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85                  90                  95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100                 105                 110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175
```

```
Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
```

405 410 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Ala
435 440 445

Ala Lys Ser Thr Thr Leu Cys
450 455

<210> 536
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434342"

<400> 536
Ile Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu
1 5 10 15

Gly Leu Ser Leu Phe Pro Arg Leu Glu Cys Gly Gly Ala Val Thr Ala
20 25 30

His Cys Ser Leu Asn Leu Leu Gly Ser Ser Asp Pro Pro Ala Ser Ala
35 40 45

Ser Arg Val Ala Glu Thr Thr Gly Cys Lys Glu Gly Thr
50 55 60

<210> 537
<211> 455
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 95; "

<220>
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<223> /note="Gene Symbol: PFKFB3; "

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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
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<223> /note="ENSP ID: ENSP00000434628"

<400> 537

```
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1               5                  10                  15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20                  25                  30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35                  40                  45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50                  55                  60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65                  70                  75                  80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85                  90                  95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100                 105                 110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

Asp Phe Lys Ala Phe Phe Ile Glu Ser Val Cys Asp Asp Pro Thr Val
```

145 150 155 160

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
165 170 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
180 185 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
195 200 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
210 215 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225 230 235 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
245 250 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
260 265 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
275 280 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
290 295 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305 310 315 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
325 330 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
340 345 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
355 360 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
370 375 380

```
Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400


Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415


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


Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Ala
        435                 440                 445


Ala Lys Ser Thr Thr Leu Cys
    450                 455


<210> 538
<211> 455
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 95; "

<220>
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<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436885"

<400> 538
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1               5                   10                  15


Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20                  25                  30


Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35                  40                  45
```

```
Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50                  55                  60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65                  70                  75                  80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85                  90                  95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100                 105                 110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
```

```
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Ala
        435                 440                 445

Ala Lys Ser Thr Thr Leu Cys
    450                 455


<210> 539
<211> 534
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
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<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
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<223> /note="Uniprot ID: Q16875; "

<220>
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<223> /note="ENSP ID: ENSP00000443319"

<400> 539

Met	Gly	Glu	Gly	Gly	Gln	Lys	Glu	Gly	Asp	Ser	Gln	Gln	Ala	Gly	Ala
1				5				10						15	

Leu	Pro	Leu	Leu	Cys	Gln	Leu	Asp	Thr	Phe	Ser	Pro	Lys	Ala	Thr	Val
			20					25					30		

Phe	Gly	Val	Ser	Ile	Asn	Pro	Ala	Cys	Gly	Pro	Lys	Leu	Thr	Asn	Ser
		35					40					45			

Pro	Thr	Val	Ile	Val	Met	Val	Gly	Leu	Pro	Ala	Arg	Gly	Lys	Thr	Tyr
	50					55					60				

Ile	Ser	Lys	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp	Ile	Gly	Val	Pro	Thr
65					70					75					80

Lys	Val	Phe	Asn	Val	Gly	Glu	Tyr	Arg	Arg	Glu	Ala	Val	Lys	Gln	Tyr
				85					90					95	

Ser	Ser	Tyr	Asn	Phe	Phe	Arg	Pro	Asp	Asn	Glu	Glu	Ala	Met	Lys	Val
			100					105					110		

Arg	Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu	Arg	Asp	Val	Lys	Ser	Tyr	Leu
		115					120					125			

Ala	Lys	Glu	Gly	Gly	Gln	Ile	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr
	130					135					140				

Arg	Glu	Arg	Arg	His	Met	Ile	Leu	His	Phe	Ala	Lys	Glu	Asn	Asp	Phe
145					150					155					160

```
Lys Ala Phe Phe Ile Glu Ser Val Cys Asp Asp Pro Thr Val Val Ala
                165                 170                 175

Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys Asp Cys
            180                 185                 190

Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser Cys Tyr
        195                 200                 205

Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg Asp Leu
    210                 215                 220

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

Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met Asn Ile
                245                 250                 255

His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu Asn Glu
            260                 265                 270

His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser Ser Arg
        275                 280                 285

Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu Gln Asn
    290                 295                 300

Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr Ile Gln
305                 310                 315                 320

Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala Leu Asn
                325                 330                 335

Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu Ile Arg
            340                 345                 350

Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys Tyr Tyr
        355                 360                 365

Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln Arg Leu
    370                 375                 380

Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile
```

```
385                 390                 395                 400

Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys
                405                 410                 415

Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu
            420                 425                 430

Lys Leu Thr Pro Val Ala Tyr Gly Cys Arg Val Glu Ser Ile Tyr Leu
        435                 440                 445

Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp Ala Lys
    450                 455                 460

Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro Leu Ala
465                 470                 475                 480

Ser Pro Glu Pro Thr Lys Lys Pro Arg Ile Asn Ser Phe Glu Glu His
                485                 490                 495

Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro Glu Val
            500                 505                 510

Pro Thr Gln Leu Pro Gly Gln Asn Met Lys Gly Ser Arg Ser Ser Ala
        515                 520                 525

Asp Ser Ser Arg Lys His
    530


<210> 540
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000486311"

<400> 540
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1   5   10   15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
            20   25   30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
        35   40   45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
    50   55   60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65   70   75   80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
                85   90   95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
            100   105   110

Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115   120   125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130   135   140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165   170   175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180   185   190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195   200   205

```
Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335

Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Ala
```

435 440 445

Ala Lys Ser Thr Thr Leu Cys
450 455

<210> 541
<211> 526
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 95; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB3; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487277"

<400> 541
Met Pro Leu Glu Leu Thr Gln Ser Arg Val Gln Lys Ile Trp Val Pro
1 5 10 15

Val Asp His Arg Pro Ser Leu Pro Arg Ser Cys Gly Pro Lys Leu Thr
20 25 30

Asn Ser Pro Thr Val Ile Val Met Val Gly Leu Pro Ala Arg Gly Lys
35 40 45

Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile Gly Val
50 55 60

Pro Thr Lys Val Phe Asn Val Gly Glu Tyr Arg Arg Glu Ala Val Lys
65 70 75 80

Gln Tyr Ser Ser Tyr Asn Phe Phe Arg Pro Asp Asn Glu Glu Ala Met
85 90 95

Lys Val Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val Lys Ser
100 105 110

```
Tyr Leu Ala Lys Glu Gly Gly Gln Ile Ala Val Phe Asp Ala Thr Asn
        115                 120                 125

Thr Thr Arg Glu Arg Arg His Met Ile Leu His Phe Ala Lys Glu Asn
    130                 135                 140

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

Val Ala Ser Asn Ile Met Glu Val Lys Ile Ser Ser Pro Asp Tyr Lys
                165                 170                 175

Asp Cys Asn Ser Ala Glu Ala Met Asp Asp Phe Met Lys Arg Ile Ser
            180                 185                 190

Cys Tyr Glu Ala Ser Tyr Gln Pro Leu Asp Pro Asp Lys Cys Asp Arg
        195                 200                 205

Asp Leu Ser Leu Ile Lys Val Ile Asp Val Gly Arg Arg Phe Leu Val
    210                 215                 220

Asn Arg Val Gln Asp His Ile Gln Ser Arg Ile Val Tyr Tyr Leu Met
225                 230                 235                 240

Asn Ile His Val Gln Pro Arg Thr Ile Tyr Leu Cys Arg His Gly Glu
                245                 250                 255

Asn Glu His Asn Leu Gln Gly Arg Ile Gly Gly Asp Ser Gly Leu Ser
            260                 265                 270

Ser Arg Gly Lys Lys Phe Ala Ser Ala Leu Ser Lys Phe Val Glu Glu
        275                 280                 285

Gln Asn Leu Lys Asp Leu Arg Val Trp Thr Ser Gln Leu Lys Ser Thr
    290                 295                 300

Ile Gln Thr Ala Glu Ala Leu Arg Leu Pro Tyr Glu Gln Trp Lys Ala
305                 310                 315                 320

Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Leu Thr Tyr Glu Glu
                325                 330                 335
```

```
Ile Arg Asp Thr Tyr Pro Glu Glu Tyr Ala Leu Arg Glu Gln Asp Lys
            340                 345                 350

Tyr Tyr Tyr Arg Tyr Pro Thr Gly Glu Ser Tyr Gln Asp Leu Val Gln
        355                 360                 365

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
    370                 375                 380

Val Ile Cys His Gln Ala Val Leu Arg Cys Leu Leu Ala Tyr Phe Leu
385                 390                 395                 400

Asp Lys Ser Ala Glu Glu Met Pro Tyr Leu Lys Cys Pro Leu His Thr
                405                 410                 415

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

Tyr Leu Asn Val Glu Ser Val Cys Thr His Arg Glu Arg Ser Glu Asp
        435                 440                 445

Ala Lys Lys Gly Pro Asn Pro Leu Met Arg Arg Asn Ser Val Thr Pro
    450                 455                 460

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

Glu His Val Ala Ser Thr Ser Ala Ala Leu Pro Ser Cys Leu Pro Pro
                485                 490                 495

Glu Val Pro Thr Gln Leu Pro Gly Gln Pro Leu Leu Gly Gln Ala Cys
            500                 505                 510

Leu Arg Thr Val Cys His Ile Phe Ser Lys Phe Ser Pro Tyr
        515                 520                 525


<210> 542
<211> 469
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "
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<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q16877; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000232375"

<400> 542
Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile Trp
1 5 10 15

Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln Arg Gly
20 25 30

Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val Gly Leu Pro
35 40 45

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

Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val Gly Gln Tyr Arg Arg
65 70 75 80

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

Glu Glu Gly Leu Lys Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg
100 105 110

Asp Val Arg Arg Phe Leu Ser Glu Glu Gly Gly His Val Ala Val Phe
115 120 125

Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ala Thr Ile Phe Asn Phe
130 135 140

Gly Glu Gln Asn Gly Tyr Lys Thr Phe Phe Val Glu Ser Ile Cys Val
145 150 155 160

```
Asp Pro Glu Val Ile Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser
                165                 170                 175

Pro Asp Tyr Val Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met
            180                 185                 190

Arg Arg Ile Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp
        195                 200                 205

Leu Asp Arg Asp Leu Ser Tyr Ile Lys Ile Met Asp Val Gly Gln Ser
    210                 215                 220

Tyr Val Val Asn Arg Val Ala Asp His Ile Gln Ser Arg Ile Val Tyr
225                 230                 235                 240

Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg
                245                 250                 255

His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg Ile Gly Gly Asp Pro
            260                 265                 270

Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys Ser Leu Ala Gln Phe
        275                 280                 285

Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val Trp Thr Ser Gln Met
    290                 295                 300

Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr Glu Gln
305                 310                 315                 320

Trp Lys Val Leu Asn Glu Ile Asp Ala Gly Val Cys Glu Glu Met Thr
                325                 330                 335

Tyr Glu Glu Ile Gln Asp Asn Tyr Pro Leu Glu Phe Ala Leu Arg Asp
            340                 345                 350

Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly Glu Ser Tyr Glu Asp
        355                 360                 365

Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu
    370                 375                 380
```

```
Asn Val Leu Val Ile Cys His Gln Ala Val Met Arg Cys Leu Leu Ala
385                 390                 395                 400

Tyr Phe Leu Asp Lys Ala Ala Glu Gln Leu Pro Tyr Leu Lys Cys Pro
                405                 410                 415

Leu His Thr Val Leu Lys Leu Thr Pro Val Ala Tyr Gly Cys Lys Val
            420                 425                 430

Glu Ser Ile Phe Leu Asn Val Ala Ala Val Asn Thr His Arg Asp Arg
        435                 440                 445

Pro Gln Asn Val Asp Ile Ser Arg Pro Pro Glu Glu Ala Leu Val Thr
    450                 455                 460

Val Pro Ala His Gln
465
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<210> 543
<211> 434
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
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<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q16877; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373240"

<400> 543

```
Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile Trp
1               5                   10                  15

Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln Arg Gly
            20                  25                  30
```

```
Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val Gly Leu Pro
        35                  40                  45

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

Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val Gly Gln Tyr Arg Arg
65                  70                  75                  80

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

Glu Glu Gly Leu Lys Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg
            100                 105                 110

Asp Val Arg Arg Phe Leu Ser Glu Glu Gly Gly His Val Ala Val Phe
        115                 120                 125

Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ala Thr Ile Phe Asn Phe
    130                 135                 140

Gly Glu Gln Asn Gly Tyr Lys Thr Phe Phe Val Glu Ser Ile Cys Val
145                 150                 155                 160

Asp Pro Glu Val Ile Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser
                165                 170                 175

Pro Asp Tyr Val Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met
            180                 185                 190

Arg Arg Ile Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp
        195                 200                 205

Leu Asp Arg Asp Leu Ser Tyr Ile Lys Ile Met Asp Val Gly Gln Ser
    210                 215                 220

Tyr Val Val Asn Arg Val Ala Asp His Ile Gln Ser Arg Ile Val Tyr
225                 230                 235                 240

Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg
                245                 250                 255
```

```
His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg Ile Gly Gly Asp Pro
            260                 265                 270

Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys Ser Leu Ala Gln Phe
        275                 280                 285

Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val Trp Thr Ser Gln Met
    290                 295                 300

Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr Glu Gln
305                 310                 315                 320

Trp Lys Val Leu Asn Glu Ile Asp Ala Ser Tyr Glu Asp Leu Val Gln
                325                 330                 335

Arg Leu Glu Pro Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu
            340                 345                 350

Val Ile Cys His Gln Ala Val Met Arg Cys Leu Leu Ala Tyr Phe Leu
        355                 360                 365

Asp Lys Ala Ala Glu Gln Leu Pro Tyr Leu Lys Cys Pro Leu His Thr
    370                 375                 380

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

Phe Leu Asn Val Ala Ala Val Asn Thr His Arg Asp Arg Pro Gln Asn
                405                 410                 415

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

His Gln
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<210> 544
<211> 462
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388394"

<400> 544
Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile Trp
1 5 10 15

Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln Arg Gly
20 25 30

Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val Gly Leu Pro
35 40 45

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

Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val Gly Gln Tyr Arg Arg
65 70 75 80

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

Glu Glu Gly Leu Lys Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg
100 105 110

Asp Val Arg Arg Phe Leu Ser Glu Glu Gly Gly His Val Ala Val Phe
115 120 125

Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ala Thr Ile Phe Asn Phe
130 135 140

Gly Glu Gln Asn Gly Tyr Lys Thr Phe Phe Val Glu Ser Ile Cys Val
145 150 155 160

Asp Pro Glu Val Ile Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser
165 170 175

```
Pro Asp Tyr Val Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met
            180                 185                 190

Arg Arg Ile Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp
        195                 200                 205

Leu Asp Arg Asp Leu Ser Tyr Ile Lys Ile Met Asp Val Gly Gln Ser
    210                 215                 220

Tyr Val Val Asn Arg Val Ala Asp His Ile Gln Ser Arg Ile Val Tyr
225                 230                 235                 240

Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg
                245                 250                 255

His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg Ile Gly Gly Asp Pro
            260                 265                 270

Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys Ser Leu Ala Gln Phe
        275                 280                 285

Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val Trp Thr Ser Gln Met
    290                 295                 300

Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr Glu Gln
305                 310                 315                 320

Trp Lys Gly Val Cys Glu Glu Met Thr Tyr Glu Glu Ile Gln Asp Asn
                325                 330                 335

Tyr Pro Leu Glu Phe Ala Leu Arg Asp Gln Asp Lys Tyr Arg Tyr Arg
            340                 345                 350

Tyr Pro Lys Gly Glu Ser Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro
        355                 360                 365

Val Ile Met Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile Cys His
    370                 375                 380

Gln Ala Val Met Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ala Ala
385                 390                 395                 400
```

```
Glu Gln Leu Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu
                405                 410                 415

Thr Pro Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Phe Leu Asn Val
            420                 425                 430

Ala Ala Val Asn Thr His Arg Asp Arg Pro Gln Asn Val Asp Ile Ser
        435                 440                 445

Arg Pro Pro Glu Glu Ala Leu Val Thr Val Pro Ala His Gln
    450                 455                 460


<210> 545
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389169"

<400> 545
Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile Trp
1               5                   10                  15

Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln Arg Gly
            20                  25                  30

Glu Leu Ser Lys Val Gly
        35


<210> 546
<211> 175
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 96; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393047"

<400> 546
Met Thr Asn Cys Pro Thr Leu Ile Val Met Val Gly Leu Pro Ala Arg
1 5 10 15

Gly Lys Thr Tyr Ile Ser Lys Lys Leu Thr Arg Tyr Leu Asn Trp Ile
20 25 30

Gly Val Pro Thr Arg Glu Phe Asn Val Gly Gln Tyr Arg Arg Asp Val
35 40 45

Val Lys Thr Tyr Lys Ser Phe Glu Phe Phe Leu Pro Asp Asn Glu Glu
50 55 60

Gly Leu Lys Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu Arg Asp Val
65 70 75 80

Arg Arg Phe Leu Ser Glu Glu Gly Gly His Val Ala Val Phe Asp Ala
85 90 95

Thr Asn Thr Thr Arg Glu Arg Arg Ala Thr Ile Phe Asn Phe Gly Glu
100 105 110

Gln Asn Gly Tyr Lys Thr Phe Phe Val Glu Ser Ile Cys Val Asp Pro
115 120 125

Glu Val Ile Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser Pro Asp
130 135 140

Tyr Val Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met Arg Arg
145 150 155 160

```
Ile Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp Leu
                165                 170                 175


<210> 547
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000400772"

<400> 547
Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile Trp
1               5                   10                  15


Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln Arg Gly
            20                  25                  30


Gly Gly Leu Val Phe Gln Gln Glu Glu Gly Cys Leu Leu Ala Leu Lys
        35                  40                  45


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


Glu Lys Tyr Ala Val Trp Ala Cys Val Cys Val Pro Gly His Cys Ala
65                  70                  75                  80


<210> 548
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "
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<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000407657"

<400> 548
Met Asp Arg Gly Ser Leu Gly Gly Ser Ser Leu Thr Asp Leu Gly Pro
1 5 10 15

Gly Ser Ser Arg Arg Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val
20 25 30

Met Val Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Lys Lys Leu
35 40 45

Thr Arg Tyr Leu Asn Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val
50 55 60

Gly Gln Tyr Arg Arg Asp Val Val Lys Thr Tyr Lys Ser Phe Glu Phe
65 70 75 80

Phe Leu Pro Asp Asn Glu Glu Gly Leu Lys Ile Arg Lys Gln Cys Ala
85 90 95

Leu Ala Ala Leu Arg Asp Val Arg Arg Phe Leu Ser Glu Glu Gly Gly
100 105 110

His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ala
115 120 125

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

Glu Ser Ile Cys Val Asp Pro Glu Val Ile Ala Ala Asn Ile Val Gln
145 150 155 160

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

```
Thr Glu Asp Phe Met Arg Arg Ile Glu Cys Tyr Glu Asn Ser Tyr Glu
            180                 185                 190

Ser Leu Asp Glu Asp Leu Asp Arg Asp Leu Ser Tyr Ile Lys Ile Met
        195                 200                 205

Asp Val Gly Gln Ser Tyr Val Val Asn Arg Val Ala Asp His Ile Gln
    210                 215                 220

Ser Arg Ile Val Tyr Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser
225                 230                 235                 240

Ile Tyr Leu Cys Arg His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg
                245                 250                 255

Ile Gly Gly Asp Pro Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys
            260                 265                 270

Ser Leu Ala Gln Phe Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val
        275                 280                 285

Trp Thr Ser Gln Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly
    290                 295                 300

Val Pro Tyr Glu Gln Trp Lys Val Leu Asn Glu Ile Asp Ala
305                 310                 315


<210> 549
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 96; "

<220>
<221> source
<223> /note="Gene Symbol: PFKFB4; "

<220>
<221> source
<223> /note="Gene Name:
      6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000415764"

<400> 549
Met Arg Ala Arg Asp Ser Thr Gly His Pro Leu Met Leu Arg Glu Gln
1 5 10 15

Thr Leu Gly Gln His Leu His Gly Glu Asp Thr Gly Glu Trp Glu His
20 25 30

Thr Cys Glu Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val
35 40 45

Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Lys Lys Leu Thr Arg
50 55 60

Tyr Leu Asn Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val Gly Gln
65 70 75 80

Tyr Arg Arg Asp Val Val Lys Thr Tyr Lys Ser Phe Glu Phe Phe Leu
85 90 95

Pro Asp Asn Glu Glu Gly Leu Lys Ile Arg Lys Gln Cys Ala Leu Ala
100 105 110

Ala Leu Arg Asp Val Arg Arg Phe Leu Ser Glu Glu Gly Gly His Val
115 120 125

Ala

<210> 550
<211> 258
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 97; "

<220>
<221> source
<223> /note="Gene Symbol: PGLS; "

<220>
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<223> /note="Gene Name:
6-phosphogluconolactonase; "

<220>
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<223> /note="Uniprot ID: O95336; "

<220>
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<400> 550
Met Ala Ala Pro Ala Pro Gly Leu Ile Ser Val Phe Ser Ser Ser Gln
1   5   10   15

Glu Leu Gly Ala Ala Leu Ala Gln Leu Val Ala Gln Arg Ala Ala Cys
            20   25   30

Cys Leu Ala Gly Ala Arg Ala Arg Phe Ala Leu Gly Leu Ser Gly Gly
        35   40   45

Ser Leu Val Ser Met Leu Ala Arg Glu Leu Pro Ala Ala Val Ala Pro
    50   55   60

Ala Gly Pro Ala Ser Leu Ala Arg Trp Thr Leu Gly Phe Cys Asp Glu
65   70   75   80

Arg Leu Val Pro Phe Asp His Ala Glu Ser Thr Tyr Gly Leu Tyr Arg
                85   90   95

Thr His Leu Leu Ser Arg Leu Pro Ile Pro Glu Ser Gln Val Ile Thr
            100   105   110

Ile Asn Pro Glu Leu Pro Val Glu Glu Ala Ala Glu Asp Tyr Ala Lys
        115   120   125

Lys Leu Arg Gln Ala Phe Gln Gly Asp Ser Ile Pro Val Phe Asp Leu
    130   135   140

Leu Ile Leu Gly Val Gly Pro Asp Gly His Thr Cys Ser Leu Phe Pro
145   150   155   160

Asp His Pro Leu Leu Gln Glu Arg Glu Lys Ile Val Ala Pro Ile Ser
                165   170   175

Asp Ser Pro Lys Pro Pro Pro Gln Arg Val Thr Leu Thr Leu Pro Val
            180   185   190

```
Leu Asn Ala Ala Arg Thr Val Ile Phe Val Ala Thr Gly Glu Gly Lys
        195                 200                 205

Ala Ala Val Leu Lys Arg Ile Leu Glu Asp Gln Glu Glu Asn Pro Leu
    210                 215                 220

Pro Ala Ala Leu Val Gln Pro His Thr Gly Lys Leu Cys Trp Phe Leu
225                 230                 235                 240

Asp Glu Ala Ala Ala Arg Leu Leu Thr Val Pro Phe Glu Lys His Ser
                245                 250                 255

Thr Leu
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<210> 551
<211> 179
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
6-phosphogluconolactonase; "

<220>
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<400> 551

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

Glu Leu Gly Ala Ala Leu Ala Gln Leu Val Ala Gln Arg Ala Ala Cys
            20                  25                  30

Cys Leu Ala Gly Ala Arg Ala Arg Phe Ala Leu Gly Leu Ser Gly Gly
        35                  40                  45

Ser Leu Val Ser Met Leu Ala Arg Glu Leu Pro Ala Ala Val Ala Pro
    50                  55                  60
```

```
Ala Gly Pro Ala Ser Leu Ala Arg Trp Thr Leu Gly Phe Cys Asp Glu
65                  70                  75                  80

Arg Leu Val Pro Phe Asp His Ala Glu Ser Thr Tyr Gly Leu Tyr Arg
                85                  90                  95

Thr His Leu Leu Ser Arg Leu Pro Ile Pro Glu Ser Gln Val Ile Thr
            100                 105                 110

Ile Asn Pro Glu Leu Pro Val Glu Glu Ala Ala Glu Asp Tyr Ala Lys
        115                 120                 125

Lys Leu Arg Gln Glu Leu Pro Gln Gly Ser Leu Ala Asp Pro Phe Glu
    130                 135                 140

Glu Ser Pro Leu Arg Gly His Ser Pro Ala Leu Gly Ser Leu Lys Ala
145                 150                 155                 160

Thr Arg Pro Leu Leu Pro Arg His Ser Lys Gly Thr Pro Ser Arg Phe
                165                 170                 175

Ser Thr Cys
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<210> 552
<211> 147
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 97; "

<220>
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<220>
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<223> /note="Gene Name:
6-phosphogluconolactonase; "

<220>
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<223> /note="ENSP ID: ENSP00000471951"

<400> 552

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Ala Gly Pro Ala Ser Leu Ala Arg Trp Thr Leu Gly Phe Cys Asp Glu
1               5                   10                  15

Arg Leu Val Pro Phe Asp His Ala Glu Ser Thr Tyr Gly Leu Tyr Arg
            20                  25                  30

Thr His Leu Leu Ser Arg Leu Pro Ile Pro Glu Ser Gln Val Ile Thr
        35                  40                  45

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

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

Leu Ile Leu Gly Val Gly Pro Asp Gly His Thr Cys Ser Leu Phe Pro
                85                  90                  95

Asp His Pro Leu Leu Gln Arg Ile Leu Glu Asp Gln Glu Glu Asn Pro
            100                 105                 110

Leu Pro Ala Ala Leu Val Gln Pro His Thr Gly Lys Leu Cys Trp Phe
        115                 120                 125

Leu Asp Glu Ala Ala Ala Arg Leu Leu Thr Val Pro Phe Glu Lys His
    130                 135                 140

Ser Thr Leu
145
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<210> 553
<211> 216
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 97; "

<220>
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<220>
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<223> /note="Gene Name:
6-phosphogluconolactonase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472345"

<400> 553
Met Ala Ala Pro Ala Pro Gly Leu Ile Ser Val Phe Ser Ser Ser Gln
1   5   10   15

Glu Leu Gly Ala Ala Leu Ala Gln Leu Val Ala Gln Arg Ala Ala Cys
            20   25   30

Cys Leu Ala Gly Ala Arg Ala Arg Phe Ala Leu Gly Leu Ser Gly Gly
        35   40   45

Ser Leu Val Ser Met Leu Ala Arg Glu Leu Pro Ala Ala Val Ala Pro
    50   55   60

Ala Gly Pro Ala Ser Leu Ala Arg Trp Thr Leu Gly Phe Cys Asp Glu
65   70   75   80

Arg Leu Val Pro Phe Asp His Ala Glu Ser Thr Tyr Gly Leu Tyr Arg
                85   90   95

Met Glu Lys Leu Arg Pro Glu Glu Thr His Leu Leu Ser Arg Leu Pro
            100   105   110

Ile Pro Glu Ser Gln Val Ile Thr Ile Asn Pro Glu Leu Pro Val Glu
        115   120   125

Glu Ala Ala Glu Asp Tyr Ala Lys Lys Leu Arg Gln Ala Phe Gln Gly
    130   135   140

Asp Ser Ile Pro Val Phe Asp Leu Leu Ile Leu Gly Val Gly Pro Asp
145   150   155   160

Gly His Thr Cys Ser Leu Phe Pro Asp His Pro Leu Leu Gln Glu Arg
                165   170   175

Glu Lys Ile Val Ala Pro Ile Ser Asp Ser Pro Lys Pro Pro Pro Gln
            180   185   190

Arg Val Thr Leu Thr Leu Pro Val Leu Asn Ala Ala Arg Thr Val Ile
        195   200   205

Phe Val Ala Thr Gly Glu Gly Lys
210 215

<210> 554
<211> 145
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 98; "

<220>
<221> source
<223> /note="Gene Symbol: PTS; "

<220>
<221> source
<223> /note="Gene Name:
6-pyruvoyltetrahydropterin synthase; "

<220>
<221> source
<223> /note="Uniprot ID: Q03393; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000280362"

<400> 554
Met Ser Thr Glu Gly Gly Gly Arg Arg Cys Gln Ala Gln Val Ser Arg
1 5 10 15

Arg Ile Ser Phe Ser Ala Ser His Arg Leu Tyr Ser Lys Phe Leu Ser
20 25 30

Asp Glu Glu Asn Leu Lys Leu Phe Gly Lys Cys Asn Asn Pro Asn Gly
35 40 45

His Gly His Asn Tyr Lys Val Val Val Thr Val His Gly Glu Ile Asp
50 55 60

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

Glu Glu Ala Ile Met Gln Pro Leu Asp His Lys Asn Leu Asp Met Asp
85 90 95

Val Pro Tyr Phe Ala Asp Val Val Ser Thr Thr Glu Asn Val Ala Val

```
            100                 105                 110

Tyr Ile Trp Asp Asn Leu Gln Lys Val Leu Pro Val Gly Val Leu Tyr
        115                 120                 125

Lys Val Lys Val Tyr Glu Thr Asp Asn Asn Ile Val Val Tyr Lys Gly
    130                 135                 140

Glu
145
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<210> 555
<211> 61
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: PTS; "

<220>
<221> source
<223> /note="Gene Name:
6-pyruvoyltetrahydropterin synthase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431750"

<400> 555

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Met Ser Thr Glu Gly Gly Gly Arg Arg Cys Gln Ala Gln Val Ser Arg
1               5                   10                  15

Arg Ile Ser Phe Ser Ala Ser His Arg Leu Tyr Ser Lys Phe Leu Ser
            20                  25                  30

Asp Glu Glu Asn Leu Lys Leu Phe Gly Lys Cys Asn Asn Pro Asn Gly
        35                  40                  45

His Gly His Asn Tyr Lys Gly Gly Asp Tyr Ala Ala Pro
    50                  55                  60
```

<210> 556
<211> 55
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 98; "

<220>
<221> source
<223> /note="Gene Symbol: PTS; "

<220>
<221> source
<223> /note="Gene Name:
6-pyruvoyltetrahydropterin synthase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433469"

<400> 556
Met Ser Thr Glu Gly Gly Gly Arg Arg Cys Gln Ala Gln Val Ser Arg
1 5 10 15

Arg Ile Ser Phe Ser Ala Ser His Arg Leu Tyr Ser Lys Phe Leu Ser
20 25 30

Asp Glu Glu Asn Leu Lys Leu Phe Gly Lys Cys Asn Asn Pro Asn Gly
35 40 45

His Gly His Asn Tyr Lys Asp
50 55

<210> 557
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 98; "

<220>
<221> source
<223> /note="Gene Symbol: PTS; "

<220>
<221> source
<223> /note="Gene Name:
6-pyruvoyltetrahydropterin synthase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434688"

<400> 557
Met Val Met Asn Leu Ala Asp Leu Lys Lys Tyr Met Glu Glu Ala Ile
1   5   10   15

Met Gln Pro Leu Asp His Lys Asn Leu Asp Met Asp Val Pro Tyr Phe
            20   25   30

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

Asn Leu Gln Lys Val Leu Pro Val Gly Val Leu Tyr Lys Val Lys Val
    50   55   60

Tyr Glu Thr Asp Asn Asn Ile Val Val Tyr Lys Gly Glu
65   70   75

<210> 558
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 98; "

<220>
<221> source
<223> /note="Gene Symbol: PTS; "

<220>
<221> source
<223> /note="Gene Name:
      6-pyruvoyltetrahydropterin synthase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435895"

<400> 558
Met Ser Thr Glu Gly Gly Gly Arg Arg Cys Gln Ala Gln Val Ser Arg
1   5   10   15

Arg Ile Ser Phe Ser Ala Ser His Arg Leu Tyr Ser Lys Phe Leu Ser
            20   25   30

Asp Glu Glu Asn Leu Lys Leu Phe Gly Lys Cys Asn Asn Pro Asn Gly
        35   40   45

```
His Gly His Asn Tyr Lys Asp
    50                  55


<210> 559
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 99; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR7; "

<220>
<221> source
<223> /note="Gene Name:
      7-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UBM7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000347717"

<400> 559
Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
1               5                   10                  15


Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
            20                  25                  30


Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
        35                  40                  45


Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
    50                  55                  60


Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
65                  70                  75                  80


Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
                85                  90                  95


Ala Gln Leu Tyr Thr Leu Trp Val Thr Phe Gln Val Leu Leu Tyr Thr
            100                 105                 110
```

```
Ser Leu Pro Asp Phe Cys His Lys Phe Leu Pro Gly Tyr Val Gly Gly
        115                 120                 125

Ile Gln Glu Gly Ala Val Thr Pro Ala Gly Val Val Asn Lys Tyr Gln
    130                 135                 140

Ile Asn Gly Leu Gln Ala Trp Leu Leu Thr His Leu Leu Trp Phe Ala
145                 150                 155                 160

Asn Ala His Leu Leu Ser Trp Phe Ser Pro Thr Ile Ile Phe Asp Asn
                165                 170                 175

Trp Ile Pro Leu Leu Trp Cys Ala Asn Ile Leu Gly Tyr Ala Val Ser
            180                 185                 190

Thr Phe Ala Met Val Lys Gly Tyr Phe Phe Pro Thr Ser Ala Arg Asp
        195                 200                 205

Cys Lys Phe Thr Gly Asn Phe Phe Tyr Asn Tyr Met Met Gly Ile Glu
    210                 215                 220

Phe Asn Pro Arg Ile Gly Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn
225                 230                 235                 240

Gly Arg Pro Gly Ile Val Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala
                245                 250                 255

Ala Lys Gln Arg Glu Leu His Ser His Val Thr Asn Ala Met Val Leu
            260                 265                 270

Val Asn Val Leu Gln Ala Ile Tyr Val Ile Asp Phe Phe Trp Asn Glu
        275                 280                 285

Thr Trp Tyr Leu Lys Thr Ile Asp Ile Cys His Asp His Phe Gly Trp
    290                 295                 300

Tyr Leu Gly Trp Gly Asp Cys Val Trp Leu Pro Tyr Leu Tyr Thr Leu
305                 310                 315                 320

Gln Gly Leu Tyr Leu Val Tyr His Pro Val Gln Leu Ser Thr Pro His
                325                 330                 335
```

```
Ala Val Gly Val Leu Leu Leu Gly Leu Val Gly Tyr Tyr Ile Phe Arg
            340                 345                 350

Val Ala Asn His Gln Lys Asp Leu Phe Arg Arg Thr Asp Gly Arg Cys
        355                 360                 365

Leu Ile Trp Gly Arg Lys Pro Lys Val Ile Glu Cys Ser Tyr Thr Ser
    370                 375                 380

Ala Asp Gly Gln Arg His His Ser Lys Leu Leu Val Ser Gly Phe Trp
385                 390                 395                 400

Gly Val Ala Arg His Phe Asn Tyr Val Gly Asp Leu Met Gly Ser Leu
                405                 410                 415

Ala Tyr Cys Leu Ala Cys Gly Gly Gly His Leu Leu Pro Tyr Phe Tyr
            420                 425                 430

Ile Ile Tyr Met Ala Ile Leu Leu Thr His Arg Cys Leu Arg Asp Glu
        435                 440                 445

His Arg Cys Ala Ser Lys Tyr Gly Arg Asp Trp Glu Arg Tyr Thr Ala
    450                 455                 460

Ala Val Pro Tyr Arg Leu Leu Pro Gly Ile Phe
465                 470                 475


<210> 560
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 99; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR7; "

<220>
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<223> /note="Gene Name:
      7-dehydrocholesterol reductase; "

<220>
<221> source
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<223> /note="Uniprot ID: Q9UBM7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384739"

<400> 560
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Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
1               5                  10                  15

Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
            20                  25                  30

Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
        35                  40                  45

Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
    50                  55                  60

Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
65                  70                  75                  80

Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
                85                  90                  95

Ala Gln Leu Tyr Thr Leu Trp Val Thr Phe Gln Val Leu Leu Tyr Thr
            100                 105                 110

Ser Leu Pro Asp Phe Cys His Lys Phe Leu Pro Gly Tyr Val Gly Gly
        115                 120                 125

Ile Gln Glu Gly Ala Val Thr Pro Ala Gly Val Val Asn Lys Tyr Gln
    130                 135                 140

Ile Asn Gly Leu Gln Ala Trp Leu Leu Thr His Leu Leu Trp Phe Ala
145                 150                 155                 160

Asn Ala His Leu Leu Ser Trp Phe Ser Pro Thr Ile Ile Phe Asp Asn
                165                 170                 175

Trp Ile Pro Leu Leu Trp Cys Ala Asn Ile Leu Gly Tyr Ala Val Ser
            180                 185                 190

Thr Phe Ala Met Val Lys Gly Tyr Phe Phe Pro Thr Ser Ala Arg Asp
        195                 200                 205
```

Cys Lys Phe Thr Gly Asn Phe Phe Tyr Asn Tyr Met Met Gly Ile Glu
210 215 220

Phe Asn Pro Arg Ile Gly Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn
225 230 235 240

Gly Arg Pro Gly Ile Val Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala
245 250 255

Ala Lys Gln Arg Glu Leu His Ser His Val Thr Asn Ala Met Val Leu
260 265 270

Val Asn Val Leu Gln Ala Ile Tyr Val Ile Asp Phe Phe Trp Asn Glu
275 280 285

Thr Trp Tyr Leu Lys Thr Ile Asp Ile Cys His Asp His Phe Gly Trp
290 295 300

Tyr Leu Gly Trp Gly Asp Cys Val Trp Leu Pro Tyr Leu Tyr Thr Leu
305 310 315 320

Gln Gly Leu Tyr Leu Val Tyr His Pro Val Gln Leu Ser Thr Pro His
325 330 335

Ala Val Gly Val Leu Leu Leu Gly Leu Val Gly Tyr Tyr Ile Phe Arg
340 345 350

Val Ala Asn His Gln Lys Asp Leu Phe Arg Arg Thr Asp Gly Arg Cys
355 360 365

Leu Ile Trp Gly Arg Lys Pro Lys Val Ile Glu Cys Ser Tyr Thr Ser
370 375 380

Ala Asp Gly Gln Arg His His Ser Lys Leu Leu Val Ser Gly Phe Trp
385 390 395 400

Gly Val Ala Arg His Phe Asn Tyr Val Gly Asp Leu Met Gly Ser Leu
405 410 415

Ala Tyr Cys Leu Ala Cys Gly Gly Gly His Leu Leu Pro Tyr Phe Tyr
420 425 430

```
Ile Ile Tyr Met Ala Ile Leu Leu Thr His Arg Cys Leu Arg Asp Glu
        435                 440                 445


His Arg Cys Ala Ser Lys Tyr Gly Arg Asp Trp Glu Arg Tyr Thr Ala
    450                 455                 460


Ala Val Pro Tyr Arg Leu Leu Pro Gly Ile Phe
465                 470                 475


<210> 561
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 99; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR7; "

<220>
<221> source
<223> /note="Gene Name:
      7-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432256"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 561
Xaa Phe Tyr Asn Tyr Met Met Gly Ile Glu Phe Asn Pro Arg Ile Gly
1               5                   10                  15


Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn Gly Arg Pro Gly Ile Val
            20                  25                  30


Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala Ala Lys Gln Arg Glu Leu
        35                  40                  45


His Ser His Val Thr Asn Ala Met Val Leu Val Asn Val Leu Gln Ala
    50                  55                  60
```

```
Ile Tyr Val Ile Asp Phe Phe Trp Asn Glu Thr Trp Tyr Leu Lys Thr
65                  70                  75                  80


Ile Asp Ile Cys His Asp His Phe Gly Trp Tyr Leu Gly Trp Gly Asp
                85                  90                  95


Cys Val Trp Leu Pro Tyr Leu Tyr Thr Leu Gln Met Arg Asn Ala Ala
            100                 105                 110


Val Glu Ala Glu
        115


<210> 562
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 99; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR7; "

<220>
<221> source
<223> /note="Gene Name:
      7-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432589"

<400> 562
Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
1               5                   10                  15


Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
            20                  25                  30


Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
        35                  40                  45


Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
    50                  55                  60


Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
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65 70 75 80

Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
85 90 95

Ala Gln Leu Tyr Thr Leu Trp Val Thr
100 105

<210> 563
<211> 221
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 99; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR7; "

<220>
<221> source
<223> /note="Gene Name:
7-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435011"

<400> 563
Ile Asn Leu Ser Phe Ala Ala Lys Gln Arg Glu Leu His Ser His Val
1 5 10 15

Thr Asn Ala Met Val Leu Val Asn Val Leu Gln Ala Ile Tyr Val Ile
20 25 30

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

His Asp His Phe Gly Trp Tyr Leu Gly Trp Gly Asp Cys Val Trp Leu
50 55 60

Pro Tyr Leu Tyr Thr Leu Gln Gly Leu Tyr Leu Val Tyr His Pro Val
65 70 75 80

Gln Leu Ser Thr Pro His Ala Val Gly Val Leu Leu Leu Gly Leu Val
85 90 95

```
Gly Tyr Tyr Ile Phe Arg Val Ala Asn His Gln Lys Asp Leu Phe Arg
            100                 105                 110

Arg Thr Asp Gly Arg Cys Leu Ile Trp Gly Arg Lys Pro Lys Val Ile
        115                 120                 125

Glu Cys Ser Tyr Thr Ser Ala Asp Gly Gln Arg His His Ser Lys Leu
    130                 135                 140

Leu Val Ser Gly Phe Trp Gly Val Ala Arg His Phe Asn Tyr Val Gly
145                 150                 155                 160

Asp Leu Met Gly Ser Leu Ala Tyr Cys Leu Ala Cys Gly Gly Gly His
                165                 170                 175

Leu Leu Pro Tyr Phe Tyr Ile Ile Tyr Met Ala Ile Leu Leu Thr His
            180                 185                 190

Arg Cys Leu Arg Asp Glu His Arg Cys Ala Ser Lys Glu Phe Arg Val
        195                 200                 205

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


<210> 564
<211> 258
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 99; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
      7-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435047"

<400> 564
Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
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1               5                   10                  15

Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
            20                  25                  30

Cys Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
        35                  40                  45

Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
    50                  55                  60

Ala Gln Leu Tyr Thr Leu Trp Val Thr Phe Gln Val Leu Leu Tyr Thr
65                  70                  75                  80

Ser Leu Pro Asp Phe Cys His Lys Phe Leu Pro Gly Tyr Val Gly Gly
                85                  90                  95

Ile Gln Glu Gly Ala Val Thr Pro Ala Gly Val Val Asn Lys Tyr Gln
            100                 105                 110

Ile Asn Gly Leu Gln Ala Trp Leu Leu Thr His Leu Leu Trp Phe Ala
        115                 120                 125

Asn Ala His Leu Leu Ser Trp Phe Ser Pro Thr Ile Ile Phe Asp Asn
    130                 135                 140

Trp Ile Pro Leu Leu Trp Cys Ala Asn Ile Leu Gly Tyr Ala Val Ser
145                 150                 155                 160

Thr Phe Ala Met Val Lys Gly Tyr Phe Phe Pro Thr Ser Ala Arg Asp
                165                 170                 175

Cys Lys Phe Thr Gly Asn Phe Phe Tyr Asn Tyr Met Met Gly Ile Glu
            180                 185                 190

Phe Asn Pro Arg Ile Gly Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn
        195                 200                 205

Gly Arg Pro Gly Ile Val Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala
    210                 215                 220

Ala Lys Gln Arg Glu Leu His Ser His Val Thr Asn Ala Met Val Leu
225                 230                 235                 240
```

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Val Asn Val Leu Gln Ala Ile Tyr Val Ile Asp Phe Phe Trp Asn Glu
                245                 250                 255


Thr Trp



<210> 565
<211> 73
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 99; "

<220>
<221> source
<223> /note="Gene Symbol: DHCR7; "

<220>
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<223> /note="Gene Name:
      7-dehydrocholesterol reductase; "

<220>
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<223> /note="ENSP ID: ENSP00000435058"

<400> 565
Met Gly Pro Ser Val Thr Ala Cys Ile Arg Pro Arg Arg Glu Val Asp
1               5                   10                  15


Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu Phe Ala Pro Phe
            20                  25                  30


Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr Ser Cys Ala Leu
        35                  40                  45


Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala Arg Leu Ser Asp
    50                  55                  60


Ile Trp Ala Lys Thr Pro Pro Ile Thr
65                  70


<210> 566
<211> 164
<212> PRT
<213> Homo sapiens
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<220>
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<220>
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<220>
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<223> /note="Gene Name:
7-dehydrocholesterol reductase; "

<220>
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<223> /note="ENSP ID: ENSP00000435668"

<400> 566
Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
1 5 10 15

Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
20 25 30

Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
35 40 45

Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
50 55 60

Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
65 70 75 80

Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
85 90 95

Ala Gln Leu Tyr Thr Leu Trp Val Thr Phe Gln Val Leu Leu Tyr Thr
100 105 110

Ser Leu Pro Asp Phe Cys His Lys Phe Leu Pro Gly Tyr Val Gly Gly
115 120 125

Ile Gln Glu Gly Ala Val Thr Pro Ala Gly Val Val Asn Lys Tyr Gln
130 135 140

Ile Asn Gly Leu Gln Ala Trp Leu Leu Thr His Leu Leu Trp Phe Ala
145 150 155 160

Asn Ala His Leu

<210> 567
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 99; "

<220>
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<220>
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<223> /note="Gene Name:
7-dehydrocholesterol reductase; "

<220>
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<223> /note="ENSP ID: ENSP00000435707"

<400> 567
Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
1 5 10 15

Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
20 25 30

Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
35 40 45

Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
50 55 60

Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
65 70 75 80

Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
85 90 95

Ala Gln Leu Tyr Thr Leu Trp Val Thr Phe Gln
100 105

<210> 568
<211> 245
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: DHCR7; "

<220>
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<223> /note="Gene Name:
7-dehydrocholesterol reductase; "

<220>
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<223> /note="ENSP ID: ENSP00000435956"

<400> 568
Thr Gly Asn Phe Phe Tyr Asn Tyr Met Met Gly Ile Glu Phe Asn Pro
1 5 10 15

Arg Ile Gly Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn Gly Arg Pro
20 25 30

Gly Ile Val Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala Ala Lys Gln
35 40 45

Arg Glu Leu His Ser His Val Thr Asn Ala Met Val Leu Val Asn Val
50 55 60

Leu Gln Ala Ile Tyr Val Ile Asp Phe Phe Trp Asn Glu Thr Trp Tyr
65 70 75 80

Leu Lys Thr Ile Asp Ile Cys His Asp His Phe Gly Trp Tyr Leu Gly
85 90 95

Trp Gly Asp Cys Val Trp Leu Pro Tyr Leu Tyr Thr Leu Gln Lys Arg
100 105 110

Thr Arg Arg Gln Gly Val Cys Gln Arg Gln Ser Trp Gly Leu Thr Pro
115 120 125

Gly Arg Trp Ala Pro Glu Pro Thr Leu Leu Ser Ser Pro Trp Ala Lys
130 135 140

```
His Arg Leu Thr Pro Ser Pro Ser Pro Pro Arg Val Cys Thr Trp Cys
145                 150                 155                 160

Thr Thr Pro Cys Ser Cys Pro Pro Arg Thr Pro Trp Ala Ser Cys Cys
                165                 170                 175

Trp Ala Trp Trp Ala Thr Thr Ser Ser Gly Trp Pro Thr Thr Arg Arg
            180                 185                 190

Thr Cys Ser Ala Ala Arg Met Gly Ala Ala Ser Ser Gly Ala Gly Ser
        195                 200                 205

Pro Arg Ser Ser Ser Ala Pro Thr His Pro Pro Met Gly Arg Gly Thr
    210                 215                 220

Thr Ala Ser Cys Trp Cys Arg Ala Ser Gly Ala Trp Pro Ala Thr Ser
225                 230                 235                 240

Thr Thr Ser Ala Thr
                245
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<210> 569
<211> 91
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
7-dehydrocholesterol reductase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436007"

<400> 569

```
Met Ala Ala Lys Ser Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
1               5                   10                  15
```

```
Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
            20                  25                  30

Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
        35                  40                  45

Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
    50                  55                  60

Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
65                  70                  75                  80

Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro
                85                  90


<210> 570
<211> 357
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
      8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID:  O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000303132"

<400> 570
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1               5                   10                  15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
            20                  25                  30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
        35                  40                  45
```

```
Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
    50                  55                  60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65                  70                  75                  80

Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85                  90                  95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100                 105                 110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115                 120                 125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130                 135                 140

Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145                 150                 155                 160

Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Gly Leu Leu Gly Asn Ala Phe
                245                 250                 255

Asp Gly His Gln Leu Leu Arg Pro Leu Ile Phe Cys Gln Asp His Leu
            260                 265                 270
```

```
Arg Glu Gly Pro Pro Ile Gly Arg Gly Asp Ser Gln Gly Glu Glu Leu
        275                 280                 285

Glu Pro Gln Leu Pro Ser Ser Leu Ser Ser Ile Pro Tyr Gly Phe Cys
    290                 295                 300

Asp His Cys Trp Thr Lys Asp Val Asp Asp Pro Pro Leu Val Thr His
305                 310                 315                 320

Pro Ser Pro Gly Ser Arg Asp Gly His Met Thr Gln Ala Trp Pro Val
                325                 330                 335

Lys Val Val Ser Pro Leu Ala Thr Val Ile Gly His Val Met Gln Ala
            340                 345                 350

Ser Leu Leu Ala Leu
        355


<210> 571
<211> 356
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
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<223> /note="Gene Name:
      8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID:  O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000305527"

<400> 571
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1               5                   10                  15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
```

```
            20                  25                  30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
        35                  40                  45

Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
    50                  55                  60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65                  70                  75                  80

Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85                  90                  95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100                 105                 110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115                 120                 125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130                 135                 140

Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145                 150                 155                 160

Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Val Ala Asp Cys Ile Cys Leu
                245                 250                 255
```

```
Met Ala Leu Asp Lys Pro Gln Ala Val Pro Val Asp Val His Met Trp
            260                 265                 270

His Ile Ala Gln Arg Asp Tyr Ser Trp His Pro Thr Thr Ser Gln Ala
        275                 280                 285

Lys Gly Pro Ser Pro Gln Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg
    290                 295                 300

Ser Leu Trp Gly Pro Tyr Ala Gly Trp Ala Gln Ala Leu Cys Gln Val
305                 310                 315                 320

Ile Thr Thr Phe Met Thr Phe Leu Gly Pro His Arg Leu Asp Gln Met
                325                 330                 335

Pro Pro Glu Glu Leu Gln Thr Ser Ser Ser Arg Leu Gly Gly Pro Pro
            340                 345                 350

Trp Gln Cys Ile
        355
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<210> 572
<211> 410
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID: O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000305584"

<400> 572

```
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1               5                  10                  15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
            20                  25                  30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
        35                  40                  45

Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
    50                  55                  60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65                  70                  75                  80

Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85                  90                  95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100                 105                 110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115                 120                 125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130                 135                 140

Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145                 150                 155                 160

Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
```

```
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Val Ala Asp Cys Ile Cys Leu
                245                 250                 255

Met Ala Leu Asp Lys Pro Gln Ala Val Pro Val Asp Val His Met Trp
            260                 265                 270

His Ile Ala Gln Arg Asp Tyr Ser Trp His Pro Thr Thr Ser Gln Ala
        275                 280                 285

Lys Gly Pro Ser Pro Gln Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg
    290                 295                 300

Ser Leu Trp Gly Pro Tyr Ala Gly Trp Ala Gln Ala Thr Pro Pro Ser
305                 310                 315                 320

Tyr Arg Cys Cys Ser Val Pro Thr Cys Ala Asn Pro Ala Met Leu Arg
                325                 330                 335

Ser His Gln Gln Ser Ala Glu Arg Val Pro Lys Gly Arg Lys Ala Arg
            340                 345                 350

Trp Gly Thr Leu Asp Lys Glu Ile Pro Gln Ala Pro Ser Pro Pro Phe
        355                 360                 365

Pro Thr Ser Leu Ser Pro Ser Pro Pro Ser Leu Met Leu Gly Arg Gly
    370                 375                 380

Leu Pro Val Thr Thr Ser Lys Ala Arg His Pro Gln Ile Lys Gln Ser
385                 390                 395                 400

Val Cys Thr Thr Arg Trp Gly Gly Gly Tyr
                405                 410


<210> 573
<211> 424
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
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<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID: O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000306561"

<400> 573

Met	Pro	Ala	Arg	Ala	Leu	Leu	Pro	Arg	Arg	Met	Gly	His	Arg	Thr	Leu
1				5				10						15	

Ala	Ser	Thr	Pro	Ala	Leu	Trp	Ala	Ser	Ile	Pro	Cys	Pro	Arg	Ser	Glu
		20					25					30			

Leu	Arg	Leu	Asp	Leu	Val	Leu	Pro	Ser	Gly	Gln	Ser	Phe	Arg	Trp	Arg
	35					40					45				

Glu	Gln	Ser	Pro	Ala	His	Trp	Ser	Gly	Val	Leu	Ala	Asp	Gln	Val	Trp
50					55					60					

Thr	Leu	Thr	Gln	Thr	Glu	Glu	Gln	Leu	His	Cys	Thr	Val	Tyr	Arg	Gly
65				70					75					80	

Asp	Lys	Ser	Gln	Ala	Ser	Arg	Pro	Thr	Pro	Asp	Glu	Leu	Glu	Ala	Val
				85					90					95	

Arg	Lys	Tyr	Phe	Gln	Leu	Asp	Val	Thr	Leu	Ala	Gln	Leu	Tyr	His	His
		100					105					110			

Trp	Gly	Ser	Val	Asp	Ser	His	Phe	Gln	Glu	Val	Ala	Gln	Lys	Phe	Gln
	115					120					125				

Gly	Val	Arg	Leu	Leu	Arg	Gln	Asp	Pro	Ile	Glu	Cys	Leu	Phe	Ser	Phe
130					135					140					

Ile	Cys	Ser	Ser	Asn	Asn	Asn	Ile	Ala	Arg	Ile	Thr	Gly	Met	Val	Glu
145					150					155					160

```
Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Val Ala Asp Cys Ile Cys Leu
                245                 250                 255

Met Ala Leu Asp Lys Pro Gln Ala Val Pro Val Asp Val His Met Trp
            260                 265                 270

His Ile Ala Gln Arg Asp Tyr Ser Trp His Pro Thr Thr Ser Gln Ala
        275                 280                 285

Lys Gly Pro Ser Pro Gln Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg
    290                 295                 300

Ser Leu Trp Gly Pro Tyr Ala Gly Trp Ala Gln Ala Gly Leu Leu Gly
305                 310                 315                 320

Asn Ala Phe Asp Gly His Gln Leu Leu Arg Pro Leu Ile Phe Cys Gln
                325                 330                 335

Asp His Leu Arg Glu Gly Pro Pro Ile Gly Arg Gly Asp Ser Gln Gly
            340                 345                 350

Glu Glu Leu Glu Pro Gln Leu Pro Ser Ser Leu Ser Ser Ile Pro Tyr
        355                 360                 365

Gly Phe Cys Asp His Cys Trp Thr Lys Asp Val Asp Asp Pro Pro Leu
    370                 375                 380

Val Thr His Pro Ser Pro Gly Ser Arg Asp Gly His Met Thr Gln Ala
```

385 390 395 400

Trp Pro Val Lys Val Val Ser Pro Leu Ala Thr Val Ile Gly His Val
405 410 415

Met Gln Ala Ser Leu Leu Ala Leu
420

<210> 574
<211> 345
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID: O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000342851"

<400> 574
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1 5 10 15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
20 25 30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
35 40 45

Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
50 55 60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65 70 75 80

```
Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85                  90                  95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100                 105                 110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115                 120                 125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130                 135                 140

Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145                 150                 155                 160

Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Val Ala Asp Cys Ile Cys Leu
                245                 250                 255

Met Ala Leu Asp Lys Pro Gln Ala Val Pro Val Asp Val His Met Trp
            260                 265                 270

His Ile Ala Gln Arg Asp Tyr Ser Trp His Pro Thr Thr Ser Gln Ala
        275                 280                 285

Lys Gly Pro Ser Pro Gln Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg
    290                 295                 300
```

```
Ser Leu Trp Gly Pro Tyr Ala Gly Trp Ala Gln Ala Val Leu Phe Ser
305                 310                 315                 320


Ala Asp Leu Arg Gln Ser Arg His Ala Gln Glu Pro Pro Ala Lys Arg
                325                 330                 335


Arg Lys Gly Ser Lys Gly Pro Glu Gly
            340                 345


<210> 575
<211> 263
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
      8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000344899"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 575
Xaa Val Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr
1               5                   10                  15


His His Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys
            20                  25                  30


Phe Gln Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe
        35                  40                  45


Ser Phe Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met
    50                  55                  60
```

```
Val Glu Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp
65                  70                  75                  80

Asp Val Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro
                85                  90                  95

Glu Val Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg
            100                 105                 110

Tyr Val Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu
        115                 120                 125

Ala Trp Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys
    130                 135                 140

Ala Leu Cys Ile Leu Pro Gly Val Gly Thr Lys Gly Leu Leu Gly Asn
145                 150                 155                 160

Ala Phe Asp Gly His Gln Leu Leu Arg Pro Leu Ile Phe Cys Gln Asp
                165                 170                 175

His Leu Arg Glu Gly Pro Pro Ile Gly Arg Gly Asp Ser Gln Gly Glu
            180                 185                 190

Glu Leu Glu Pro Gln Leu Pro Ser Ser Leu Ser Ser Ile Pro Tyr Gly
        195                 200                 205

Phe Cys Asp His Cys Trp Thr Lys Asp Val Asp Asp Pro Pro Leu Val
    210                 215                 220

Thr His Pro Ser Pro Gly Ser Arg Asp Gly His Met Thr Gln Ala Trp
225                 230                 235                 240

Pro Val Lys Val Val Ser Pro Leu Ala Thr Val Ile Gly His Val Met
                245                 250                 255

Gln Ala Ser Leu Leu Ala Leu
            260
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<210> 576
<211> 324
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID: O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000345520"

<400> 576
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1   5   10   15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
            20   25   30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
        35   40   45

Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
    50   55   60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65   70   75   80

Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85   90   95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100   105   110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115   120   125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130   135   140

```
Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145                 150                 155                 160

Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Val Ala Asp Cys Ile Cys Leu
                245                 250                 255

Met Ala Leu Asp Lys Pro Gln Ala Val Pro Val Asp Val His Met Trp
            260                 265                 270

His Ile Ala Gln Arg Asp Tyr Ser Trp His Pro Thr Thr Ser Gln Ala
        275                 280                 285

Lys Gly Pro Ser Pro Gln Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg
    290                 295                 300

Ser Leu Trp Gly Pro Tyr Ala Gly Trp Ala Gln Ala Val Ser Val Pro
305                 310                 315                 320

Arg Cys Pro Pro
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<210> 577
<211> 195
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 100; "

<220>
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<223> /note="Gene Symbol: OGG1; "

<220>
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<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID: O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373337"

<400> 577
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1   5   10   15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
            20   25   30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
        35   40   45

Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
    50   55   60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65   70   75   80

Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85   90   95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100   105   110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115   120   125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130   135   140

Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145   150   155   160

```
Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175


Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Pro Trp
            180                 185                 190


Gln Cys Ile
        195


<210> 578
<211> 222
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000390337"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 578
Xaa Pro Cys Gly Pro Pro Ser Arg Ala Leu Ala Leu Ser Cys Ala Trp
1               5                   10                  15


Thr Trp Phe Cys Leu Leu Asp Asn Leu Ser Gly Val Arg Leu Leu Arg
            20                  25                  30


Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe Ile Cys Ser Ser Asn Asn
        35                  40                  45


Asn Ile Ala Arg Ile Thr Gly Met Val Glu Arg Leu Cys Gln Ala Phe
    50                  55                  60
```

```
Gly Pro Arg Leu Ile Gln Leu Asp Asp Val Thr Tyr His Gly Phe Pro
65                  70                  75                  80

Ser Leu Gln Ala Leu Ala Gly Pro Glu Val Glu Ala His Leu Arg Lys
                85                  90                  95

Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val Ser Ala Ser Ala Arg Ala
            100                 105                 110

Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp Leu Gln Gln Leu Arg Glu
        115                 120                 125

Ser Ser Tyr Glu Glu Ala His Lys Ala Leu Cys Ile Leu Pro Gly Val
    130                 135                 140

Gly Thr Lys Val Ala Asp Cys Ile Cys Leu Met Ala Leu Asp Lys Pro
145                 150                 155                 160

Gln Ala Val Pro Val Asp Val His Met Trp His Ile Ala Gln Arg Asp
                165                 170                 175

Tyr Ser Trp His Pro Thr Thr Ser Gln Ala Lys Gly Pro Ser Pro Gln
            180                 185                 190

Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg Ser Leu Trp Gly Pro Tyr
        195                 200                 205

Ala Gly Trp Ala Gln Ala Val Ser Val Pro Arg Cys Pro Pro
    210                 215                 220


<210> 579
<211> 168
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
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<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393726"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 579

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Xaa Ala Ser Ile Pro Cys Pro Arg Ser Glu Leu Arg Leu Asp Leu Val
1               5                   10                  15

Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg Glu Gln Ser Pro Ala His
            20                  25                  30

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

Glu Gln Leu His Cys Thr Val Tyr Arg Gly Asp Lys Ser Gln Ala Ser
    50                  55                  60

Arg Pro Thr Pro Asp Glu Leu Glu Ala Val Arg Lys Tyr Phe Gln Leu
65                  70                  75                  80

Asp Val Thr Leu Ala Gln Leu Tyr His His Trp Gly Ser Val Asp Ser
                85                  90                  95

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

Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe Ile Cys Ser Ser Asn Asn
        115                 120                 125

Asn Ile Ala Arg Ile Thr Gly Met Val Glu Arg Leu Cys Gln Ala Phe
    130                 135                 140

Gly Pro Arg Leu Ile Gln Leu Asp Asp Val Thr Tyr His Gly Phe Pro
145                 150                 155                 160

Ser Leu Gln Ala Leu Ala Gly Gly
                165
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<210> 580
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
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<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396034"

<400> 580
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1 5 10 15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
20 25 30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Leu
35 40 45

Thr Ala Ser Ala
50

<210> 581
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
<221> source
<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399810"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 581
Xaa Glu Leu Glu Ala Val Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu
1 5 10 15

Ala Gln Leu Tyr His His Trp Gly Ser Val Asp Ser His Phe Gln Glu
20 25 30

Val Ala Gln Lys Phe Gln Gly Val Arg Leu Leu Arg Gln Asp Pro Ile
35 40 45

Glu Cys Leu Phe Ser Phe Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg
50 55 60

Ile Thr Gly Met Val Glu Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu
65 70 75 80

Ile Gln Leu Asp Asp Val Thr Tyr His Gly Phe Pro Ser Leu Gln Ala
85 90 95

Leu Ala Gly Val Pro Val Pro Ala Glu Gly Leu Leu Thr Ser Ala Ser
100 105 110

Ala Phe Gln Ser Pro Leu Arg Ser Arg Gln Pro Glu Ala Asp Arg Arg
115 120 125

<210> 582
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
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<223> /note="Gene Symbol: OGG1; "

<220>
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<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402713"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 582
Xaa Met Met Ser Pro Thr Met Ala Ser Pro Ala Cys Arg Pro Trp Leu
1 5 10 15

Val Ala Asp Cys Ile Cys Leu Met Ala Leu Asp Lys Pro Gln Ala Val
20 25 30

Pro Val Asp Val His Met Trp His Ile Ala Gln Arg Asp Tyr Ser Trp
35 40 45

His Pro Thr Thr Ser Gln Ala Lys Gly Pro Ser Pro Gln Thr Asn Lys
50 55 60

Glu Leu Gly Asn Phe Phe Arg Ser Leu Trp Gly Pro Tyr Ala Gly Trp
65 70 75 80

Ala Gln Ala Thr Pro Pro Ser Tyr Arg Cys Cys Ser Val Pro Thr Cys
85 90 95

Ala Asn Pro Ala Met Leu Arg Ser His Gln Gln Ser Ala Glu Arg Val
100 105 110

Pro Lys Gly Arg Lys Ala Arg Trp Gly Thr Leu Asp Lys Glu Ile Pro
115 120 125

Gln Ala Pro Ser
130

<210> 583
<211> 322
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 100; "

<220>
<221> source
<223> /note="Gene Symbol: OGG1; "

<220>
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<223> /note="Gene Name:
8-oxoguanine DNA glycosylase; "

<220>
<221> source
<223> /note="Uniprot ID: O15527; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403598"

<400> 583
Met Pro Ala Arg Ala Leu Leu Pro Arg Arg Met Gly His Arg Thr Leu
1   5   10   15

Ala Ser Thr Pro Ala Leu Trp Ala Ser Ile Pro Cys Pro Arg Ser Glu
            20   25   30

Leu Arg Leu Asp Leu Val Leu Pro Ser Gly Gln Ser Phe Arg Trp Arg
        35   40   45

Glu Gln Ser Pro Ala His Trp Ser Gly Val Leu Ala Asp Gln Val Trp
    50   55   60

Thr Leu Thr Gln Thr Glu Glu Gln Leu His Cys Thr Val Tyr Arg Gly
65   70   75   80

Asp Lys Ser Gln Ala Ser Arg Pro Thr Pro Asp Glu Leu Glu Ala Val
                85   90   95

Arg Lys Tyr Phe Gln Leu Asp Val Thr Leu Ala Gln Leu Tyr His His
            100   105   110

Trp Gly Ser Val Asp Ser His Phe Gln Glu Val Ala Gln Lys Phe Gln
        115   120   125

Gly Val Arg Leu Leu Arg Gln Asp Pro Ile Glu Cys Leu Phe Ser Phe
    130   135   140

```
Ile Cys Ser Ser Asn Asn Asn Ile Ala Arg Ile Thr Gly Met Val Glu
145                 150                 155                 160

Arg Leu Cys Gln Ala Phe Gly Pro Arg Leu Ile Gln Leu Asp Asp Val
                165                 170                 175

Thr Tyr His Gly Phe Pro Ser Leu Gln Ala Leu Ala Gly Pro Glu Val
            180                 185                 190

Glu Ala His Leu Arg Lys Leu Gly Leu Gly Tyr Arg Ala Arg Tyr Val
        195                 200                 205

Ser Ala Ser Ala Arg Ala Ile Leu Glu Glu Gln Gly Gly Leu Ala Trp
    210                 215                 220

Leu Gln Gln Leu Arg Glu Ser Ser Tyr Glu Glu Ala His Lys Ala Leu
225                 230                 235                 240

Cys Ile Leu Pro Gly Val Gly Thr Lys Val Ala Asp Cys Ile Cys Leu
                245                 250                 255

Met Ala Leu Asp Lys Pro Gln Ala Val Pro Val Asp Val His Met Trp
            260                 265                 270

His Ile Ala Gln Arg Asp Tyr Ser Trp His Pro Thr Thr Ser Gln Ala
        275                 280                 285

Lys Gly Pro Ser Pro Gln Thr Asn Lys Glu Leu Gly Asn Phe Phe Arg
    290                 295                 300

Ser Leu Trp Gly Pro Tyr Ala Gly Trp Ala Gln Ala Ala Gly Ser Asp
305                 310                 315                 320

Ala Ser
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<210> 584
<211> 593
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000314075"

<400> 584
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1   5   10   15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20   25   30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35   40   45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50   55   60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65   70   75   80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
                85   90   95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
            100   105   110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
        115   120   125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130   135   140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145   150   155   160

```
Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165                 170                 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
            180                 185                 190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
        195                 200                 205

Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
    210                 215                 220

Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240

Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350

Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380
```

```
Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
    450                 455                 460

Leu Ala Leu Thr Thr Pro Ser Glu Glu Leu Pro Asp Arg Ala Gly Ile
465                 470                 475                 480

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Val Ala Ala Pro Pro
                565                 570                 575

Pro Gly Lys Arg Gly Thr Leu Ile Thr Arg Cys Pro Gly Phe Phe Glu
            580                 585                 590

Cys
```

<210> 585
<211> 903
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<220>
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A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000337736"

<400> 585
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1   5   10   15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20   25   30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35   40   45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50   55   60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65   70   75   80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
                85   90   95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
            100   105   110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
        115   120   125

```
Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130                 135                 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145                 150                 155                 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165                 170                 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
            180                 185                 190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
        195                 200                 205

Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
    210                 215                 220

Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240

Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350
```

```
Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380

Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
    450                 455                 460

Leu Ala Leu Thr Thr Pro Ser Glu Glu Leu Pro Asp Arg Ala Gly Ile
465                 470                 475                 480

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Gly Ser Asp Arg Asn
                565                 570                 575
```

```
Ser Met Asp Ser Val Asp Ser Cys Cys Ser Leu Lys Lys Thr Glu Ser
            580                 585                 590

Phe Gln Asn Ala Gln Ala Gly Ser Asn Pro Lys Lys Val Asp Leu Ile
        595                 600                 605

Ile Trp Glu Ile Glu Val Pro Lys His Leu Val Gly Arg Leu Ile Gly
    610                 615                 620

Lys Gln Gly Arg Tyr Val Ser Phe Leu Lys Gln Thr Ser Gly Ala Lys
625                 630                 635                 640

Ile Tyr Ile Ser Thr Leu Pro Tyr Thr Gln Ser Val Gln Ile Cys His
                645                 650                 655

Ile Glu Gly Ser Gln His His Val Asp Lys Ala Leu Asn Leu Ile Gly
            660                 665                 670

Lys Lys Phe Lys Glu Leu Asn Leu Thr Asn Ile Tyr Ala Pro Pro Leu
        675                 680                 685

Pro Ser Leu Ala Leu Pro Ser Leu Pro Met Thr Ser Trp Leu Met Leu
    690                 695                 700

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

Gly His Leu Phe Val Gln Gln His Thr His Pro Thr Phe His Ala Leu
                725                 730                 735

Arg Ser Leu Asp Gln Gln Met Tyr Leu Cys Tyr Ser Gln Pro Gly Ile
            740                 745                 750

Pro Thr Leu Pro Thr Pro Val Glu Ile Thr Val Ile Cys Ala Ala Pro
        755                 760                 765

Gly Ala Asp Gly Ala Trp Trp Arg Ala Gln Val Val Ala Ser Tyr Glu
    770                 775                 780

Glu Thr Asn Glu Val Glu Ile Arg Tyr Val Asp Tyr Gly Gly Tyr Lys
785                 790                 795                 800

Arg Val Lys Val Asp Val Leu Arg Gln Ile Arg Ser Asp Phe Val Thr
```

```
                805                 810                 815

Leu Pro Phe Gln Gly Ala Glu Val Leu Leu Asp Ser Val Met Pro Leu
            820                 825                 830

Ser Asp Asp Asp Gln Phe Ser Pro Glu Ala Asp Ala Ala Met Ser Glu
        835                 840                 845

Met Thr Gly Asn Thr Ala Leu Leu Ala Gln Val Thr Ser Tyr Ser Pro
    850                 855                 860

Thr Gly Leu Pro Leu Ile Gln Leu Trp Ser Val Val Gly Asp Glu Val
865                 870                 875                 880

Val Leu Ile Asn Arg Ser Leu Val Glu Arg Gly Leu Ala Gln Trp Val
                885                 890                 895

Asp Ser Tyr Tyr Thr Ser Leu
            900


<210> 586
<211> 593
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 1; "

<220>
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<223> /note="Uniprot ID:  Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433212"

<400> 586
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1               5                   10                  15
```

```
Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20                  25                  30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35                  40                  45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50                  55                  60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65                  70                  75                  80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
                85                  90                  95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
            100                 105                 110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
        115                 120                 125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130                 135                 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145                 150                 155                 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165                 170                 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
            180                 185                 190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
        195                 200                 205

Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
    210                 215                 220

Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240
```

```
Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350

Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380

Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
    450                 455                 460

Leu Ala Leu Thr Thr Pro Ser Glu Glu Leu Pro Asp Arg Ala Gly Ile
```

```
465                 470                 475                 480

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Val Ala Ala Pro Pro
                565                 570                 575

Pro Gly Lys Arg Gly Thr Leu Ile Thr Arg Cys Pro Gly Phe Phe Glu
            580                 585                 590

Cys
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<210> 587
<211> 903
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443139"

<400> 587
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1   5   10   15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20   25   30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35   40   45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50   55   60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65   70   75   80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
                85   90   95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
            100   105   110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
        115   120   125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130   135   140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145   150   155   160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165   170   175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
            180   185   190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
        195   200   205

```
Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
    210                 215                 220

Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240

Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350

Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380

Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
```

```
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
    450                 455                 460

Leu Ala Leu Thr Thr Pro Ser Glu Glu Leu Pro Asp Arg Ala Gly Ile
465                 470                 475                 480

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Gly Ser Asp Arg Asn
                565                 570                 575

Ser Met Asp Ser Val Asp Ser Cys Cys Ser Leu Lys Lys Thr Glu Ser
            580                 585                 590

Phe Gln Asn Ala Gln Ala Gly Ser Asn Pro Lys Lys Val Asp Leu Ile
        595                 600                 605

Ile Trp Glu Ile Glu Val Pro Lys His Leu Val Gly Arg Leu Ile Gly
    610                 615                 620

Lys Gln Gly Arg Tyr Val Ser Phe Leu Lys Gln Thr Ser Gly Ala Lys
625                 630                 635                 640

Ile Tyr Ile Ser Thr Leu Pro Tyr Thr Gln Ser Val Gln Ile Cys His
                645                 650                 655

Ile Glu Gly Ser Gln His His Val Asp Lys Ala Leu Asn Leu Ile Gly
            660                 665                 670
```

Lys Lys Phe Lys Glu Leu Asn Leu Thr Asn Ile Tyr Ala Pro Pro Leu
675 680 685

Pro Ser Leu Ala Leu Pro Ser Leu Pro Met Thr Ser Trp Leu Met Leu
690 695 700

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

Gly His Leu Phe Val Gln Gln His Thr His Pro Thr Phe His Ala Leu
725 730 735

Arg Ser Leu Asp Gln Gln Met Tyr Leu Cys Tyr Ser Gln Pro Gly Ile
740 745 750

Pro Thr Leu Pro Thr Pro Val Glu Ile Thr Val Ile Cys Ala Ala Pro
755 760 765

Gly Ala Asp Gly Ala Trp Trp Arg Ala Gln Val Val Ala Ser Tyr Glu
770 775 780

Glu Thr Asn Glu Val Glu Ile Arg Tyr Val Asp Tyr Gly Gly Tyr Lys
785 790 795 800

Arg Val Lys Val Asp Val Leu Arg Gln Ile Arg Ser Asp Phe Val Thr
805 810 815

Leu Pro Phe Gln Gly Ala Glu Val Leu Leu Asp Ser Val Met Pro Leu
820 825 830

Ser Asp Asp Asp Gln Phe Ser Pro Glu Ala Asp Ala Ala Met Ser Glu
835 840 845

Met Thr Gly Asn Thr Ala Leu Leu Ala Gln Val Thr Ser Tyr Ser Pro
850 855 860

Thr Gly Leu Pro Leu Ile Gln Leu Trp Ser Val Val Gly Asp Glu Val
865 870 875 880

Val Leu Ile Asn Arg Ser Leu Val Glu Arg Gly Leu Ala Gln Trp Val
885 890 895

Asp Ser Tyr Tyr Thr Ser Leu
900

<210> 588
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458164"

<400> 588
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1 5 10 15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
20 25 30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
35 40 45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
50 55 60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65 70 75 80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
85 90 95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
100 105 110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser

```
        115                 120                 125

Thr Lys Leu Glu Leu Ala Leu Thr Gly
    130                 135


<210> 589
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000458370"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 589
Xaa Gly Ala Asp Gly Ala Trp Trp Arg Ala Gln Val Val Ala Ser Tyr
1               5                   10                  15


Glu Glu Thr Asn Glu Val Glu Ile Arg Tyr Val Asp Tyr Gly Gly Tyr
            20                  25                  30


Lys Arg Val Lys Val Asp Val Leu Arg Gln Ile Arg Ser Asp Phe Val
        35                  40                  45


Thr Leu Pro Phe Gln Gly Ala Glu Val Leu Leu Asp Ser Val Met Pro
    50                  55                  60


Leu Ser Asp Asp Asp Gln Phe Ser Pro Glu Ala Asp Ala Ala Met Ser
65                  70                  75                  80


Glu Met Thr Gly Asn Thr Ala Leu Leu Ala Gln Val Thr Ser Tyr Ser
```

```
                85                  90                  95

Pro Thr Gly Leu Pro Leu Ile Gln Leu Trp Ser Val Val Gly Asp Glu
            100                 105                 110

Val Val Leu Ile Asn Arg Ser Leu Val Glu Arg Gly Leu Ala Gln Leu
        115                 120                 125

Ala Ser Ala Leu Cys Ser Leu Lys Ile Ser Lys
    130                 135


<210> 590
<211> 204
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458378"

<400> 590
Ala Glu Lys Arg Ser Ser Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala
1               5                   10                  15

Glu Gly Thr Gly Asp Ala Val Leu Gly Glu Lys Val Leu Glu Glu Ala
            20                  25                  30

Leu Leu Ser Arg Glu His Val Leu Glu Leu Glu Asn Ser Lys Gly Pro
        35                  40                  45

Ser Leu Ala Ser Leu Glu Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser
    50                  55                  60

Ser Gln Val Val Gly Pro Val Gln Glu Glu Glu Tyr Val Ala Glu Lys
65                  70                  75                  80
```

```
Leu Pro Ser Arg Phe Ile Glu Ser Ala His Thr Glu Leu Ala Lys Asp
                85                  90                  95

Asp Ala Ala Pro Ala Pro Pro Val Ala Asp Ala Lys Ala Gln Asp Arg
            100                 105                 110

Gly Val Glu Gly Glu Leu Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu
        115                 120                 125

Glu Asp Leu Gly Ala Glu Asp Gly Trp Thr Met Asp Ala Glu Ala Asp
    130                 135                 140

His Ser Gly Gly Ser Asp Arg Asn Ser Met Asp Ser Val Asp Ser Cys
145                 150                 155                 160

Cys Ser Leu Lys Lys Thr Glu Ser Phe Gln Asn Ala Gln Ala Gly Ser
                165                 170                 175

Asn Pro Lys Lys Val Asp Leu Ile Ile Trp Glu Ile Glu Val Pro Lys
            180                 185                 190

His Leu Val Gly Arg Leu Ile Gly Lys Gln Gly Arg
        195                 200


<210> 591
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458982"

<400> 591
Met Ala Ile Gln Phe Arg Ser
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1 5

<210> 592
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459521"

<400> 592
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1 5 10 15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
20 25 30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
35 40 45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
50 55 60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65 70 75 80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
85 90 95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
100 105 110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
115 120 125

```
Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130                 135                 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145                 150                 155                 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165                 170                 175

Lys Val Gln Pro Gly Tyr
            180


<210> 593
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459808"

<400> 593
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1               5                   10                  15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20                  25                  30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35                  40                  45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50                  55                  60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
```

65 70 75 80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
85 90 95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
100 105 110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
115 120 125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
130 135 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145 150 155 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
165 170 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro
180 185

<210> 594
<211> 903
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID: Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459895"

<400> 594
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1 5 10 15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
20 25 30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
35 40 45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
50 55 60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65 70 75 80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
85 90 95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
100 105 110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
115 120 125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
130 135 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145 150 155 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
165 170 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
180 185 190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
195 200 205

Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
210 215 220

```
Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240

Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350

Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380

Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
```

```
    450                 455                 460

Leu Ala Leu Thr Thr Pro Ser Glu Glu Leu Pro Asp Arg Ala Gly Ile
465                 470                 475                 480

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Gly Ser Asp Arg Asn
                565                 570                 575

Ser Met Asp Ser Val Asp Ser Cys Cys Ser Leu Lys Lys Thr Glu Ser
            580                 585                 590

Phe Gln Asn Ala Gln Ala Gly Ser Asn Pro Lys Lys Val Asp Leu Ile
        595                 600                 605

Ile Trp Glu Ile Glu Val Pro Lys His Leu Val Gly Arg Leu Ile Gly
    610                 615                 620

Lys Gln Gly Arg Tyr Val Ser Phe Leu Lys Gln Thr Ser Gly Ala Lys
625                 630                 635                 640

Ile Tyr Ile Ser Thr Leu Pro Tyr Thr Gln Ser Val Gln Ile Cys His
                645                 650                 655

Ile Glu Gly Ser Gln His His Val Asp Lys Ala Leu Asn Leu Ile Gly
            660                 665                 670

Lys Lys Phe Lys Glu Leu Asn Leu Thr Asn Ile Tyr Ala Pro Pro Leu
        675                 680                 685
```

Pro Ser Leu Ala Leu Pro Ser Leu Pro Met Thr Ser Trp Leu Met Leu
690 695 700

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

Gly His Leu Phe Val Gln Gln His Thr His Pro Thr Phe His Ala Leu
725 730 735

Arg Ser Leu Asp Gln Gln Met Tyr Leu Cys Tyr Ser Gln Pro Gly Ile
740 745 750

Pro Thr Leu Pro Thr Pro Val Glu Ile Thr Val Ile Cys Ala Ala Pro
755 760 765

Gly Ala Asp Gly Ala Trp Trp Arg Ala Gln Val Val Ala Ser Tyr Glu
770 775 780

Glu Thr Asn Glu Val Glu Ile Arg Tyr Val Asp Tyr Gly Gly Tyr Lys
785 790 795 800

Arg Val Lys Val Asp Val Leu Arg Gln Ile Arg Ser Asp Phe Val Thr
805 810 815

Leu Pro Phe Gln Gly Ala Glu Val Leu Leu Asp Ser Val Met Pro Leu
820 825 830

Ser Asp Asp Asp Gln Phe Ser Pro Glu Ala Asp Ala Ala Met Ser Glu
835 840 845

Met Thr Gly Asn Thr Ala Leu Leu Ala Gln Val Thr Ser Tyr Ser Pro
850 855 860

Thr Gly Leu Pro Leu Ile Gln Leu Trp Ser Val Val Gly Asp Glu Val
865 870 875 880

Val Leu Ile Asn Arg Ser Leu Val Glu Arg Gly Leu Ala Gln Trp Val
885 890 895

Asp Ser Tyr Tyr Thr Ser Leu
900

<210> 595
<211> 903
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 101; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP1; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 1; "

<220>
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<223> /note="Uniprot ID: Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459968"

<400> 595
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1   5   10   15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20   25   30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35   40   45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50   55   60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65   70   75   80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
                85   90   95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
            100   105   110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser

```
        115                 120                 125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130                 135                 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145                 150                 155                 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165                 170                 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
            180                 185                 190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
        195                 200                 205

Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
    210                 215                 220

Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240

Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350
```

```
Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380

Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
    450                 455                 460

Leu Ala Leu Thr Thr Pro Ser Glu Glu Leu Pro Asp Arg Ala Gly Ile
465                 470                 475                 480

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Gly Ser Asp Arg Asn
                565                 570                 575
```

```
Ser Met Asp Ser Val Asp Ser Cys Cys Ser Leu Lys Lys Thr Glu Ser
            580                 585                 590

Phe Gln Asn Ala Gln Ala Gly Ser Asn Pro Lys Lys Val Asp Leu Ile
        595                 600                 605

Ile Trp Glu Ile Glu Val Pro Lys His Leu Val Gly Arg Leu Ile Gly
    610                 615                 620

Lys Gln Gly Arg Tyr Val Ser Phe Leu Lys Gln Thr Ser Gly Ala Lys
625                 630                 635                 640

Ile Tyr Ile Ser Thr Leu Pro Tyr Thr Gln Ser Val Gln Ile Cys His
                645                 650                 655

Ile Glu Gly Ser Gln His His Val Asp Lys Ala Leu Asn Leu Ile Gly
            660                 665                 670

Lys Lys Phe Lys Glu Leu Asn Leu Thr Asn Ile Tyr Ala Pro Pro Leu
        675                 680                 685

Pro Ser Leu Ala Leu Pro Ser Leu Pro Met Thr Ser Trp Leu Met Leu
    690                 695                 700

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

Gly His Leu Phe Val Gln Gln His Thr His Pro Thr Phe His Ala Leu
                725                 730                 735

Arg Ser Leu Asp Gln Gln Met Tyr Leu Cys Tyr Ser Gln Pro Gly Ile
            740                 745                 750

Pro Thr Leu Pro Thr Pro Val Glu Ile Thr Val Ile Cys Ala Ala Pro
        755                 760                 765

Gly Ala Asp Gly Ala Trp Trp Arg Ala Gln Val Val Ala Ser Tyr Glu
    770                 775                 780

Glu Thr Asn Glu Val Glu Ile Arg Tyr Val Asp Tyr Gly Gly Tyr Lys
785                 790                 795                 800
```

```
Arg Val Lys Val Asp Val Leu Arg Gln Ile Arg Ser Asp Phe Val Thr
                805                 810                 815

Leu Pro Phe Gln Gly Ala Glu Val Leu Leu Asp Ser Val Met Pro Leu
            820                 825                 830

Ser Asp Asp Asp Gln Phe Ser Pro Glu Ala Asp Ala Ala Met Ser Glu
        835                 840                 845

Met Thr Gly Asn Thr Ala Leu Leu Ala Gln Val Thr Ser Tyr Ser Pro
    850                 855                 860

Thr Gly Leu Pro Leu Ile Gln Leu Trp Ser Val Val Gly Asp Glu Val
865                 870                 875                 880

Val Leu Ile Asn Arg Ser Leu Val Glu Arg Gly Leu Ala Gln Trp Val
                885                 890                 895

Asp Ser Tyr Tyr Thr Ser Leu
            900


<210> 596
<211> 95
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AKAP1; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 1; "

<220>
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<223> /note="ENSP ID: ENSP00000460209"

<400> 596
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1               5                   10                  15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20                  25                  30
```

```
Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35                  40                  45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50                  55                  60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65                  70                  75                  80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu
                85                  90                  95


<210> 597
<211> 83
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<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<400> 597
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1               5                  10                  15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20                  25                  30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35                  40                  45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50                  55                  60
```

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65 70 75 80

Glu Leu Ser

<210> 598
<211> 47
<212> PRT
<213> Homo sapiens

<220>
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<220>
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A kinase (PRKA) anchor prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460557"

<400> 598
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1 5 10 15

Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
20 25 30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln
35 40 45

<210> 599
<211> 179
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>

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A kinase (PRKA) anchor prt 1; "

<220>
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<400> 599

```
Val Ile Val Val Asn Gln Val Asn Ala Gly His Leu Phe Val Gln Gln
1               5                   10                  15

His Thr His Pro Thr Phe His Ala Leu Arg Ser Leu Asp Gln Gln Met
            20                  25                  30

Tyr Leu Cys Tyr Ser Gln Pro Gly Ile Pro Thr Leu Pro Thr Pro Val
        35                  40                  45

Glu Ile Thr Val Ile Cys Ala Ala Pro Gly Ala Asp Gly Ala Trp Trp
    50                  55                  60

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

Arg Tyr Val Asp Tyr Gly Gly Tyr Lys Arg Val Lys Val Asp Val Leu
                85                  90                  95

Arg Gln Ile Arg Ser Asp Phe Val Thr Leu Pro Phe Gln Gly Ala Glu
            100                 105                 110

Val Leu Leu Asp Ser Val Met Pro Leu Ser Asp Asp Asp Gln Phe Ser
        115                 120                 125

Pro Glu Ala Asp Ala Ala Met Ser Glu Met Thr Gly Asn Thr Ala Leu
    130                 135                 140

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

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

Lys Asn Lys
```

<210> 600
<211> 7
<212> PRT
<213> Homo sapiens

<220>
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<220>
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A kinase (PRKA) anchor prt 1; "

<220>
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<223> /note="ENSP ID: ENSP00000461418"

<400> 600
Met Ala Ile Gln Phe Arg Ser
1 5

<210> 601
<211> 360
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 1; "

<220>
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<223> /note="ENSP ID: ENSP00000461854"

<400> 601
Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro Lys Thr
1 5 10 15

Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys Asp Ser
20 25 30

```
Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys Leu Ala
        35                  40                  45

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

Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln Ser Val
65                  70                  75                  80

Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser Thr Ser
                85                  90                  95

Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg Asp Lys
            100                 105                 110

Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser Asn Gly
        115                 120                 125

Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly Trp Thr
    130                 135                 140

Met Asp Ala Glu Ala Asp His Ser Gly Gly Ser Asp Arg Asn Ser Met
145                 150                 155                 160

Asp Ser Val Asp Ser Cys Cys Ser Leu Lys Lys Thr Glu Ser Phe Gln
                165                 170                 175

Asn Ala Gln Ala Gly Ser Asn Pro Lys Lys Val Asp Leu Ile Ile Trp
            180                 185                 190

Glu Ile Glu Val Pro Lys His Leu Val Gly Arg Leu Ile Gly Lys Gln
        195                 200                 205

Gly Arg Tyr Val Ser Phe Leu Lys Gln Thr Ser Gly Ala Lys Ile Tyr
    210                 215                 220

Ile Ser Thr Leu Pro Tyr Thr Gln Ser Val Gln Ile Cys His Ile Glu
225                 230                 235                 240

Gly Ser Gln His His Val Asp Lys Ala Leu Asn Leu Ile Gly Lys Lys
                245                 250                 255
```

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

Leu Ala Leu Pro Ser Leu Pro Met Thr Ser Trp Leu Met Leu Pro Asp
        275                 280                 285

Gly Ile Thr Val Glu Val Ile Val Val Asn Gln Val Asn Ala Gly His
    290                 295                 300

Leu Phe Val Gln Gln His Thr His Pro Thr Phe His Ala Leu Arg Ser
305                 310                 315                 320

Leu Asp Gln Gln Met Tyr Leu Cys Tyr Ser Gln Pro Gly Ile Pro Thr
                325                 330                 335

Leu Pro Thr Pro Val Glu Ser Leu Thr Leu Ser Pro Cys Arg Phe Arg
            340                 345                 350

Glu Gln Lys Ser Phe Trp Thr Val
        355                 360


<210> 602
<211> 903
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Uniprot ID:  Q92667; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478212"

<400> 602
Met Ala Ile Gln Phe Arg Ser Leu Phe Pro Leu Ala Leu Pro Gly Met
1               5                   10                  15
```

```
Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg Lys Lys Gly His
            20                  25                  30

Val Ser Ser His Asp Glu Gln Gln Val Glu Ala Gly Ala Val Gln Leu
        35                  40                  45

Arg Ala Asp Pro Ala Ile Lys Glu Pro Leu Pro Val Glu Asp Val Cys
    50                  55                  60

Pro Lys Val Val Ser Thr Pro Pro Ser Val Thr Glu Pro Pro Glu Lys
65                  70                  75                  80

Glu Leu Ser Thr Val Ser Lys Leu Pro Ala Glu Pro Pro Ala Leu Leu
                85                  90                  95

Gln Thr His Pro Pro Cys Arg Arg Ser Glu Ser Ser Gly Ile Leu Pro
            100                 105                 110

Asn Thr Thr Asp Met Arg Leu Arg Pro Gly Thr Arg Arg Asp Asp Ser
        115                 120                 125

Thr Lys Leu Glu Leu Ala Leu Thr Gly Gly Glu Ala Lys Ser Ile Pro
    130                 135                 140

Leu Glu Cys Pro Leu Ser Ser Pro Lys Gly Val Leu Phe Ser Ser Lys
145                 150                 155                 160

Ser Ala Glu Val Cys Lys Gln Asp Ser Pro Phe Ser Arg Val Pro Arg
                165                 170                 175

Lys Val Gln Pro Gly Tyr Pro Val Val Pro Ala Glu Lys Arg Ser Ser
            180                 185                 190

Gly Glu Arg Ala Arg Glu Thr Gly Gly Ala Glu Gly Thr Gly Asp Ala
        195                 200                 205

Val Leu Gly Glu Lys Val Leu Glu Glu Ala Leu Leu Ser Arg Glu His
    210                 215                 220

Val Leu Glu Leu Glu Asn Ser Lys Gly Pro Ser Leu Ala Ser Leu Glu
225                 230                 235                 240
```

```
Gly Glu Glu Asp Lys Gly Lys Ser Ser Ser Ser Gln Val Val Gly Pro
                245                 250                 255

Val Gln Glu Glu Glu Tyr Val Ala Glu Lys Leu Pro Ser Arg Phe Ile
            260                 265                 270

Glu Ser Ala His Thr Glu Leu Ala Lys Asp Asp Ala Ala Pro Ala Pro
        275                 280                 285

Pro Val Ala Asp Ala Lys Ala Gln Asp Arg Gly Val Glu Gly Glu Leu
    290                 295                 300

Gly Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu Gly Leu Asp Arg Asn
305                 310                 315                 320

Glu Glu Gly Leu Asp Arg Asn Glu Glu Ser Leu Asp Arg Asn Glu Glu
                325                 330                 335

Gly Leu Asp Arg Asn Glu Glu Ile Lys Arg Ala Ala Phe Gln Ile Ile
            340                 345                 350

Ser Gln Val Ile Ser Glu Ala Thr Glu Gln Val Leu Ala Thr Thr Val
        355                 360                 365

Gly Lys Val Ala Gly Arg Val Cys Gln Ala Ser Gln Leu Gln Gly Gln
    370                 375                 380

Lys Glu Glu Ser Cys Val Pro Val His Gln Lys Thr Val Leu Gly Pro
385                 390                 395                 400

Asp Thr Ala Glu Pro Ala Thr Ala Glu Ala Ala Val Ala Pro Pro Asp
                405                 410                 415

Ala Gly Leu Pro Leu Pro Gly Leu Pro Ala Glu Gly Ser Pro Pro Pro
            420                 425                 430

Lys Thr Tyr Val Ser Cys Leu Lys Ser Leu Leu Ser Ser Pro Thr Lys
        435                 440                 445

Asp Ser Lys Pro Asn Ile Ser Ala His His Ile Ser Leu Ala Ser Cys
    450                 455                 460
```

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

Leu Val Glu Asp Ala Thr Cys Val Thr Cys Met Ser Asp Ser Ser Gln
                485                 490                 495

Ser Val Pro Leu Val Ala Ser Pro Gly His Cys Ser Asp Ser Phe Ser
            500                 505                 510

Thr Ser Gly Leu Glu Asp Ser Cys Thr Glu Thr Ser Ser Ser Pro Arg
        515                 520                 525

Asp Lys Ala Ile Thr Pro Pro Leu Pro Glu Ser Thr Val Pro Phe Ser
    530                 535                 540

Asn Gly Val Leu Lys Gly Glu Leu Ser Asp Leu Gly Ala Glu Asp Gly
545                 550                 555                 560

Trp Thr Met Asp Ala Glu Ala Asp His Ser Gly Gly Ser Asp Arg Asn
                565                 570                 575

Ser Met Asp Ser Val Asp Ser Cys Cys Ser Leu Lys Lys Thr Glu Ser
            580                 585                 590

Phe Gln Asn Ala Gln Ala Gly Ser Asn Pro Lys Lys Val Asp Leu Ile
        595                 600                 605

Ile Trp Glu Ile Glu Val Pro Lys His Leu Val Gly Arg Leu Ile Gly
    610                 615                 620

Lys Gln Gly Arg Tyr Val Ser Phe Leu Lys Gln Thr Ser Gly Ala Lys
625                 630                 635                 640

Ile Tyr Ile Ser Thr Leu Pro Tyr Thr Gln Ser Val Gln Ile Cys His
                645                 650                 655

Ile Glu Gly Ser Gln His His Val Asp Lys Ala Leu Asn Leu Ile Gly
            660                 665                 670

Lys Lys Phe Lys Glu Leu Asn Leu Thr Asn Ile Tyr Ala Pro Pro Leu
        675                 680                 685

Pro Ser Leu Ala Leu Pro Ser Leu Pro Met Thr Ser Trp Leu Met Leu
```

690 695 700

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

Gly His Leu Phe Val Gln Gln His Thr His Pro Thr Phe His Ala Leu
725 730 735

Arg Ser Leu Asp Gln Gln Met Tyr Leu Cys Tyr Ser Gln Pro Gly Ile
740 745 750

Pro Thr Leu Pro Thr Pro Val Glu Ile Thr Val Ile Cys Ala Ala Pro
755 760 765

Gly Ala Asp Gly Ala Trp Trp Arg Ala Gln Val Val Ala Ser Tyr Glu
770 775 780

Glu Thr Asn Glu Val Glu Ile Arg Tyr Val Asp Tyr Gly Gly Tyr Lys
785 790 795 800

Arg Val Lys Val Asp Val Leu Arg Gln Ile Arg Ser Asp Phe Val Thr
805 810 815

Leu Pro Phe Gln Gly Ala Glu Val Leu Leu Asp Ser Val Met Pro Leu
820 825 830

Ser Asp Asp Asp Gln Phe Ser Pro Glu Ala Asp Ala Ala Met Ser Glu
835 840 845

Met Thr Gly Asn Thr Ala Leu Leu Ala Gln Val Thr Ser Tyr Ser Pro
850 855 860

Thr Gly Leu Pro Leu Ile Gln Leu Trp Ser Val Val Gly Asp Glu Val
865 870 875 880

Val Leu Ile Asn Arg Ser Leu Val Glu Arg Gly Leu Ala Gln Trp Val
885 890 895

Asp Ser Tyr Tyr Thr Ser Leu
900

<210> 603
<211> 662

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 102; "

<220>
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<223> /note="Gene Symbol: AKAP10; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 10; "

<220>
<221> source
<223> /note="Uniprot ID: O43572; "

<220>
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<223> /note="ENSP ID: ENSP00000225737"

<400> 603

Met	Arg	Gly	Ala	Gly	Pro	Ser	Pro	Arg	Gln	Ser	Pro	Arg	Thr	Leu	Arg
1				5					10						15

Pro	Asp	Pro	Gly	Pro	Ala	Met	Ser	Phe	Phe	Arg	Arg	Lys	Val	Lys	Gly
			20					25					30		

Lys	Glu	Gln	Glu	Lys	Thr	Ser	Asp	Val	Lys	Ser	Ile	Lys	Ala	Ser	Ile
		35					40					45			

Ser	Val	His	Ser	Pro	Gln	Lys	Ser	Thr	Lys	Asn	His	Ala	Leu	Leu	Glu
	50					55					60				

Ala	Ala	Gly	Pro	Ser	His	Val	Ala	Ile	Asn	Ala	Ile	Ser	Ala	Asn	Met
65					70					75					80

Asp	Ser	Phe	Ser	Ser	Ser	Arg	Thr	Ala	Thr	Leu	Lys	Lys	Gln	Pro	Ser
				85					90					95	

His	Met	Glu	Ala	Ala	His	Phe	Gly	Asp	Leu	Gly	Arg	Ser	Cys	Leu	Asp
			100					105					110		

Tyr	Gln	Thr	Gln	Glu	Thr	Lys	Ser	Ser	Leu	Ser	Lys	Thr	Leu	Glu	Gln
		115					120					125			

```
Val Leu His Asp Thr Ile Val Leu Pro Tyr Phe Ile Gln Phe Met Glu
    130                 135                 140

Leu Arg Arg Met Glu His Leu Val Lys Phe Trp Leu Glu Ala Glu Ser
145                 150                 155                 160

Phe His Ser Thr Thr Trp Ser Arg Ile Arg Ala His Ser Leu Asn Thr
                165                 170                 175

Val Lys Gln Ser Ser Leu Ala Glu Pro Val Ser Pro Ser Lys Lys His
            180                 185                 190

Glu Thr Thr Ala Ser Phe Leu Thr Asp Ser Leu Asp Lys Arg Leu Glu
        195                 200                 205

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

Leu Asn Asn Arg Thr Asn Ser Thr Gln Asn His Leu Leu Leu Ser Gln
225                 230                 235                 240

Glu Cys Asp Ser Ala His Ser Leu Arg Leu Glu Met Ala Arg Ala Gly
                245                 250                 255

Thr His Gln Val Ser Met Glu Thr Gln Glu Ser Ser Ser Thr Leu Thr
            260                 265                 270

Val Ala Ser Arg Asn Ser Pro Ala Ser Pro Leu Lys Glu Leu Ser Gly
        275                 280                 285

Lys Leu Met Lys Ser Ile Glu Gln Asp Ala Val Asn Thr Phe Thr Lys
    290                 295                 300

Tyr Ile Ser Pro Asp Ala Ala Lys Pro Ile Pro Ile Thr Glu Ala Met
305                 310                 315                 320

Arg Asn Asp Ile Ile Ala Arg Ile Cys Gly Glu Asp Gly Gln Val Asp
                325                 330                 335

Pro Asn Cys Phe Val Leu Ala Gln Ser Ile Val Phe Ser Ala Met Glu
            340                 345                 350

Gln Glu His Phe Ser Glu Phe Leu Arg Ser His His Phe Cys Lys Tyr
```

355 360 365

Gln Ile Glu Val Leu Thr Ser Gly Thr Val Tyr Leu Ala Asp Ile Leu
370 375 380

Phe Cys Glu Ser Ala Leu Phe Tyr Phe Ser Glu Tyr Met Glu Lys Glu
385 390 395 400

Asp Ala Val Asn Ile Leu Gln Phe Trp Leu Ala Ala Asp Asn Phe Gln
405 410 415

Ser Gln Leu Ala Ala Lys Lys Gly Gln Tyr Asp Gly Gln Glu Ala Gln
420 425 430

Asn Asp Ala Met Ile Leu Tyr Asp Lys Tyr Phe Ser Leu Gln Ala Thr
435 440 445

His Pro Leu Gly Phe Asp Asp Val Val Arg Leu Glu Ile Glu Ser Asn
450 455 460

Ile Cys Arg Glu Gly Gly Pro Leu Pro Asn Cys Phe Thr Thr Pro Leu
465 470 475 480

Arg Gln Ala Trp Thr Thr Met Glu Lys Val Phe Leu Pro Gly Phe Leu
485 490 495

Ser Ser Asn Leu Tyr Tyr Lys Tyr Leu Asn Asp Leu Ile His Ser Val
500 505 510

Arg Gly Asp Glu Phe Leu Gly Gly Asn Val Ser Leu Thr Ala Pro Gly
515 520 525

Ser Val Gly Pro Pro Asp Glu Ser His Pro Gly Ser Ser Asp Ser Ser
530 535 540

Ala Ser Gln Ser Ser Val Lys Lys Ala Ser Ile Lys Ile Leu Lys Asn
545 550 555 560

Phe Asp Glu Ala Ile Ile Val Asp Ala Ala Ser Leu Asp Pro Glu Ser
565 570 575

Leu Tyr Gln Arg Thr Tyr Ala Gly Lys Met Thr Phe Gly Arg Val Ser
580 585 590

```
Asp Leu Gly Gln Phe Ile Arg Glu Ser Glu Pro Glu Pro Asp Val Arg
        595                 600                 605

Lys Ser Lys Gly Ser Met Phe Ser Gln Ala Met Lys Lys Trp Val Gln
    610                 615                 620

Gly Asn Thr Asp Glu Ala Gln Glu Glu Leu Ala Trp Lys Ile Ala Lys
625                 630                 635                 640

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

Glu Lys Ser Thr Lys Leu
            660


<210> 604
<211> 604
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 102; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP10; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378907"

<400> 604
Met Arg Gly Ala Gly Pro Ser Pro Arg Gln Ser Pro Arg Thr Leu Arg
1               5                   10                  15

Pro Asp Pro Gly Pro Ala Met Ser Phe Phe Arg Arg Lys Val Lys Gly
            20                  25                  30

Lys Glu Gln Glu Lys Thr Ser Asp Val Lys Ser Ile Lys Ala Ser Ile
        35                  40                  45
```

```
Ser Val His Ser Pro Gln Lys Ser Thr Lys Asn His Ala Leu Leu Glu
    50                  55                  60

Ala Ala Gly Pro Ser His Val Ala Ile Asn Ala Ile Ser Ala Asn Met
65                  70                  75                  80

Asp Ser Phe Ser Ser Ser Arg Thr Ala Thr Leu Lys Lys Gln Pro Ser
                85                  90                  95

His Met Glu Ala Ala His Phe Gly Asp Leu Gly Arg Ser Cys Leu Asp
            100                 105                 110

Tyr Gln Thr Gln Glu Thr Lys Ser Ser Leu Ser Lys Thr Leu Glu Gln
        115                 120                 125

Val Leu His Asp Thr Ile Val Leu Pro Tyr Phe Ile Gln Phe Met Glu
    130                 135                 140

Leu Arg Arg Met Glu His Leu Val Lys Phe Trp Leu Glu Ala Glu Ser
145                 150                 155                 160

Phe His Ser Thr Thr Trp Ser Arg Ile Arg Ala His Ser Leu Asn Thr
                165                 170                 175

Val Lys Gln Ser Ser Leu Ala Glu Pro Val Ser Pro Ser Lys Lys His
            180                 185                 190

Glu Thr Thr Ala Ser Phe Leu Thr Asp Ser Leu Asp Lys Arg Leu Glu
        195                 200                 205

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

Leu Asn Asn Arg Thr Asn Ser Thr Gln Asn His Leu Leu Leu Ser Gln
225                 230                 235                 240

Glu Cys Asp Ser Ala His Ser Leu Arg Leu Glu Met Ala Arg Ala Gly
                245                 250                 255

Thr His Gln Val Ser Met Glu Thr Gln Glu Ser Ser Ser Thr Leu Thr
            260                 265                 270

Val Ala Ser Arg Asn Ser Pro Ala Ser Pro Leu Lys Glu Leu Ser Gly
```

```
        275                 280                 285

Lys Leu Met Lys Ser Ile Glu Gln Asp Ala Val Asn Thr Phe Thr Lys
    290                 295                 300

Tyr Ile Ser Pro Asp Ala Ala Lys Pro Ile Pro Ile Thr Glu Ala Met
305                 310                 315                 320

Arg Asn Asp Ile Ile Ala Arg Ile Cys Gly Glu Asp Gly Gln Val Asp
                325                 330                 335

Pro Asn Cys Phe Val Leu Ala Gln Ser Ile Val Phe Ser Ala Met Glu
            340                 345                 350

Gln Glu His Phe Ser Glu Phe Leu Arg Ser His His Phe Cys Lys Tyr
        355                 360                 365

Gln Ile Glu Val Leu Thr Ser Gly Thr Val Tyr Leu Ala Asp Ile Leu
    370                 375                 380

Phe Cys Glu Ser Ala Leu Phe Tyr Phe Ser Glu Tyr Met Glu Lys Glu
385                 390                 395                 400

Asp Ala Val Asn Ile Leu Gln Phe Trp Leu Ala Ala Asp Asn Phe Gln
                405                 410                 415

Ser Gln Leu Ala Ala Lys Lys Gly Gln Tyr Asp Gly Gln Glu Ala Gln
            420                 425                 430

Asn Asp Ala Met Ile Leu Tyr Asp Lys Tyr Phe Ser Leu Gln Ala Thr
        435                 440                 445

His Pro Leu Gly Phe Asp Asp Val Val Arg Leu Glu Ile Glu Ser Asn
    450                 455                 460

Ile Cys Arg Glu Gly Gly Pro Leu Pro Asn Cys Phe Thr Thr Pro Leu
465                 470                 475                 480

Arg Gln Ala Trp Thr Thr Met Glu Lys Ser Ser Val Lys Lys Ala Ser
                485                 490                 495

Ile Lys Ile Leu Lys Asn Phe Asp Glu Ala Ile Ile Val Asp Ala Ala
            500                 505                 510
```

```
Ser Leu Asp Pro Glu Ser Leu Tyr Gln Arg Thr Tyr Ala Gly Lys Met
        515                 520                 525

Thr Phe Gly Arg Val Ser Asp Leu Gly Gln Phe Ile Arg Glu Ser Glu
    530                 535                 540

Pro Glu Pro Asp Val Arg Lys Ser Lys Gly Ser Met Phe Ser Gln Ala
545                 550                 555                 560

Met Lys Lys Trp Val Gln Gly Asn Thr Asp Glu Ala Gln Glu Glu Leu
                565                 570                 575

Ala Trp Lys Ile Ala Lys Met Ile Val Ser Asp Ile Met Gln Gln Ala
            580                 585                 590

Gln Tyr Asp Gln Pro Leu Glu Lys Ser Thr Lys Leu
        595                 600


<210> 605
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 102; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP10; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458637"

<400> 605
Met Arg Gly Ala Gly Pro Ser Pro Arg Gln Ser Pro Arg Thr Leu Arg
1               5                   10                  15

Pro Asp Pro Gly Pro Ala Met Ser Phe Phe Arg Arg Lys Val Lys Gly
            20                  25                  30
```

```
Lys Glu Gln Glu Lys Thr Ser Asp Val Lys Ser Ile Lys Ala Leu Lys
        35                  40                  45

Ile Met Pro Cys Trp Arg Leu Gln Asp Gln Val Met Leu Gln Ser Met
    50                  55                  60

Pro Phe Leu Pro Thr Trp Thr Pro Phe Gln Val Ala Gly Gln Pro His
65                  70                  75                  80

Leu Arg Ser Ser Gln Ala Thr Trp Arg Pro Leu Ile Leu Val Thr Trp
                85                  90                  95

Ala Asp Leu Val Trp Thr Thr Arg Leu Lys Arg Pro Asn Gln Ala Phe
            100                 105                 110

Leu Arg Pro Leu Asn Lys Ser Cys Thr Thr Leu Leu Ser Ser Leu Thr
        115                 120                 125

Ser Phe Asn Ser Trp Asn Phe Gly Glu Trp
    130                 135


<210> 606
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<223> /note="Gene Symbol: AKAP10; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461040"

<400> 606
Met Arg Gly Ala Gly Pro Ser Pro Arg Gln Ser Pro Arg Thr Leu Arg
1               5                   10                  15

Pro Asp Pro Gly Pro Ala Met Ser Phe Phe Arg Arg Lys Val Lys Gly
            20                  25                  30
```

Lys Glu Gln Glu Lys Thr Ser Asp Val Lys Ser Ile Lys Gly Cys Arg
35 40 45

Thr Lys Ser Cys Cys Asn Gln Cys His Phe Cys Gln His Gly Leu Leu
50 55 60

Phe Lys
65

<210> 607
<211> 63
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 102; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP10; "

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<223> /note="Gene Name:
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<220>
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<400> 607
Met Arg Gly Ala Gly Pro Ser Pro Arg Gln Ser Pro Arg Thr Leu Arg
1 5 10 15

Pro Asp Pro Gly Pro Ala Met Ser Phe Phe Arg Arg Lys Val Lys Gly
20 25 30

Lys Glu Gln Glu Lys Thr Ser Asp Val Lys Ser Ile Lys Val Glu Thr
35 40 45

Glu Phe His His Val Ser Gln Tyr Gly Leu Asp Leu Leu Thr Leu
50 55 60

<210> 608
<211> 78
<212> PRT
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<220>
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<220>
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<220>
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<400> 608
Leu Ala Leu Leu Ala Leu Leu Met Ser Leu Thr Gln Gly Val Leu Thr
1 5 10 15

Ala Leu Arg Leu Arg Lys Met Thr Phe Gly Arg Val Ser Asp Leu Gly
20 25 30

Gln Phe Ile Arg Glu Ser Glu Pro Glu Pro Asp Val Arg Lys Ser Lys
35 40 45

Gly Ser Met Phe Ser Gln Ala Met Lys Lys Trp Val Gln Gly Asn Thr
50 55 60

Asp Glu Ala Gln Glu Glu Leu Ala Trp Lys Ile Ala Lys Met
65 70 75

<210> 609
<211> 150
<212> PRT
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<220>
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<220>
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<220>
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<400> 609
Met Arg Gly Ala Gly Pro Ser Pro Arg Gln Ser Pro Arg Thr Leu Arg
1   5   10   15

Pro Asp Pro Gly Pro Ala Met Ser Phe Phe Arg Arg Lys Val Lys Gly
            20   25   30

Lys Glu Gln Glu Lys Thr Ser Asp Val Lys Ser Ile Lys Ala Ser Ile
        35   40   45

Ser Val His Ser Pro Gln Lys Ser Thr Lys Asn His Ala Leu Leu Glu
    50   55   60

Ala Ala Gly Pro Ser His Val Ala Ile Asn Ala Ile Ser Ala Asn Met
65   70   75   80

Asp Ser Phe Ser Ser Ser Arg Thr Ala Thr Leu Lys Lys Gln Pro Ser
                85   90   95

His Met Glu Ala Ala His Phe Gly Asp Leu Asp Leu Val Trp Thr Thr
            100   105   110

Arg Leu Lys Arg Pro Asn Gln Ala Phe Leu Arg Pro Leu Asn Lys Ser
        115   120   125

Cys Thr Thr Leu Leu Ser Ser Leu Thr Ser Phe Asn Ser Trp Asn Phe
    130   135   140

Gly Glu Trp Ser Ile Trp
145   150

<210> 610
<211> 59
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="ENSP ID: ENSP00000464294"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 610
Xaa Lys Tyr Ile Ser Pro Asp Ala Ala Lys Pro Ile Pro Ile Thr Glu
1 5 10 15

Ala Met Arg Asn Asp Ile Ile Ala Arg Ile Cys Gly Glu Asp Gly Gln
20 25 30

Val Asp Pro Asn Cys Phe Val Leu Ala Gln Ser Ile Val Phe Ser Ala
35 40 45

Met Glu Gln Asp Thr Trp Lys Lys Arg Met Gln
50 55

<210> 611
<211> 31
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AKAP10; "

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<220>
<221> source
<223> /note="ENSP ID: ENSP00000466329"

<220>

<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 611
Xaa Leu Thr Ala Pro Gly Ser Val Gly Pro Pro Asp Glu Ser His Pro
1   5   10   15

Gly Ser Ser Asp Ser Ser Ala Ser Gln Cys Glu Lys Ser Gln Tyr
            20   25   30

<210> 612
<211> 1901
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AKAP11; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID: Q9UKA4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000025301"

<400> 612
Met Ala Thr Phe Arg Asn Asn His Met Lys Thr Lys Ala Ser Val Arg
1   5   10   15

Lys Ser Phe Ser Glu Asp Val Phe Gln Ser Val Lys Ser Leu Leu Gln
            20   25   30

Ser Gln Lys Glu Leu Cys Ser Val Thr Ala Glu Asp Cys Leu Gln Gln
        35   40   45

Asp Glu His Ala Asn Leu Thr Glu Val Thr Phe Leu Gly Phe Asn Glu
    50   55   60

Glu Thr Asp Ala Ala His Ile Gln Asp Leu Ala Ala Val Ser Leu Glu

65 70 75 80

Leu Pro Asp Ile Leu Asn Ser Leu His Phe Cys Ser Leu Asn Glu Asn
85 90 95

Glu Ile Ile Cys Met Lys Asn Ile Asn Lys Pro Leu Asp Ile Ser Ser
100 105 110

Asp Pro Leu Asn Gln Ser His Pro Ser Gly Met Leu Cys Val Met Arg
115 120 125

Val Ser Pro Thr Ser Pro Arg Leu Arg Ile Asp Phe Ile Phe Ser Leu
130 135 140

Leu Ser Lys Tyr Ala Thr Gly Ile Arg Tyr Thr Leu Asp Thr Phe Leu
145 150 155 160

His Gln Lys His Gln Leu Glu Thr Thr Asp Glu Asp Asp Asp Asp Thr
165 170 175

Asn Gln Ser Val Ser Ser Ile Glu Asp Asp Phe Val Thr Ala Phe Glu
180 185 190

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

Ile Thr Val Leu Arg Ser Gln Cys Asp Ala Ala Ser Gln Thr Val Thr
210 215 220

Gly His His Leu Glu Thr His Asp Leu Lys Ile Leu Ile Ser Ser Gly
225 230 235 240

Gln Gln Lys Ser Leu Ala Lys Pro Ser Thr Ser Ser Val Asn Val Leu
245 250 255

Gly His Lys Glu Leu Pro Ser Val Lys Thr Ser Val Thr Thr Ser Ile
260 265 270

Ser Glu Pro Trp Thr Gln Arg Ser Phe Tyr Arg Ser Ser Asn Ala Ser
275 280 285

Asp Lys Asp Ser Asp Leu Gln Lys Thr Phe Phe Ser Ser Ser Pro Ala
290 295 300

```
Tyr Ser Ser Glu Ser Glu Cys Ser Ser Pro Ser Pro Val Ile Phe Leu
305                 310                 315                 320

Asp Glu Glu Gly Tyr Gln Lys Ser Leu Lys Ala Lys Leu Glu Leu Pro
                325                 330                 335

Lys Ile Pro Val Met Lys Asp Asp Ile Glu Asp Ser Asp Ser Glu Val
            340                 345                 350

Ser Glu Phe Phe Asp Ser Phe Asp Gln Phe Asp Glu Leu Glu Gln Thr
        355                 360                 365

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

Gln Arg Lys Gly His Lys His Gly Lys Ser Cys Met Asn Pro Gln Lys
385                 390                 395                 400

Phe Lys Phe Asp Arg Pro Ala Leu Pro Ala Asn Val Arg Lys Pro Thr
                405                 410                 415

Pro Arg Lys Pro Glu Ser Pro Tyr Gly Asn Leu Cys Asp Ala Pro Asp
            420                 425                 430

Ser Pro Arg Pro Val Lys Ala Ser Arg Glu Asp Ser Gly Leu Phe Ser
        435                 440                 445

Pro Ile Arg Ser Ser Ala Phe Ser Pro Leu Gly Gly Cys Thr Pro Ala
    450                 455                 460

Glu Cys Phe Cys Gln Thr Asp Ile Gly Gly Asp Arg Ile His Glu Asn
465                 470                 475                 480

His Asp Ser Val Tyr Tyr Thr Tyr Glu Asp Tyr Ala Lys Ser Ile Ser
                485                 490                 495

Cys Glu Val Leu Gly Ser Val Leu Arg Thr His His Thr Asn Thr Leu
            500                 505                 510

Ser Asn Ile Asn Ser Ile Lys His Gly Glu Asn Lys Thr Val Thr Phe
        515                 520                 525
```

Lys His Gly Asn Leu Asp Gln Lys Asn Lys Ser Lys Asn Lys Ser Leu
530 535 540

Met Ile Lys Asp Ser Ile Gln Lys Phe Ala Ala Asp Leu Val Glu Lys
545 550 555 560

Ser Phe Gly Ser Ala Phe Lys Asp Leu Gln Lys Gly Val Ser Ser Cys
565 570 575

Thr Asn Ala Leu Tyr His Leu Ala Ile Lys Leu Thr Ser Ser Val Leu
580 585 590

Gln Met Ala Phe Asp Glu Leu Arg Arg Gln Arg Ala Phe Ser Leu Lys
595 600 605

Glu Arg Ala Ile Ser Gly Leu Ala Asn Phe Leu Val Ser Glu Ala Leu
610 615 620

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

Asn Thr Val Ala Arg Phe Ala Ala Asp Leu Ala Glu Glu Leu Val Phe
645 650 655

Glu Gly Ile Met Glu Val Cys Gln Phe Ser Tyr Pro Gln Thr Pro Ala
660 665 670

Ser Pro Gln Cys Gly Ser Phe Asp Phe Glu Asp Lys Val Val Lys Leu
675 680 685

Tyr Ala Lys Asp Leu Ser Glu Ser Val Ile Gln Glu Ala Phe Ile Glu
690 695 700

Leu Ser Gln Val Asp Val Thr Phe Thr Thr Lys Ala Ala Val Ser Val
705 710 715 720

Ser Thr Asp Asn Ile Lys Tyr Val Ser Ala Glu Ser Val Val Pro Ser
725 730 735

Thr Gln Ala Val Thr Phe Ser Pro Ser Phe His Asn Gln Ala Ile Met
740 745 750

```
Val Thr Lys Pro Val Gln Glu Tyr Lys Lys Glu Tyr Thr Val Gln Gln
        755                 760                 765

Ala Leu Phe Cys Thr Ser Gly Ile Val Thr Ser Ile Pro Val Pro Leu
    770                 775                 780

Ala Gly Ser Ala Leu Leu Pro Tyr His Ile Ser Ser Thr Ala Cys Gln
785                 790                 795                 800

Ala Lys Ala His Leu Ser Ser Asp Asp Ser Asn Ser Asn Gly Asp Ser
                805                 810                 815

Ala Gln Val His Ile Ala Thr Lys Asn Arg Glu Glu Lys Ala Ala Cys
            820                 825                 830

Leu Arg Asn Ile Cys Leu Pro Ser Glu His Asn Pro Gly Asn Gln Asn
        835                 840                 845

Asp Phe Lys Pro Thr Asn Asp Asp Ile Glu Met Gln Ser Ser Ser Lys
    850                 855                 860

Leu Pro Asn Asp Pro Ala Ile Ile Ser Asn Phe Ser Ala Ala Val Val
865                 870                 875                 880

His Thr Ile Val Asn Glu Thr Leu Glu Ser Met Thr Ser Leu Glu Val
                885                 890                 895

Thr Lys Met Val Asp Glu Arg Thr Asp Tyr Leu Thr Lys Ser Leu Lys
            900                 905                 910

Glu Lys Thr Pro Pro Phe Ser His Cys Asp Gln Ala Val Leu Gln Cys
        915                 920                 925

Ser Glu Ala Ser Ser Asn Lys Asp Met Phe Ala Asp Arg Leu Ser Lys
    930                 935                 940

Ser Ile Ile Lys His Ser Ile Asp Lys Ser Lys Ser Val Ile Pro Asn
945                 950                 955                 960

Ile Asp Lys Asn Ala Val Tyr Lys Glu Ser Leu Pro Val Ser Gly Glu
                965                 970                 975

Glu Ser Gln Leu Thr Pro Glu Lys Ser Pro Lys Phe Pro Asp Ser Gln
```

980 985 990

Asn Gln Leu Thr His Cys Ser Leu Ser Ala Ala Lys Asp Cys Val Pro
995 1000 1005

Glu Cys Lys Val Ser Met Val His Gly Ser Ser Leu Glu Thr Leu
1010 1015 1020

Pro Ser Cys Pro Ala Val Thr Gly Gln Lys Ser Asp Leu Lys Glu
1025 1030 1035

Ser Ala Lys Asp Gln Pro Leu Lys Lys His Asn Leu Asn Ser Thr
1040 1045 1050

Ser Leu Glu Ala Leu Ser Phe Gly Gln Glu Asn Pro Phe Pro His
1055 1060 1065

Ser His Thr Phe Ser Ser Thr Ala Leu Thr Cys Val Asp Gly Leu
1070 1075 1080

His Val Glu Asp Lys Gln Lys Val Arg Asp Arg Asn Val Ile Pro
1085 1090 1095

Asp Thr Pro Pro Ser Thr Pro Leu Val Pro Ser Arg Ala Ser Ser
1100 1105 1110

Glu Trp Asp Ile Lys Lys Leu Thr Lys Lys Leu Lys Gly Glu Leu
1115 1120 1125

Ala Lys Glu Phe Ala Pro Ala Thr Pro Pro Ser Thr Pro His Asn
1130 1135 1140

Ser Ser Val Gly Ser Leu Ser Glu Asn Glu Gln Asn Thr Ile Glu
1145 1150 1155

Lys Glu Glu Phe Met Leu Lys Leu Met Arg Ser Leu Ser Glu Glu
1160 1165 1170

Val Glu Ser Ser Glu Ser Gly Glu Leu Pro Glu Val Asp Val Lys
1175 1180 1185

Ser Glu His Ser Gly Lys Lys Val Gln Phe Ala Glu Ala Leu Ala

1190 1195 1200

Thr His Ile Leu Ser Leu Ala Thr Glu Met Ala Ala Ser His Leu
1205 1210 1215

Asp Asn Lys Ile Ile Gln Glu Pro Lys Val Lys Asn Pro Cys Leu
1220 1225 1230

Asn Val Gln Ser Gln Arg Ser Val Ser Pro Thr Phe Leu Asn Pro
1235 1240 1245

Ser Asp Glu Asn Leu Lys Thr Leu Cys Asn Phe Ala Gly Asp Leu
1250 1255 1260

Ala Ala Glu Val Ile Thr Glu Ala Glu Lys Ile Ala Lys Val Arg
1265 1270 1275

Asn Cys Met Leu Phe Lys Gln Lys Lys Asn Ser Cys Tyr Ala Asp
1280 1285 1290

Gly Asp Glu Asp Tyr Lys Val Glu Glu Lys Leu Asp Ile Glu Ala
1295 1300 1305

Val Val His Pro Arg Glu Val Asp Pro Phe Ile Leu Ser Leu Pro
1310 1315 1320

Pro Ser Ser Cys Met Ser Gly Leu Met Tyr Lys Tyr Pro Ser Cys
1325 1330 1335

Glu Ser Val Thr Asp Glu Tyr Ala Gly His Leu Ile Gln Ile Leu
1340 1345 1350

Lys Gln Glu Gly Gly Asn Ser Glu Leu Ile Met Asp Gln Tyr Ala
1355 1360 1365

Asn Arg Leu Ala Tyr Arg Ser Val Lys Ser Gly Leu Gln Glu Ala
1370 1375 1380

Ala Lys Thr Thr Lys Val Gln Cys Asn Ser Arg Met Phe Pro Val
1385 1390 1395

Pro Ser Ser Gln Val Lys Thr Asn Lys Glu Leu Leu Met Phe Ser
1400 1405 1410

```
Asn Lys  Glu His His Gln Glu  Ala Asp Lys Lys Arg  Gln Ser Lys
    1415                 1420                 1425

Arg Asn  Glu Gly Tyr Phe Cys  Lys Asn Gln Thr Cys  Glu Arg Thr
    1430                 1435                 1440

Leu Asp  Pro Tyr Arg Asn Glu  Val Ser Gln Leu Tyr  Ser Phe Ser
    1445                 1450                 1455

Thr Ser  Leu Val His Ser Ile  Thr Lys Asp Ala Lys  Glu Glu Leu
    1460                 1465                 1470

Thr Ala  Ser Leu Val Gly Leu  Pro Lys Ser Leu Thr  Asp Ser Cys
    1475                 1480                 1485

Leu Phe  Glu Lys Ser Gly Tyr  Glu Glu Asp Asn Glu  Cys His Val
    1490                 1495                 1500

Thr Pro  Glu Leu Pro Lys Ser  Leu Gln Pro Ser Ser  Gln Asn His
    1505                 1510                 1515

Arg Phe  Tyr His Ser Thr Gly  Ser Leu Asn Gly Tyr  Gly Cys Gly
    1520                 1525                 1530

Asp Asn  Val Val Gln Ala Val  Glu Gln Tyr Ala Lys  Lys Val Val
    1535                 1540                 1545

Asp Asp  Thr Leu Glu Leu Thr  Leu Gly Ser Thr Val  Phe Arg Val
    1550                 1555                 1560

Ser Glu  Thr Thr Lys Ser Ala  Asp Arg Val Thr Tyr  Ala Glu Lys
    1565                 1570                 1575

Leu Ser  Pro Leu Thr Gly Gln  Ala Cys Arg Tyr Cys  Asp Leu Lys
    1580                 1585                 1590

Glu Leu  His Asn Cys Thr Gly  Asn Ser Ser Gln His  Phe Phe Arg
    1595                 1600                 1605

Gln Gly  Ser Leu Ala Ser Ser  Lys Pro Ala Ser Asn  Pro Lys Phe
    1610                 1615                 1620
```

```
Ser Ser  Arg Tyr Gln Lys Ser  Arg Ile Phe His Leu  Ser Val Pro
    1625                1630                1635

Gln Ile  His Val Asn Leu Asp  Lys Lys Ala Val Leu  Ala Glu Lys
    1640                1645                1650

Ile Val  Ala Glu Ala Ile Glu  Lys Ala Glu Arg Glu  Leu Ser Ser
    1655                1660                1665

Thr Ser  Leu Ala Ala Asp Ser  Gly Ile Gly Gln Glu  Gly Ala Ser
    1670                1675                1680

Phe Ala  Glu Ser Leu Ala Thr  Glu Thr Met Thr Ala  Ala Val Thr
    1685                1690                1695

Asn Val  Gly His Ala Val Ser  Ser Ser Lys Glu Ile  Glu Asp Phe
    1700                1705                1710

Gln Ser  Thr Glu Ser Val Ser  Ser Gln Gln Met Asn  Leu Ser Ile
    1715                1720                1725

Gly Asp  Asp Ser Thr Gly Ser  Trp Ser Asn Leu Ser  Phe Glu Asp
    1730                1735                1740

Glu His  Gln Asp Glu Ser Ser  Ser Phe His His Leu  Ser Glu Ser
    1745                1750                1755

Asn Gly  Asn Ser Ser Ser Trp  Ser Ser Leu Gly Leu  Glu Gly Asp
    1760                1765                1770

Leu Tyr  Glu Asp Asn Leu Ser  Phe Pro Thr Ser Asp  Ser Asp Gly
    1775                1780                1785

Pro Asp  Asp Lys Asp Glu Glu  His Glu Asp Glu Val  Glu Gly Leu
    1790                1795                1800

Gly Gln  Asp Gly Lys Thr Leu  Leu Ile Thr Asn Ile  Asp Met Glu
    1805                1810                1815

Pro Cys  Thr Val Asp Pro Gln  Leu Arg Ile Ile Leu  Gln Trp Leu
    1820                1825                1830
```

```
Ile Ala  Ser Glu Ala Glu Val  Ala Glu Leu Tyr Phe  His Asp Ser
    1835                1840                1845


Ala Asn  Lys Glu Phe Met Leu  Leu Ser Lys Gln Leu  Gln Glu Lys
    1850                1855                1860


Gly Trp  Lys Val Gly Asp Leu  Leu Gln Ala Val Leu  Gln Tyr Tyr
    1865                1870                1875


Glu Val  Met Glu Lys Ala Ser  Ser Glu Glu Arg Cys  Lys Ser Leu
    1880                1885                1890


Phe Asp  Trp Leu Leu Glu Asn  Ala
    1895                1900


<210> 613
<211> 1782
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: AKAP12; "

<220>
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<220>
<221> source
<223> /note="Uniprot ID:  Q02952; "

<220>
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<400> 613
Met Gly Ala Gly Ser Ser Thr Glu Gln Arg Ser Pro Glu Gln Pro Pro
1               5                  10                  15


Glu Gly Ser Ser Thr Pro Ala Glu Pro Glu Pro Ser Gly Gly Gly Pro
            20                  25                  30


Ser Ala Glu Ala Ala Pro Asp Thr Thr Ala Asp Pro Ala Ile Ala Ala
        35                  40                  45
```

```
Ser Asp Pro Ala Thr Lys Leu Leu Gln Lys Asn Gly Gln Leu Ser Thr
    50                  55                  60

Ile Asn Gly Val Ala Glu Gln Asp Glu Leu Ser Leu Gln Glu Gly Asp
65                  70                  75                  80

Leu Asn Gly Gln Lys Gly Ala Leu Asn Gly Gln Gly Ala Leu Asn Ser
                85                  90                  95

Gln Glu Glu Glu Glu Val Ile Val Thr Glu Val Gly Gln Arg Asp Ser
            100                 105                 110

Glu Asp Val Ser Lys Arg Asp Ser Asp Lys Glu Met Ala Thr Lys Ser
        115                 120                 125

Ala Val Val His Asp Ile Thr Asp Asp Gly Gln Glu Glu Thr Pro Glu
    130                 135                 140

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

Gln Pro Thr Glu Ser Gln Ala Asn Asp Ile Gly Phe Lys Lys Val Phe
                165                 170                 175

Lys Phe Val Gly Phe Lys Phe Thr Val Lys Lys Asp Lys Thr Glu Lys
            180                 185                 190

Pro Asp Thr Val Gln Leu Leu Thr Val Lys Lys Asp Glu Gly Glu Gly
        195                 200                 205

Ala Ala Gly Ala Gly Asp His Lys Asp Pro Ser Leu Gly Ala Gly Glu
    210                 215                 220

Ala Ala Ser Lys Glu Ser Glu Pro Lys Gln Ser Thr Glu Lys Pro Glu
225                 230                 235                 240

Glu Thr Leu Lys Arg Glu Gln Ser His Ala Glu Ile Ser Pro Pro Ala
                245                 250                 255

Glu Ser Gly Gln Ala Val Glu Glu Cys Lys Glu Glu Gly Glu Glu Lys
            260                 265                 270
```

```
Gln Glu Lys Glu Pro Ser Lys Ser Ala Glu Ser Pro Thr Ser Pro Val
        275                 280                 285

Thr Ser Glu Thr Gly Ser Thr Phe Lys Lys Phe Phe Thr Gln Gly Trp
    290                 295                 300

Ala Gly Trp Arg Lys Lys Thr Ser Phe Arg Lys Pro Lys Glu Asp Glu
305                 310                 315                 320

Val Glu Ala Ser Glu Lys Lys Lys Glu Gln Glu Pro Glu Lys Val Asp
                325                 330                 335

Thr Glu Glu Asp Gly Lys Ala Glu Val Ala Ser Glu Lys Leu Thr Ala
            340                 345                 350

Ser Glu Gln Ala His Pro Gln Glu Pro Ala Glu Ser Ala His Glu Pro
        355                 360                 365

Arg Leu Ser Ala Glu Tyr Glu Lys Val Glu Leu Pro Ser Glu Glu Gln
    370                 375                 380

Val Ser Gly Ser Gln Gly Pro Ser Glu Glu Lys Pro Ala Pro Leu Ala
385                 390                 395                 400

Thr Glu Val Phe Asp Glu Lys Ile Glu Val His Gln Glu Glu Val Val
                405                 410                 415

Ala Glu Val His Val Ser Thr Val Glu Glu Arg Thr Glu Glu Gln Lys
            420                 425                 430

Thr Glu Val Glu Glu Thr Ala Gly Ser Val Pro Ala Glu Glu Leu Val
        435                 440                 445

Glu Met Asp Ala Glu Pro Gln Glu Ala Glu Pro Ala Lys Glu Leu Val
    450                 455                 460

Lys Leu Lys Glu Thr Cys Val Ser Gly Glu Asp Pro Thr Gln Gly Ala
465                 470                 475                 480

Asp Leu Ser Pro Asp Glu Lys Val Leu Ser Lys Pro Pro Glu Gly Val
                485                 490                 495
```

```
Val Ser Glu Val Glu Met Leu Ser Ser Gln Glu Arg Met Lys Val Gln
            500                 505                 510

Gly Ser Pro Leu Lys Lys Leu Phe Thr Ser Thr Gly Leu Lys Lys Leu
        515                 520                 525

Ser Gly Lys Lys Gln Lys Gly Lys Arg Gly Gly Gly Asp Glu Glu Ser
    530                 535                 540

Gly Glu His Thr Gln Val Pro Ala Asp Ser Pro Asp Ser Gln Glu Glu
545                 550                 555                 560

Gln Lys Gly Glu Ser Ser Ala Ser Ser Pro Glu Glu Pro Glu Glu Ile
                565                 570                 575

Thr Cys Leu Glu Lys Gly Leu Ala Glu Val Gln Gln Asp Gly Glu Ala
            580                 585                 590

Glu Glu Gly Ala Thr Ser Asp Gly Glu Lys Lys Arg Glu Gly Val Thr
        595                 600                 605

Pro Trp Ala Ser Phe Lys Lys Met Val Thr Pro Lys Lys Arg Val Arg
    610                 615                 620

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

Ala Thr Leu Ser Ser Thr Glu Ser Thr Ala Ser Glu Met Gln Glu Glu
                645                 650                 655

Met Lys Gly Ser Val Glu Glu Pro Lys Pro Glu Glu Pro Lys Arg Lys
            660                 665                 670

Val Asp Thr Ser Val Ser Trp Glu Ala Leu Ile Cys Val Gly Ser Ser
        675                 680                 685

Lys Lys Arg Ala Arg Arg Gly Ser Ser Ser Asp Glu Glu Gly Gly Pro
    690                 695                 700

Lys Ala Met Gly Gly Asp His Gln Lys Ala Asp Glu Ala Gly Lys Asp
705                 710                 715                 720

Lys Glu Thr Gly Thr Asp Gly Ile Leu Ala Gly Ser Gln Glu His Asp
```

```
                725                 730                 735

Pro Gly Gln Gly Ser Ser Ser Pro Glu Gln Ala Gly Ser Pro Thr Glu
            740                 745                 750

Gly Glu Gly Val Ser Thr Trp Glu Ser Phe Lys Arg Leu Val Thr Pro
        755                 760                 765

Arg Lys Lys Ser Lys Ser Lys Leu Glu Glu Lys Ser Glu Asp Ser Ile
    770                 775                 780

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

Glu Glu Ser Trp Val Ser Ile Lys Lys Phe Ile Pro Gly Arg Arg Lys
                805                 810                 815

Lys Arg Pro Asp Gly Lys Gln Glu Gln Ala Pro Val Glu Asp Ala Gly
            820                 825                 830

Pro Thr Gly Ala Asn Glu Asp Asp Ser Asp Val Pro Ala Val Val Pro
        835                 840                 845

Leu Ser Glu Tyr Asp Ala Val Glu Arg Glu Lys Met Glu Ala Gln Gln
    850                 855                 860

Ala Gln Lys Ser Ala Glu Gln Pro Glu Gln Lys Ala Ala Thr Glu Val
865                 870                 875                 880

Ser Lys Glu Leu Ser Glu Ser Gln Val His Met Met Ala Ala Ala Val
                885                 890                 895

Ala Asp Gly Thr Arg Ala Ala Thr Ile Ile Glu Glu Arg Ser Pro Ser
            900                 905                 910

Trp Ile Ser Ala Ser Val Thr Glu Pro Leu Glu Gln Val Glu Ala Glu
        915                 920                 925

Ala Ala Leu Leu Thr Glu Glu Val Leu Glu Arg Glu Val Ile Ala Glu
    930                 935                 940

Glu Glu Pro Pro Thr Val Thr Glu Pro Leu Pro Glu Asn Arg Glu Ala
945                 950                 955                 960
```

```
Arg Gly Asp Thr Val Val Ser Glu Ala Glu Leu Thr Pro Glu Ala Val
                965                 970                 975

Thr Ala Ala Glu Thr Ala Gly Pro Leu Gly Ala Glu Glu Gly Thr Glu
            980                 985                 990

Ala Ser Ala Ala Glu Glu Thr Thr  Glu Met Val Ser Ala  Val Ser
Gln
        995                 1000                1005

Leu Thr  Asp Ser Pro Asp Thr  Thr Glu Glu Ala Thr  Pro Val Gln
    1010                1015                1020

Glu Val  Glu Gly Gly Val Pro  Asp Ile Glu Glu Gln  Glu Arg Arg
    1025                1030                1035

Thr Gln  Glu Val Leu Gln Ala  Val Ala Glu Lys Val  Lys Glu Glu
    1040                1045                1050

Ser Gln  Leu Pro Gly Thr Gly  Gly Pro Glu Asp Val  Leu Gln Pro
    1055                1060                1065

Val Gln  Arg Ala Glu Ala Glu  Arg Pro Glu Glu Gln  Ala Glu Ala
    1070                1075                1080

Ser Gly  Leu Lys Lys Glu Thr  Asp Val Val Leu Lys  Val Asp Ala
    1085                1090                1095

Gln Glu  Ala Lys Thr Glu Pro  Phe Thr Gln Gly Lys  Val Val Gly
    1100                1105                1110

Gln Thr  Thr Pro Glu Ser Phe  Glu Lys Ala Pro Gln  Val Thr Glu
    1115                1120                1125

Ser Ile  Glu Ser Ser Glu Leu  Val Thr Thr Cys Gln  Ala Glu Thr
    1130                1135                1140

Leu Ala  Gly Val Lys Ser Gln  Glu Met Val Met Glu  Gln Ala Ile
    1145                1150                1155

Pro Pro  Asp Ser Val Glu Thr  Pro Thr Asp Ser Glu  Thr Asp Gly
    1160                1165                1170
```

```
Ser Thr  Pro Val Ala Asp Phe  Asp Ala Pro Gly Thr  Thr Gln Lys
    1175                1180                1185

Asp Glu  Ile Val Glu Ile His  Glu Glu Asn Glu Val  Ala Ser Gly
    1190                1195                1200

Thr Gln  Ser Gly Gly Thr Glu  Ala Glu Ala Val Pro  Ala Gln Lys
    1205                1210                1215

Glu Arg  Pro Pro Ala Pro Ser  Ser Phe Val Phe Gln  Glu Glu Thr
    1220                1225                1230

Lys Glu  Gln Ser Lys Met Glu  Asp Thr Leu Glu His  Thr Asp Lys
    1235                1240                1245

Glu Val  Ser Val Glu Thr Val  Ser Ile Leu Ser Lys  Thr Glu Gly
    1250                1255                1260

Thr Gln  Glu Ala Asp Gln Tyr  Ala Asp Glu Lys Thr  Lys Asp Val
    1265                1270                1275

Pro Phe  Phe Glu Gly Leu Glu  Gly Ser Ile Asp Thr  Gly Ile Thr
    1280                1285                1290

Val Ser  Arg Glu Lys Val Thr  Glu Val Ala Leu Lys  Gly Glu Gly
    1295                1300                1305

Thr Glu  Glu Ala Glu Cys Lys  Lys Asp Asp Ala Leu  Glu Leu Gln
    1310                1315                1320

Ser His  Ala Lys Ser Pro Pro  Ser Pro Val Glu Arg  Glu Met Val
    1325                1330                1335

Val Gln  Val Glu Arg Glu Lys  Thr Glu Ala Glu Pro  Thr His Val
    1340                1345                1350

Asn Glu  Glu Lys Leu Glu His  Glu Thr Ala Val Thr  Val Ser Glu
    1355                1360                1365

Glu Val  Ser Lys Gln Leu Leu  Gln Thr Val Asn Val  Pro Ile Ile
    1370                1375                1380
```

```
Asp Gly  Ala Lys Glu Val Ser  Ser Leu Glu Gly Ser  Pro Pro Pro
    1385                1390                1395

Cys Leu  Gly Gln Glu Glu Ala  Val Cys Thr Lys Ile  Gln Val Gln
    1400                1405                1410

Ser Ser  Glu Ala Ser Phe Thr  Leu Thr Ala Ala Ala  Glu Glu Glu
    1415                1420                1425

Lys Val  Leu Gly Glu Thr Ala  Asn Ile Leu Glu Thr  Gly Glu Thr
    1430                1435                1440

Leu Glu  Pro Ala Gly Ala His  Leu Val Leu Glu Glu  Lys Ser Ser
    1445                1450                1455

Glu Lys  Asn Glu Asp Phe Ala  Ala His Pro Gly Glu  Asp Ala Val
    1460                1465                1470

Pro Thr  Gly Pro Asp Cys Gln  Ala Lys Ser Thr Pro  Val Ile Val
    1475                1480                1485

Ser Ala  Thr Thr Lys Lys Gly  Leu Ser Ser Asp Leu  Glu Gly Glu
    1490                1495                1500

Lys Thr  Thr Ser Leu Lys Trp  Lys Ser Asp Glu Val  Asp Glu Gln
    1505                1510                1515

Val Ala  Cys Gln Glu Val Lys  Val Ser Val Ala Ile  Glu Asp Leu
    1520                1525                1530

Glu Pro  Glu Asn Gly Ile Leu  Glu Leu Glu Thr Lys  Ser Ser Lys
    1535                1540                1545

Leu Val  Gln Asn Ile Ile Gln  Thr Ala Val Asp Gln  Phe Val Arg
    1550                1555                1560

Thr Glu  Glu Thr Ala Thr Glu  Met Leu Thr Ser Glu  Leu Gln Thr
    1565                1570                1575

Gln Ala  His Val Ile Lys Ala  Asp Ser Gln Asp Ala  Gly Gln Glu
    1580                1585                1590
```

```
Thr Glu  Lys Glu Gly Glu Glu  Pro Gln Ala Ser Ala  Gln Asp Glu
    1595                1600                1605

Thr Pro  Ile Thr Ser Ala Lys  Glu Glu Ser Glu Ser  Thr Ala Val
    1610                1615                1620

Gly Gln  Ala His Ser Asp Ile  Ser Lys Asp Met Ser  Glu Ala Ser
    1625                1630                1635

Glu Lys  Thr Met Thr Val Glu  Val Glu Gly Ser Thr  Val Asn Asp
    1640                1645                1650

Gln Gln  Leu Glu Glu Val Val  Leu Pro Ser Glu Glu  Glu Gly Gly
    1655                1660                1665

Gly Ala  Gly Thr Lys Ser Val  Pro Glu Asp Asp Gly  His Ala Leu
    1670                1675                1680

Leu Ala  Glu Arg Ile Glu Lys  Ser Leu Val Glu Pro  Lys Glu Asp
    1685                1690                1695

Glu Lys  Gly Asp Asp Val Asp  Asp Pro Glu Asn Gln  Asn Ser Ala
    1700                1705                1710

Leu Ala  Asp Thr Asp Ala Ser  Gly Gly Leu Thr Lys  Glu Ser Pro
    1715                1720                1725

Asp Thr  Asn Gly Pro Lys Gln  Lys Glu Lys Glu Asp  Ala Gln Glu
    1730                1735                1740

Val Glu  Leu Gln Glu Gly Lys  Val His Ser Glu Ser  Asp Lys Ala
    1745                1750                1755

Ile Thr  Pro Gln Ala Gln Glu  Glu Leu Gln Lys Gln  Glu Arg Glu
    1760                1765                1770

Ser Ala  Lys Ser Glu Leu Thr  Glu Ser
    1775                1780
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<210> 614
<211> 1684
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 104; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP12; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 12; "

<220>
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<223> /note="Uniprot ID: Q02952; "

<220>
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<223> /note="ENSP ID: ENSP00000346702"

<400> 614

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

Val Ser Lys Arg Asp Ser Asp Lys Glu Met Ala Thr Lys Ser Ala Val
            20                  25                  30

Val His Asp Ile Thr Asp Asp Gly Gln Glu Glu Thr Pro Glu Ile Ile
        35                  40                  45

Glu Gln Ile Pro Ser Ser Glu Ser Asn Leu Glu Glu Leu Thr Gln Pro
    50                  55                  60

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

Val Gly Phe Lys Phe Thr Val Lys Lys Asp Lys Thr Glu Lys Pro Asp
                85                  90                  95

Thr Val Gln Leu Leu Thr Val Lys Lys Asp Glu Gly Glu Gly Ala Ala
            100                 105                 110

Gly Ala Gly Asp His Lys Asp Pro Ser Leu Gly Ala Gly Glu Ala Ala
        115                 120                 125

Ser Lys Glu Ser Glu Pro Lys Gln Ser Thr Glu Lys Pro Glu Glu Thr
    130                 135                 140
```

```
Leu Lys Arg Glu Gln Ser His Ala Glu Ile Ser Pro Pro Ala Glu Ser
145                 150                 155                 160

Gly Gln Ala Val Glu Glu Cys Lys Glu Glu Gly Glu Glu Lys Gln Glu
                165                 170                 175

Lys Glu Pro Ser Lys Ser Ala Glu Ser Pro Thr Ser Pro Val Thr Ser
            180                 185                 190

Glu Thr Gly Ser Thr Phe Lys Lys Phe Phe Thr Gln Gly Trp Ala Gly
        195                 200                 205

Trp Arg Lys Lys Thr Ser Phe Arg Lys Pro Lys Glu Asp Glu Val Glu
    210                 215                 220

Ala Ser Glu Lys Lys Lys Glu Gln Glu Pro Glu Lys Val Asp Thr Glu
225                 230                 235                 240

Glu Asp Gly Lys Ala Glu Val Ala Ser Glu Lys Leu Thr Ala Ser Glu
                245                 250                 255

Gln Ala His Pro Gln Glu Pro Ala Glu Ser Ala His Glu Pro Arg Leu
            260                 265                 270

Ser Ala Glu Tyr Glu Lys Val Glu Leu Pro Ser Glu Glu Gln Val Ser
        275                 280                 285

Gly Ser Gln Gly Pro Ser Glu Glu Lys Pro Ala Pro Leu Ala Thr Glu
    290                 295                 300

Val Phe Asp Glu Lys Ile Glu Val His Gln Glu Glu Val Val Ala Glu
305                 310                 315                 320

Val His Val Ser Thr Val Glu Glu Arg Thr Glu Glu Gln Lys Thr Glu
                325                 330                 335

Val Glu Glu Thr Ala Gly Ser Val Pro Ala Glu Glu Leu Val Glu Met
            340                 345                 350

Asp Ala Glu Pro Gln Glu Ala Glu Pro Ala Lys Glu Leu Val Lys Leu
        355                 360                 365
```

```
Lys Glu Thr Cys Val Ser Gly Glu Asp Pro Thr Gln Gly Ala Asp Leu
    370                 375                 380

Ser Pro Asp Glu Lys Val Leu Ser Lys Pro Pro Glu Gly Val Val Ser
385                 390                 395                 400

Glu Val Glu Met Leu Ser Ser Gln Glu Arg Met Lys Val Gln Gly Ser
                405                 410                 415

Pro Leu Lys Lys Leu Phe Thr Ser Thr Gly Leu Lys Lys Leu Ser Gly
            420                 425                 430

Lys Lys Gln Lys Gly Lys Arg Gly Gly Gly Asp Glu Glu Ser Gly Glu
        435                 440                 445

His Thr Gln Val Pro Ala Asp Ser Pro Asp Ser Gln Glu Glu Gln Lys
    450                 455                 460

Gly Glu Ser Ser Ala Ser Ser Pro Glu Glu Pro Glu Glu Ile Thr Cys
465                 470                 475                 480

Leu Glu Lys Gly Leu Ala Glu Val Gln Gln Asp Gly Glu Ala Glu Glu
                485                 490                 495

Gly Ala Thr Ser Asp Gly Glu Lys Lys Arg Glu Gly Val Thr Pro Trp
            500                 505                 510

Ala Ser Phe Lys Lys Met Val Thr Pro Lys Lys Arg Val Arg Arg Pro
        515                 520                 525

Ser Glu Ser Asp Lys Glu Asp Glu Leu Asp Lys Val Lys Ser Ala Thr
    530                 535                 540

Leu Ser Ser Thr Glu Ser Thr Ala Ser Glu Met Gln Glu Glu Met Lys
545                 550                 555                 560

Gly Ser Val Glu Glu Pro Lys Pro Glu Glu Pro Lys Arg Lys Val Asp
                565                 570                 575

Thr Ser Val Ser Trp Glu Ala Leu Ile Cys Val Gly Ser Ser Lys Lys
            580                 585                 590

Arg Ala Arg Arg Gly Ser Ser Ser Asp Glu Glu Gly Gly Pro Lys Ala
```

595 600 605

Met Gly Gly Asp His Gln Lys Ala Asp Glu Ala Gly Lys Asp Lys Glu
610 615 620

Thr Gly Thr Asp Gly Ile Leu Ala Gly Ser Gln Glu His Asp Pro Gly
625 630 635 640

Gln Gly Ser Ser Ser Pro Glu Gln Ala Gly Ser Pro Thr Glu Gly Glu
645 650 655

Gly Val Ser Thr Trp Glu Ser Phe Lys Arg Leu Val Thr Pro Arg Lys
660 665 670

Lys Ser Lys Ser Lys Leu Glu Glu Lys Ser Glu Asp Ser Ile Ala Gly
675 680 685

Ser Gly Val Glu His Ser Thr Pro Asp Thr Glu Pro Gly Lys Glu Glu
690 695 700

Ser Trp Val Ser Ile Lys Lys Phe Ile Pro Gly Arg Arg Lys Lys Arg
705 710 715 720

Pro Asp Gly Lys Gln Glu Gln Ala Pro Val Glu Asp Ala Gly Pro Thr
725 730 735

Gly Ala Asn Glu Asp Asp Ser Asp Val Pro Ala Val Val Pro Leu Ser
740 745 750

Glu Tyr Asp Ala Val Glu Arg Glu Lys Met Glu Ala Gln Gln Ala Gln
755 760 765

Lys Ser Ala Glu Gln Pro Glu Gln Lys Ala Ala Thr Glu Val Ser Lys
770 775 780

Glu Leu Ser Glu Ser Gln Val His Met Met Ala Ala Ala Val Ala Asp
785 790 795 800

Gly Thr Arg Ala Ala Thr Ile Ile Glu Glu Arg Ser Pro Ser Trp Ile
805 810 815

Ser Ala Ser Val Thr Glu Pro Leu Glu Gln Val Glu Ala Glu Ala Ala
820 825 830

```
Leu Leu Thr Glu Glu Val Leu Glu Arg Glu Val Ile Ala Glu Glu Glu
        835                 840                 845

Pro Pro Thr Val Thr Glu Pro Leu Pro Glu Asn Arg Glu Ala Arg Gly
    850                 855                 860

Asp Thr Val Val Ser Glu Ala Glu Leu Thr Pro Glu Ala Val Thr Ala
865                 870                 875                 880

Ala Glu Thr Ala Gly Pro Leu Gly Ala Glu Glu Gly Thr Glu Ala Ser
                885                 890                 895

Ala Ala Glu Glu Thr Thr Glu Met Val Ser Ala Val Ser Gln Leu Thr
            900                 905                 910

Asp Ser Pro Asp Thr Thr Glu Glu Ala Thr Pro Val Gln Glu Val Glu
        915                 920                 925

Gly Gly Val Pro Asp Ile Glu Glu Gln Glu Arg Arg Thr Gln Glu Val
    930                 935                 940

Leu Gln Ala Val Ala Glu Lys Val Lys Glu Glu Ser Gln Leu Pro Gly
945                 950                 955                 960

Thr Gly Gly Pro Glu Asp Val Leu Gln Pro Val Gln Arg Ala Glu Ala
                965                 970                 975

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

Asp Val Val Leu Lys Val Asp Ala  Gln Glu Ala Lys Thr  Glu Pro
Phe
        995                 1000                1005

Thr Gln  Gly Lys Val Val Gly  Gln Thr Thr Pro Glu  Ser Phe Glu
    1010                1015                1020

Lys Ala  Pro Gln Val Thr Glu  Ser Ile Glu Ser Ser  Glu Leu Val
    1025                1030                1035

Thr Thr  Cys Gln Ala Glu Thr  Leu Ala Gly Val Lys  Ser Gln Glu
    1040                1045                1050
```

```
Met Val  Met Glu Gln Ala Ile  Pro Pro Asp Ser Val  Glu Thr Pro
    1055                1060                1065

Thr Asp  Ser Glu Thr Asp Gly  Ser Thr Pro Val Ala  Asp Phe Asp
    1070                1075                1080

Ala Pro  Gly Thr Thr Gln Lys  Asp Glu Ile Val Glu  Ile His Glu
    1085                1090                1095

Glu Asn  Glu Val Ala Ser Gly  Thr Gln Ser Gly Gly  Thr Glu Ala
    1100                1105                1110

Glu Ala  Val Pro Ala Gln Lys  Glu Arg Pro Pro Ala  Pro Ser Ser
    1115                1120                1125

Phe Val  Phe Gln Glu Glu Thr  Lys Glu Gln Ser Lys  Met Glu Asp
    1130                1135                1140

Thr Leu  Glu His Thr Asp Lys  Glu Val Ser Val Glu  Thr Val Ser
    1145                1150                1155

Ile Leu  Ser Lys Thr Glu Gly  Thr Gln Glu Ala Asp  Gln Tyr Ala
    1160                1165                1170

Asp Glu  Lys Thr Lys Asp Val  Pro Phe Phe Glu Gly  Leu Glu Gly
    1175                1180                1185

Ser Ile  Asp Thr Gly Ile Thr  Val Ser Arg Glu Lys  Val Thr Glu
    1190                1195                1200

Val Ala  Leu Lys Gly Glu Gly  Thr Glu Glu Ala Glu  Cys Lys Lys
    1205                1210                1215

Asp Asp  Ala Leu Glu Leu Gln  Ser His Ala Lys Ser  Pro Pro Ser
    1220                1225                1230

Pro Val  Glu Arg Glu Met Val  Val Gln Val Glu Arg  Glu Lys Thr
    1235                1240                1245

Glu Ala  Glu Pro Thr His Val  Asn Glu Glu Lys Leu  Glu His Glu
    1250                1255                1260
```

```
Thr Ala  Val Thr Val Ser Glu  Glu Val Ser Lys Gln  Leu Leu Gln
    1265                1270                1275

Thr Val  Asn Val Pro Ile Ile  Asp Gly Ala Lys Glu  Val Ser Ser
    1280                1285                1290

Leu Glu  Gly Ser Pro Pro Pro  Cys Leu Gly Gln Glu  Glu Ala Val
    1295                1300                1305

Cys Thr  Lys Ile Gln Val Gln  Ser Ser Glu Ala Ser  Phe Thr Leu
    1310                1315                1320

Thr Ala  Ala Ala Glu Glu Glu  Lys Val Leu Gly Glu  Thr Ala Asn
    1325                1330                1335

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

Val Leu  Glu Glu Lys Ser Ser  Glu Lys Asn Glu Asp  Phe Ala Ala
    1355                1360                1365

His Pro  Gly Glu Asp Ala Val  Pro Thr Gly Pro Asp  Cys Gln Ala
    1370                1375                1380

Lys Ser  Thr Pro Val Ile Val  Ser Ala Thr Thr Lys  Lys Gly Leu
    1385                1390                1395

Ser Ser  Asp Leu Glu Gly Glu  Lys Thr Thr Ser Leu  Lys Trp Lys
    1400                1405                1410

Ser Asp  Glu Val Asp Glu Gln  Val Ala Cys Gln Glu  Val Lys Val
    1415                1420                1425

Ser Val  Ala Ile Glu Asp Leu  Glu Pro Glu Asn Gly  Ile Leu Glu
    1430                1435                1440

Leu Glu  Thr Lys Ser Ser Lys  Leu Val Gln Asn Ile  Ile Gln Thr
    1445                1450                1455

Ala Val  Asp Gln Phe Val Arg  Thr Glu Glu Thr Ala  Thr Glu Met
    1460                1465                1470
```

```
Leu Thr  Ser Glu Leu Gln Thr  Gln Ala His Val Ile  Lys Ala Asp
    1475                1480                1485

Ser Gln  Asp Ala Gly Gln Glu  Thr Glu Lys Glu Gly  Glu Glu Pro
    1490                1495                1500

Gln Ala  Ser Ala Gln Asp Glu  Thr Pro Ile Thr Ser  Ala Lys Glu
    1505                1510                1515

Glu Ser  Glu Ser Thr Ala Val  Gly Gln Ala His Ser  Asp Ile Ser
    1520                1525                1530

Lys Asp  Met Ser Glu Ala Ser  Glu Lys Thr Met Thr  Val Glu Val
    1535                1540                1545

Glu Gly  Ser Thr Val Asn Asp  Gln Gln Leu Glu Glu  Val Val Leu
    1550                1555                1560

Pro Ser  Glu Glu Glu Gly Gly  Gly Ala Gly Thr Lys  Ser Val Pro
    1565                1570                1575

Glu Asp  Asp Gly His Ala Leu  Leu Ala Glu Arg Ile  Glu Lys Ser
    1580                1585                1590

Leu Val  Glu Pro Lys Glu Asp  Glu Lys Gly Asp Asp  Val Asp Asp
    1595                1600                1605

Pro Glu  Asn Gln Asn Ser Ala  Leu Ala Asp Thr Asp  Ala Ser Gly
    1610                1615                1620

Gly Leu  Thr Lys Glu Ser Pro  Asp Thr Asn Gly Pro  Lys Gln Lys
    1625                1630                1635

Glu Lys  Glu Asp Ala Gln Glu  Val Glu Leu Gln Glu  Gly Lys Val
    1640                1645                1650

His Ser  Glu Ser Asp Lys Ala  Ile Thr Pro Gln Ala  Gln Glu Glu
    1655                1660                1665

Leu Gln  Lys Gln Glu Arg Glu  Ser Ala Lys Ser Glu  Leu Thr Glu
    1670                1675                1680

Ser
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<210> 615
<211> 1677
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: AKAP12; "

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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 12; "

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<223> /note="Uniprot ID: Q02952; "

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Met Val Gly Gln Arg Asp Ser Glu Asp Val Ser Lys Arg Asp Ser Asp
1   5   10   15

Lys Glu Met Ala Thr Lys Ser Ala Val Val His Asp Ile Thr Asp Asp
            20   25   30

Gly Gln Glu Glu Thr Pro Glu Ile Ile Glu Gln Ile Pro Ser Ser Glu
        35   40   45

Ser Asn Leu Glu Glu Leu Thr Gln Pro Thr Glu Ser Gln Ala Asn Asp
    50   55   60

Ile Gly Phe Lys Lys Val Phe Lys Phe Val Gly Phe Lys Phe Thr Val
65   70   75   80

Lys Lys Asp Lys Thr Glu Lys Pro Asp Thr Val Gln Leu Leu Thr Val
                85   90   95

Lys Lys Asp Glu Gly Glu Gly Ala Ala Gly Ala Gly Asp His Lys Asp
            100   105   110

```
Pro Ser Leu Gly Ala Gly Glu Ala Ala Ser Lys Glu Ser Glu Pro Lys
        115                 120                 125

Gln Ser Thr Glu Lys Pro Glu Glu Thr Leu Lys Arg Glu Gln Ser His
    130                 135                 140

Ala Glu Ile Ser Pro Pro Ala Glu Ser Gly Gln Ala Val Glu Glu Cys
145                 150                 155                 160

Lys Glu Glu Gly Glu Glu Lys Gln Glu Lys Glu Pro Ser Lys Ser Ala
                165                 170                 175

Glu Ser Pro Thr Ser Pro Val Thr Ser Glu Thr Gly Ser Thr Phe Lys
            180                 185                 190

Lys Phe Phe Thr Gln Gly Trp Ala Gly Trp Arg Lys Lys Thr Ser Phe
        195                 200                 205

Arg Lys Pro Lys Glu Asp Glu Val Glu Ala Ser Glu Lys Lys Lys Glu
    210                 215                 220

Gln Glu Pro Glu Lys Val Asp Thr Glu Glu Asp Gly Lys Ala Glu Val
225                 230                 235                 240

Ala Ser Glu Lys Leu Thr Ala Ser Glu Gln Ala His Pro Gln Glu Pro
                245                 250                 255

Ala Glu Ser Ala His Glu Pro Arg Leu Ser Ala Glu Tyr Glu Lys Val
            260                 265                 270

Glu Leu Pro Ser Glu Glu Gln Val Ser Gly Ser Gln Gly Pro Ser Glu
        275                 280                 285

Glu Lys Pro Ala Pro Leu Ala Thr Glu Val Phe Asp Glu Lys Ile Glu
    290                 295                 300

Val His Gln Glu Glu Val Val Ala Glu Val His Val Ser Thr Val Glu
305                 310                 315                 320

Glu Arg Thr Glu Glu Gln Lys Thr Glu Val Glu Glu Thr Ala Gly Ser
                325                 330                 335
```

```
Val Pro Ala Glu Glu Leu Val Glu Met Asp Ala Glu Pro Gln Glu Ala
            340                 345                 350

Glu Pro Ala Lys Glu Leu Val Lys Leu Lys Glu Thr Cys Val Ser Gly
        355                 360                 365

Glu Asp Pro Thr Gln Gly Ala Asp Leu Ser Pro Asp Glu Lys Val Leu
    370                 375                 380

Ser Lys Pro Pro Glu Gly Val Val Ser Glu Val Glu Met Leu Ser Ser
385                 390                 395                 400

Gln Glu Arg Met Lys Val Gln Gly Ser Pro Leu Lys Lys Leu Phe Thr
                405                 410                 415

Ser Thr Gly Leu Lys Lys Leu Ser Gly Lys Lys Gln Lys Gly Lys Arg
            420                 425                 430

Gly Gly Gly Asp Glu Glu Ser Gly Glu His Thr Gln Val Pro Ala Asp
        435                 440                 445

Ser Pro Asp Ser Gln Glu Glu Gln Lys Gly Glu Ser Ser Ala Ser Ser
    450                 455                 460

Pro Glu Glu Pro Glu Glu Ile Thr Cys Leu Glu Lys Gly Leu Ala Glu
465                 470                 475                 480

Val Gln Gln Asp Gly Glu Ala Glu Glu Gly Ala Thr Ser Asp Gly Glu
                485                 490                 495

Lys Lys Arg Glu Gly Val Thr Pro Trp Ala Ser Phe Lys Lys Met Val
            500                 505                 510

Thr Pro Lys Lys Arg Val Arg Arg Pro Ser Glu Ser Asp Lys Glu Asp
        515                 520                 525

Glu Leu Asp Lys Val Lys Ser Ala Thr Leu Ser Ser Thr Glu Ser Thr
    530                 535                 540

Ala Ser Glu Met Gln Glu Glu Met Lys Gly Ser Val Glu Glu Pro Lys
545                 550                 555                 560

Pro Glu Glu Pro Lys Arg Lys Val Asp Thr Ser Val Ser Trp Glu Ala
```

565 570 575

Leu Ile Cys Val Gly Ser Ser Lys Lys Arg Ala Arg Arg Gly Ser Ser
580 585 590

Ser Asp Glu Glu Gly Gly Pro Lys Ala Met Gly Gly Asp His Gln Lys
595 600 605

Ala Asp Glu Ala Gly Lys Asp Lys Glu Thr Gly Thr Asp Gly Ile Leu
610 615 620

Ala Gly Ser Gln Glu His Asp Pro Gly Gln Gly Ser Ser Ser Pro Glu
625 630 635 640

Gln Ala Gly Ser Pro Thr Glu Gly Glu Gly Val Ser Thr Trp Glu Ser
645 650 655

Phe Lys Arg Leu Val Thr Pro Arg Lys Lys Ser Lys Ser Lys Leu Glu
660 665 670

Glu Lys Ser Glu Asp Ser Ile Ala Gly Ser Gly Val Glu His Ser Thr
675 680 685

Pro Asp Thr Glu Pro Gly Lys Glu Glu Ser Trp Val Ser Ile Lys Lys
690 695 700

Phe Ile Pro Gly Arg Arg Lys Lys Arg Pro Asp Gly Lys Gln Glu Gln
705 710 715 720

Ala Pro Val Glu Asp Ala Gly Pro Thr Gly Ala Asn Glu Asp Asp Ser
725 730 735

Asp Val Pro Ala Val Val Pro Leu Ser Glu Tyr Asp Ala Val Glu Arg
740 745 750

Glu Lys Met Glu Ala Gln Gln Ala Gln Lys Ser Ala Glu Gln Pro Glu
755 760 765

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

His Met Met Ala Ala Ala Val Ala Asp Gly Thr Arg Ala Ala Thr Ile
785 790 795 800

```
Ile Glu Glu Arg Ser Pro Ser Trp Ile Ser Ala Ser Val Thr Glu Pro
                805                 810                 815

Leu Glu Gln Val Glu Ala Glu Ala Ala Leu Leu Thr Glu Glu Val Leu
            820                 825                 830

Glu Arg Glu Val Ile Ala Glu Glu Glu Pro Pro Thr Val Thr Glu Pro
        835                 840                 845

Leu Pro Glu Asn Arg Glu Ala Arg Gly Asp Thr Val Val Ser Glu Ala
    850                 855                 860

Glu Leu Thr Pro Glu Ala Val Thr Ala Ala Glu Thr Ala Gly Pro Leu
865                 870                 875                 880

Gly Ala Glu Glu Gly Thr Glu Ala Ser Ala Ala Glu Glu Thr Thr Glu
                885                 890                 895

Met Val Ser Ala Val Ser Gln Leu Thr Asp Ser Pro Asp Thr Thr Glu
            900                 905                 910

Glu Ala Thr Pro Val Gln Glu Val Glu Gly Gly Val Pro Asp Ile Glu
        915                 920                 925

Glu Gln Glu Arg Arg Thr Gln Glu Val Leu Gln Ala Val Ala Glu Lys
    930                 935                 940

Val Lys Glu Glu Ser Gln Leu Pro Gly Thr Gly Gly Pro Glu Asp Val
945                 950                 955                 960

Leu Gln Pro Val Gln Arg Ala Glu Ala Glu Arg Pro Glu Glu Gln Ala
                965                 970                 975

Glu Ala Ser Gly Leu Lys Lys Glu Thr Asp Val Val Leu Lys Val Asp
            980                 985                 990

Ala Gln Glu Ala Lys Thr Glu Pro  Phe Thr Gln Gly Lys  Val Val
Gly
        995                 1000                1005

Gln Thr  Thr Pro Glu Ser Phe  Glu Lys Ala Pro Gln  Val Thr Glu
    1010                1015                1020
```

```
Ser Ile  Glu Ser Ser Glu Leu  Val Thr Thr Cys Gln  Ala Glu Thr
    1025                1030                1035

Leu Ala  Gly Val Lys Ser Gln  Glu Met Val Met Glu  Gln Ala Ile
    1040                1045                1050

Pro Pro  Asp Ser Val Glu Thr  Pro Thr Asp Ser Glu  Thr Asp Gly
    1055                1060                1065

Ser Thr  Pro Val Ala Asp Phe  Asp Ala Pro Gly Thr  Thr Gln Lys
    1070                1075                1080

Asp Glu  Ile Val Glu Ile His  Glu Glu Asn Glu Val  Ala Ser Gly
    1085                1090                1095

Thr Gln  Ser Gly Gly Thr Glu  Ala Glu Ala Val Pro  Ala Gln Lys
    1100                1105                1110

Glu Arg  Pro Pro Ala Pro Ser  Ser Phe Val Phe Gln  Glu Glu Thr
    1115                1120                1125

Lys Glu  Gln Ser Lys Met Glu  Asp Thr Leu Glu His  Thr Asp Lys
    1130                1135                1140

Glu Val  Ser Val Glu Thr Val  Ser Ile Leu Ser Lys  Thr Glu Gly
    1145                1150                1155

Thr Gln  Glu Ala Asp Gln Tyr  Ala Asp Glu Lys Thr  Lys Asp Val
    1160                1165                1170

Pro Phe  Phe Glu Gly Leu Glu  Gly Ser Ile Asp Thr  Gly Ile Thr
    1175                1180                1185

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

Thr Glu  Glu Ala Glu Cys Lys  Lys Asp Asp Ala Leu  Glu Leu Gln
    1205                1210                1215

Ser His  Ala Lys Ser Pro Pro  Ser Pro Val Glu Arg  Glu Met Val
    1220                1225                1230
```

```
Val Gln  Val Glu Arg Glu Lys  Thr Glu Ala Glu Pro  Thr His Val
    1235                1240                1245

Asn Glu  Glu Lys Leu Glu His  Glu Thr Ala Val Thr  Val Ser Glu
    1250                1255                1260

Glu Val  Ser Lys Gln Leu Leu  Gln Thr Val Asn Val  Pro Ile Ile
    1265                1270                1275

Asp Gly  Ala Lys Glu Val Ser  Ser Leu Glu Gly Ser  Pro Pro Pro
    1280                1285                1290

Cys Leu  Gly Gln Glu Glu Ala  Val Cys Thr Lys Ile  Gln Val Gln
    1295                1300                1305

Ser Ser  Glu Ala Ser Phe Thr  Leu Thr Ala Ala Ala  Glu Glu Glu
    1310                1315                1320

Lys Val  Leu Gly Glu Thr Ala  Asn Ile Leu Glu Thr  Gly Glu Thr
    1325                1330                1335

Leu Glu  Pro Ala Gly Ala His  Leu Val Leu Glu Glu  Lys Ser Ser
    1340                1345                1350

Glu Lys  Asn Glu Asp Phe Ala  Ala His Pro Gly Glu  Asp Ala Val
    1355                1360                1365

Pro Thr  Gly Pro Asp Cys Gln  Ala Lys Ser Thr Pro  Val Ile Val
    1370                1375                1380

Ser Ala  Thr Thr Lys Lys Gly  Leu Ser Ser Asp Leu  Glu Gly Glu
    1385                1390                1395

Lys Thr  Thr Ser Leu Lys Trp  Lys Ser Asp Glu Val  Asp Glu Gln
    1400                1405                1410

Val Ala  Cys Gln Glu Val Lys  Val Ser Val Ala Ile  Glu Asp Leu
    1415                1420                1425

Glu Pro  Glu Asn Gly Ile Leu  Glu Leu Glu Thr Lys  Ser Ser Lys
    1430                1435                1440
```

```
Leu Val  Gln Asn Ile Ile Gln  Thr Ala Val Asp Gln  Phe Val Arg
    1445                1450                1455

Thr Glu  Glu Thr Ala Thr Glu  Met Leu Thr Ser Glu  Leu Gln Thr
    1460                1465                1470

Gln Ala  His Val Ile Lys Ala  Asp Ser Gln Asp Ala  Gly Gln Glu
    1475                1480                1485

Thr Glu  Lys Glu Gly Glu Glu  Pro Gln Ala Ser Ala  Gln Asp Glu
    1490                1495                1500

Thr Pro  Ile Thr Ser Ala Lys  Glu Glu Ser Glu Ser  Thr Ala Val
    1505                1510                1515

Gly Gln  Ala His Ser Asp Ile  Ser Lys Asp Met Ser  Glu Ala Ser
    1520                1525                1530

Glu Lys  Thr Met Thr Val Glu  Val Glu Gly Ser Thr  Val Asn Asp
    1535                1540                1545

Gln Gln  Leu Glu Glu Val Val  Leu Pro Ser Glu Glu  Glu Gly Gly
    1550                1555                1560

Gly Ala  Gly Thr Lys Ser Val  Pro Glu Asp Asp Gly  His Ala Leu
    1565                1570                1575

Leu Ala  Glu Arg Ile Glu Lys  Ser Leu Val Glu Pro  Lys Glu Asp
    1580                1585                1590

Glu Lys  Gly Asp Asp Val Asp  Asp Pro Glu Asn Gln  Asn Ser Ala
    1595                1600                1605

Leu Ala  Asp Thr Asp Ala Ser  Gly Gly Leu Thr Lys  Glu Ser Pro
    1610                1615                1620

Asp Thr  Asn Gly Pro Lys Gln  Lys Glu Lys Glu Asp  Ala Gln Glu
    1625                1630                1635

Val Glu  Leu Gln Glu Gly Lys  Val His Ser Glu Ser  Asp Lys Ala
    1640                1645                1650

Ile Thr  Pro Gln Ala Gln Glu  Glu Leu Gln Lys Gln  Glu Arg Glu
```

```
    1655                1660                1665


Ser Ala  Lys Ser Glu Leu Thr  Glu Ser
    1670                1675


<210> 616
<211> 1782
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 104; "

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<223> /note="Gene Symbol: AKAP12; "

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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 12; "

<220>
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<223> /note="Uniprot ID:  Q02952; "

<220>
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<223> /note="ENSP ID: ENSP00000384537"

<400> 616
Met Gly Ala Gly Ser Ser Thr Glu Gln Arg Ser Pro Glu Gln Pro Pro
1               5                  10                  15


Glu Gly Ser Ser Thr Pro Ala Glu Pro Glu Pro Ser Gly Gly Gly Pro
            20                  25                  30


Ser Ala Glu Ala Ala Pro Asp Thr Thr Ala Asp Pro Ala Ile Ala Ala
        35                  40                  45


Ser Asp Pro Ala Thr Lys Leu Leu Gln Lys Asn Gly Gln Leu Ser Thr
    50                  55                  60


Ile Asn Gly Val Ala Glu Gln Asp Glu Leu Ser Leu Gln Glu Gly Asp
65                  70                  75                  80


Leu Asn Gly Gln Lys Gly Ala Leu Asn Gly Gln Gly Ala Leu Asn Ser
                85                  90                  95
```

```
Gln Glu Glu Glu Glu Val Ile Val Thr Glu Val Gly Gln Arg Asp Ser
            100                 105                 110

Glu Asp Val Ser Lys Arg Asp Ser Asp Lys Glu Met Ala Thr Lys Ser
        115                 120                 125

Ala Val Val His Asp Ile Thr Asp Asp Gly Gln Glu Glu Thr Pro Glu
    130                 135                 140

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

Gln Pro Thr Glu Ser Gln Ala Asn Asp Ile Gly Phe Lys Lys Val Phe
                165                 170                 175

Lys Phe Val Gly Phe Lys Phe Thr Val Lys Lys Asp Lys Thr Glu Lys
            180                 185                 190

Pro Asp Thr Val Gln Leu Leu Thr Val Lys Lys Asp Glu Gly Glu Gly
        195                 200                 205

Ala Ala Gly Ala Gly Asp His Lys Asp Pro Ser Leu Gly Ala Gly Glu
    210                 215                 220

Ala Ala Ser Lys Glu Ser Glu Pro Lys Gln Ser Thr Glu Lys Pro Glu
225                 230                 235                 240

Glu Thr Leu Lys Arg Glu Gln Ser His Ala Glu Ile Ser Pro Pro Ala
                245                 250                 255

Glu Ser Gly Gln Ala Val Glu Glu Cys Lys Glu Glu Gly Glu Glu Lys
            260                 265                 270

Gln Glu Lys Glu Pro Ser Lys Ser Ala Glu Ser Pro Thr Ser Pro Val
        275                 280                 285

Thr Ser Glu Thr Gly Ser Thr Phe Lys Lys Phe Phe Thr Gln Gly Trp
    290                 295                 300

Ala Gly Trp Arg Lys Lys Thr Ser Phe Arg Lys Pro Lys Glu Asp Glu
305                 310                 315                 320
```

```
Val Glu Ala Ser Glu Lys Lys Lys Glu Gln Glu Pro Glu Lys Val Asp
                325                 330                 335

Thr Glu Glu Asp Gly Lys Ala Glu Val Ala Ser Glu Lys Leu Thr Ala
            340                 345                 350

Ser Glu Gln Ala His Pro Gln Glu Pro Ala Glu Ser Ala His Glu Pro
        355                 360                 365

Arg Leu Ser Ala Glu Tyr Glu Lys Val Glu Leu Pro Ser Glu Glu Gln
    370                 375                 380

Val Ser Gly Ser Gln Gly Pro Ser Glu Glu Lys Pro Ala Pro Leu Ala
385                 390                 395                 400

Thr Glu Val Phe Asp Glu Lys Ile Glu Val His Gln Glu Glu Val Val
                405                 410                 415

Ala Glu Val His Val Ser Thr Val Glu Glu Arg Thr Glu Glu Gln Lys
            420                 425                 430

Thr Glu Val Glu Glu Thr Ala Gly Ser Val Pro Ala Glu Glu Leu Val
        435                 440                 445

Glu Met Asp Ala Glu Pro Gln Glu Ala Glu Pro Ala Lys Glu Leu Val
    450                 455                 460

Lys Leu Lys Glu Thr Cys Val Ser Gly Glu Asp Pro Thr Gln Gly Ala
465                 470                 475                 480

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

Val Ser Glu Val Glu Met Leu Ser Ser Gln Glu Arg Met Lys Val Gln
            500                 505                 510

Gly Ser Pro Leu Lys Lys Leu Phe Thr Ser Thr Gly Leu Lys Lys Leu
        515                 520                 525

Ser Gly Lys Lys Gln Lys Gly Lys Arg Gly Gly Gly Asp Glu Glu Ser
    530                 535                 540

Gly Glu His Thr Gln Val Pro Ala Asp Ser Pro Asp Ser Gln Glu Glu
```

545 550 555 560

Gln Lys Gly Glu Ser Ser Ala Ser Ser Pro Glu Glu Pro Glu Glu Ile
565 570 575

Thr Cys Leu Glu Lys Gly Leu Ala Glu Val Gln Gln Asp Gly Glu Ala
580 585 590

Glu Glu Gly Ala Thr Ser Asp Gly Glu Lys Lys Arg Glu Gly Val Thr
595 600 605

Pro Trp Ala Ser Phe Lys Lys Met Val Thr Pro Lys Lys Arg Val Arg
610 615 620

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

Ala Thr Leu Ser Ser Thr Glu Ser Thr Ala Ser Glu Met Gln Glu Glu
645 650 655

Met Lys Gly Ser Val Glu Glu Pro Lys Pro Glu Glu Pro Lys Arg Lys
660 665 670

Val Asp Thr Ser Val Ser Trp Glu Ala Leu Ile Cys Val Gly Ser Ser
675 680 685

Lys Lys Arg Ala Arg Arg Gly Ser Ser Ser Asp Glu Glu Gly Gly Pro
690 695 700

Lys Ala Met Gly Gly Asp His Gln Lys Ala Asp Glu Ala Gly Lys Asp
705 710 715 720

Lys Glu Thr Gly Thr Asp Gly Ile Leu Ala Gly Ser Gln Glu His Asp
725 730 735

Pro Gly Gln Gly Ser Ser Ser Pro Glu Gln Ala Gly Ser Pro Thr Glu
740 745 750

Gly Glu Gly Val Ser Thr Trp Glu Ser Phe Lys Arg Leu Val Thr Pro
755 760 765

Arg Lys Lys Ser Lys Ser Lys Leu Glu Glu Lys Ser Glu Asp Ser Ile
770 775 780

```
Ala Gly Ser Gly Val Glu His Ser Thr Pro Asp Thr Glu Pro Gly Lys
785                 790                 795                 800

Glu Glu Ser Trp Val Ser Ile Lys Lys Phe Ile Pro Gly Arg Arg Lys
                805                 810                 815

Lys Arg Pro Asp Gly Lys Gln Glu Gln Ala Pro Val Glu Asp Ala Gly
            820                 825                 830

Pro Thr Gly Ala Asn Glu Asp Asp Ser Asp Val Pro Ala Val Val Pro
        835                 840                 845

Leu Ser Glu Tyr Asp Ala Val Glu Arg Glu Lys Met Glu Ala Gln Gln
    850                 855                 860

Ala Gln Lys Ser Ala Glu Gln Pro Glu Gln Lys Ala Ala Thr Glu Val
865                 870                 875                 880

Ser Lys Glu Leu Ser Glu Ser Gln Val His Met Met Ala Ala Ala Val
                885                 890                 895

Ala Asp Gly Thr Arg Ala Ala Thr Ile Ile Glu Glu Arg Ser Pro Ser
            900                 905                 910

Trp Ile Ser Ala Ser Val Thr Glu Pro Leu Glu Gln Val Glu Ala Glu
        915                 920                 925

Ala Ala Leu Leu Thr Glu Glu Val Leu Glu Arg Glu Val Ile Ala Glu
    930                 935                 940

Glu Glu Pro Pro Thr Val Thr Glu Pro Leu Pro Glu Asn Arg Glu Ala
945                 950                 955                 960

Arg Gly Asp Thr Val Val Ser Glu Ala Glu Leu Thr Pro Glu Ala Val
                965                 970                 975

Thr Ala Ala Glu Thr Ala Gly Pro Leu Gly Ala Glu Glu Gly Thr Glu
            980                 985                 990

Ala Ser Ala Ala Glu Glu Thr Thr  Glu Met Val Ser Ala  Val Ser
Gln
        995                 1000                1005
```

```
Leu Thr  Asp Ser Pro Asp Thr  Thr Glu Glu Ala Thr  Pro Val Gln
    1010                1015                1020

Glu Val  Glu Gly Gly Val Pro  Asp Ile Glu Glu Gln  Glu Arg Arg
    1025                1030                1035

Thr Gln  Glu Val Leu Gln Ala  Val Ala Glu Lys Val  Lys Glu Glu
    1040                1045                1050

Ser Gln  Leu Pro Gly Thr Gly  Gly Pro Glu Asp Val  Leu Gln Pro
    1055                1060                1065

Val Gln  Arg Ala Glu Ala Glu  Arg Pro Glu Glu Gln  Ala Glu Ala
    1070                1075                1080

Ser Gly  Leu Lys Lys Glu Thr  Asp Val Val Leu Lys  Val Asp Ala
    1085                1090                1095

Gln Glu  Ala Lys Thr Glu Pro  Phe Thr Gln Gly Lys  Val Val Gly
    1100                1105                1110

Gln Thr  Thr Pro Glu Ser Phe  Glu Lys Ala Pro Gln  Val Thr Glu
    1115                1120                1125

Ser Ile  Glu Ser Ser Glu Leu  Val Thr Thr Cys Gln  Ala Glu Thr
    1130                1135                1140

Leu Ala  Gly Val Lys Ser Gln  Glu Met Val Met Glu  Gln Ala Ile
    1145                1150                1155

Pro Pro  Asp Ser Val Glu Thr  Pro Thr Asp Ser Glu  Thr Asp Gly
    1160                1165                1170

Ser Thr  Pro Val Ala Asp Phe  Asp Ala Pro Gly Thr  Thr Gln Lys
    1175                1180                1185

Asp Glu  Ile Val Glu Ile His  Glu Glu Asn Glu Val  Ala Ser Gly
    1190                1195                1200

Thr Gln  Ser Gly Gly Thr Glu  Ala Glu Ala Val Pro  Ala Gln Lys
    1205                1210                1215
```

```
Glu Arg  Pro Pro Ala Pro Ser  Ser Phe Val Phe Gln  Glu Glu Thr
    1220                1225                1230

Lys Glu  Gln Ser Lys Met Glu  Asp Thr Leu Glu His  Thr Asp Lys
    1235                1240                1245

Glu Val  Ser Val Glu Thr Val  Ser Ile Leu Ser Lys  Thr Glu Gly
    1250                1255                1260

Thr Gln  Glu Ala Asp Gln Tyr  Ala Asp Glu Lys Thr  Lys Asp Val
    1265                1270                1275

Pro Phe  Phe Glu Gly Leu Glu  Gly Ser Ile Asp Thr  Gly Ile Thr
    1280                1285                1290

Val Ser  Arg Glu Lys Val Thr  Glu Val Ala Leu Lys  Gly Glu Gly
    1295                1300                1305

Thr Glu  Glu Ala Glu Cys Lys  Lys Asp Asp Ala Leu  Glu Leu Gln
    1310                1315                1320

Ser His  Ala Lys Ser Pro Pro  Ser Pro Val Glu Arg  Glu Met Val
    1325                1330                1335

Val Gln  Val Glu Arg Glu Lys  Thr Glu Ala Glu Pro  Thr His Val
    1340                1345                1350

Asn Glu  Glu Lys Leu Glu His  Glu Thr Ala Val Thr  Val Ser Glu
    1355                1360                1365

Glu Val  Ser Lys Gln Leu Leu  Gln Thr Val Asn Val  Pro Ile Ile
    1370                1375                1380

Asp Gly  Ala Lys Glu Val Ser  Ser Leu Glu Gly Ser  Pro Pro Pro
    1385                1390                1395

Cys Leu  Gly Gln Glu Glu Ala  Val Cys Thr Lys Ile  Gln Val Gln
    1400                1405                1410

Ser Ser  Glu Ala Ser Phe Thr  Leu Thr Ala Ala Ala  Glu Glu Glu
    1415                1420                1425
```

```
Lys Val  Leu Gly Glu Thr Ala  Asn Ile Leu Glu Thr  Gly Glu Thr
    1430                1435                1440

Leu Glu  Pro Ala Gly Ala His  Leu Val Leu Glu Glu  Lys Ser Ser
    1445                1450                1455

Glu Lys  Asn Glu Asp Phe Ala  Ala His Pro Gly Glu  Asp Ala Val
    1460                1465                1470

Pro Thr  Gly Pro Asp Cys Gln  Ala Lys Ser Thr Pro  Val Ile Val
    1475                1480                1485

Ser Ala  Thr Thr Lys Lys Gly  Leu Ser Ser Asp Leu  Glu Gly Glu
    1490                1495                1500

Lys Thr  Thr Ser Leu Lys Trp  Lys Ser Asp Glu Val  Asp Glu Gln
    1505                1510                1515

Val Ala  Cys Gln Glu Val Lys  Val Ser Val Ala Ile  Glu Asp Leu
    1520                1525                1530

Glu Pro  Glu Asn Gly Ile Leu  Glu Leu Glu Thr Lys  Ser Ser Lys
    1535                1540                1545

Leu Val  Gln Asn Ile Ile Gln  Thr Ala Val Asp Gln  Phe Val Arg
    1550                1555                1560

Thr Glu  Glu Thr Ala Thr Glu  Met Leu Thr Ser Glu  Leu Gln Thr
    1565                1570                1575

Gln Ala  His Val Ile Lys Ala  Asp Ser Gln Asp Ala  Gly Gln Glu
    1580                1585                1590

Thr Glu  Lys Glu Gly Glu Glu  Pro Gln Ala Ser Ala  Gln Asp Glu
    1595                1600                1605

Thr Pro  Ile Thr Ser Ala Lys  Glu Glu Ser Glu Ser  Thr Ala Val
    1610                1615                1620

Gly Gln  Ala His Ser Asp Ile  Ser Lys Asp Met Ser  Glu Ala Ser
    1625                1630                1635

Glu Lys  Thr Met Thr Val Glu  Val Glu Gly Ser Thr  Val Asn Asp
```

```
    1640                1645                1650

Gln Gln  Leu Glu Glu Val Val  Leu Pro Ser Glu Glu  Glu Gly Gly
    1655                1660                1665

Gly Ala  Gly Thr Lys Ser Val  Pro Glu Asp Asp Gly  His Ala Leu
    1670                1675                1680

Leu Ala  Glu Arg Ile Glu Lys  Ser Leu Val Glu Pro  Lys Glu Asp
    1685                1690                1695

Glu Lys  Gly Asp Asp Val Asp  Asp Pro Glu Asn Gln  Asn Ser Ala
    1700                1705                1710

Leu Ala  Asp Thr Asp Ala Ser  Gly Gly Leu Thr Lys  Glu Ser Pro
    1715                1720                1725

Asp Thr  Asn Gly Pro Lys Gln  Lys Glu Lys Glu Asp  Ala Gln Glu
    1730                1735                1740

Val Glu  Leu Gln Glu Gly Lys  Val His Ser Glu Ser  Asp Lys Ala
    1745                1750                1755

Ile Thr  Pro Gln Ala Gln Glu  Glu Leu Gln Lys Gln  Glu Arg Glu
    1760                1765                1770

Ser Ala  Lys Ser Glu Leu Thr  Glu Ser
    1775                1780


<210> 617
<211> 2817
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 105; "

<220>
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<223> /note="Gene Symbol: AKAP13; "

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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 13; "
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<220>
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<223> /note="Uniprot ID: Q12802; "

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Met Lys Leu Asn Pro Gln Gln Ala Pro Leu Tyr Gly Asp Cys Val Val
1   5   10   15

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

Tyr Leu Val Phe Leu Gly Ser Thr Leu Arg His Cys Thr Ser Thr Arg
        35   40   45

Lys Val Ser Ser Asp Thr Leu Glu Thr Ile Ala Pro Gly His Asp Cys
    50   55   60

Cys Glu Thr Val Lys Val Gln Leu Cys Ala Ser Lys Glu Gly Leu Pro
65   70   75   80

Val Phe Val Val Ala Glu Glu Asp Phe His Phe Val Gln Asp Glu Ala
                85   90   95

Tyr Asp Ala Ala Gln Phe Leu Ala Thr Ser Ala Gly Asn Gln Gln Ala
            100   105   110

Leu Asn Phe Thr Arg Phe Leu Asp Gln Ser Gly Pro Pro Ser Gly Asp
        115   120   125

Val Asn Ser Leu Asp Lys Lys Leu Val Leu Ala Phe Arg His Leu Lys
    130   135   140

Leu Pro Thr Glu Trp Asn Val Leu Gly Thr Asp Gln Ser Leu His Asp
145   150   155   160

Ala Gly Pro Arg Glu Thr Leu Met His Phe Ala Val Arg Leu Gly Leu
                165   170   175

Leu Arg Leu Thr Trp Phe Leu Leu Gln Lys Pro Gly Gly Arg Gly Ala
            180   185   190

```
Leu Ser Ile His Asn Gln Glu Gly Ala Thr Pro Val Ser Leu Ala Leu
        195                 200                 205

Glu Arg Gly Tyr His Lys Leu His Gln Leu Leu Thr Glu Glu Asn Ala
    210                 215                 220

Gly Glu Pro Asp Ser Trp Ser Ser Leu Ser Tyr Glu Ile Pro Tyr Gly
225                 230                 235                 240

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

Ser Glu Ser Asp Ser His His Glu His Pro Phe Pro Gly Asp Gly Cys
            260                 265                 270

Thr Gly Pro Ile Phe Lys Leu Met Asn Ile Gln Gln Gln Leu Met Lys
        275                 280                 285

Thr Asn Leu Lys Gln Met Asp Ser Leu Met Pro Leu Met Met Thr Ala
    290                 295                 300

Gln Asp Pro Ser Ser Ala Pro Glu Thr Asp Gly Gln Phe Leu Pro Cys
305                 310                 315                 320

Ala Pro Glu Pro Thr Asp Pro Gln Arg Leu Ser Ser Ser Glu Glu Thr
                325                 330                 335

Glu Ser Thr Gln Cys Cys Pro Gly Ser Pro Val Ala Gln Thr Glu Ser
            340                 345                 350

Pro Cys Asp Leu Ser Ser Ile Val Glu Glu Glu Asn Thr Asp Arg Ser
        355                 360                 365

Cys Arg Lys Lys Asn Lys Gly Val Glu Arg Lys Gly Glu Glu Val Glu
    370                 375                 380

Pro Ala Pro Ile Val Asp Ser Gly Thr Val Ser Asp Gln Asp Ser Cys
385                 390                 395                 400

Leu Gln Ser Leu Pro Asp Cys Gly Val Lys Gly Thr Glu Gly Leu Ser
                405                 410                 415

Ser Cys Gly Asn Arg Asn Glu Glu Thr Gly Thr Lys Ser Ser Gly Met
```

```
            420                 425                 430

Pro Thr Asp Gln Glu Ser Leu Ser Ser Gly Asp Ala Val Leu Gln Arg
        435                 440                 445

Asp Leu Val Met Glu Pro Gly Thr Ala Gln Tyr Ser Ser Gly Gly Glu
    450                 455                 460

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

Glu Met Glu His Gly Leu Met Asn Pro Asp Ala Thr Val Trp Lys Asn
                485                 490                 495

Val Leu Gln Gly Gly Glu Ser Thr Lys Glu Arg Phe Glu Asn Ser Asn
            500                 505                 510

Ile Gly Thr Ala Gly Ala Ser Asp Val His Val Thr Ser Lys Pro Val
        515                 520                 525

Asp Lys Ile Ser Val Pro Asn Cys Ala Pro Ala Ala Ser Ser Leu Asp
    530                 535                 540

Gly Asn Lys Pro Ala Glu Ser Ser Leu Ala Phe Ser Asn Glu Glu Thr
545                 550                 555                 560

Ser Thr Glu Lys Thr Ala Glu Thr Glu Thr Ser Arg Ser Arg Glu Glu
                565                 570                 575

Ser Ala Asp Ala Pro Val Asp Gln Asn Ser Val Val Ile Pro Ala Ala
            580                 585                 590

Ala Lys Asp Lys Ile Ser Asp Gly Leu Glu Pro Tyr Thr Leu Leu Ala
        595                 600                 605

Ala Gly Ile Gly Glu Ala Met Ser Pro Ser Asp Leu Ala Leu Leu Gly
    610                 615                 620

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

His Ala Gln Ser Gln Lys Gly Lys Ser Ser Pro Ile Cys Ser Thr Thr
                645                 650                 655
```

```
Gly Asp Asp Lys Leu Cys Ala Asp Ser Ala Cys Gln Gln Asn Thr Val
            660                 665                 670

Thr Ser Ser Gly Asp Leu Val Ala Lys Leu Cys Asp Asn Ile Val Ser
        675                 680                 685

Glu Ser Glu Ser Thr Thr Ala Arg Gln Pro Ser Ser Gln Asp Pro Pro
    690                 695                 700

Asp Ala Ser His Cys Glu Asp Pro Gln Ala His Thr Val Thr Ser Asp
705                 710                 715                 720

Pro Val Arg Asp Thr Gln Glu Arg Ala Asp Phe Cys Pro Phe Lys Val
                725                 730                 735

Val Asp Asn Lys Gly Gln Arg Lys Asp Val Lys Leu Asp Lys Pro Leu
            740                 745                 750

Thr Asn Met Leu Glu Val Val Ser His Pro His Pro Val Val Pro Lys
        755                 760                 765

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

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

Ala Leu Ser Phe Val Pro Ser Gln Lys Glu Lys Gly Thr Ala Thr Pro
                805                 810                 815

Glu Leu His Thr Ala Thr Asp Tyr Arg Asp Gly Pro Asp Gly Asn Ser
            820                 825                 830

Asn Glu Pro Asp Thr Arg Pro Leu Glu Asp Arg Ala Val Gly Leu Ser
        835                 840                 845

Thr Ser Ser Thr Ala Ala Glu Leu Gln His Gly Met Gly Asn Thr Ser
    850                 855                 860

Leu Thr Gly Leu Gly Gly Glu His Glu Gly Pro Ala Pro Pro Ala Ile
865                 870                 875                 880
```

```
Pro Glu Ala Leu Asn Ile Lys Gly Asn Thr Asp Ser Ser Leu Gln Ser
               885                 890                 895

Val Gly Lys Ala Thr Leu Ala Leu Asp Ser Val Leu Thr Glu Glu Gly
           900                 905                 910

Lys Leu Leu Val Val Ser Glu Ser Ser Ala Ala Gln Glu Gln Asp Lys
       915                 920                 925

Asp Lys Ala Val Thr Cys Ser Ser Ile Lys Glu Asn Ala Leu Ser Ser
   930                 935                 940

Gly Thr Leu Gln Glu Glu Gln Arg Thr Pro Pro Pro Gly Gln Asp Thr
945                 950                 955                 960

Gln Gln Phe His Glu Lys Ser Ile Ser Ala Asp Cys Ala Lys Asp Lys
               965                 970                 975

Ala Leu Gln Leu Ser Asn Ser Pro Gly Ala Ser Ser Ala Phe Leu Lys
           980                 985                 990

Ala Glu Thr Glu His Asn Lys Glu  Val Ala Pro Gln Val  Ser Leu
Leu
       995                 1000                1005

Thr Gln  Gly Gly Ala Ala Gln  Ser Leu Val Pro Pro  Gly Ala Ser
   1010                1015                1020

Leu Ala  Thr Glu Ser Arg Gln  Glu Ala Leu Gly Ala  Glu His Asn
   1025                1030                1035

Ser Ser  Ala Leu Leu Pro Cys  Leu Leu Pro Asp Gly  Ser Asp Gly
   1040                1045                1050

Ser Asp  Ala Leu Asn Cys Ser  Gln Pro Ser Pro Leu  Asp Val Gly
   1055                1060                1065

Val Lys  Asn Thr Gln Ser Gln  Gly Lys Thr Ser Ala  Cys Glu Val
   1070                1075                1080

Ser Gly  Asp Val Thr Val Asp  Val Thr Gly Val Asn  Ala Leu Gln
   1085                1090                1095
```

```
Gly Met  Ala Glu Pro Arg Arg  Glu Asn Ile Ser His  Asn Thr Gln
    1100                1105                1110

Asp Ile  Leu Ile Pro Asn Val  Leu Leu Ser Gln Glu  Lys Asn Ala
    1115                1120                1125

Val Leu  Gly Leu Pro Val Ala  Leu Gln Asp Lys Ala  Val Thr Asp
    1130                1135                1140

Pro Gln  Gly Val Gly Thr Pro  Glu Met Ile Pro Leu  Asp Trp Glu
    1145                1150                1155

Lys Gly  Lys Leu Glu Gly Ala  Asp His Ser Cys Thr  Met Gly Asp
    1160                1165                1170

Ala Glu  Glu Ala Gln Ile Asp  Asp Glu Ala His Pro  Val Leu Leu
    1175                1180                1185

Gln Pro  Val Ala Lys Glu Leu  Pro Thr Asp Met Glu  Leu Ser Ala
    1190                1195                1200

His Asp  Asp Gly Ala Pro Ala  Gly Val Arg Glu Val  Met Arg Ala
    1205                1210                1215

Pro Pro  Ser Gly Arg Glu Arg  Ser Thr Pro Ser Leu  Pro Cys Met
    1220                1225                1230

Val Ser  Ala Gln Asp Ala Pro  Leu Pro Lys Gly Ala  Asp Leu Ile
    1235                1240                1245

Glu Glu  Ala Ala Ser Arg Ile  Val Asp Ala Val Ile  Glu Gln Val
    1250                1255                1260

Lys Ala  Ala Gly Ala Leu Leu  Thr Glu Gly Glu Ala  Cys His Met
    1265                1270                1275

Ser Leu  Ser Ser Pro Glu Leu  Gly Pro Leu Thr Lys  Gly Leu Glu
    1280                1285                1290

Ser Ala  Phe Thr Glu Lys Val  Ser Thr Phe Pro Pro  Gly Glu Ser
    1295                1300                1305
```

```
Leu Pro  Met Gly Ser Thr Pro  Glu Glu Ala Thr Gly  Ser Leu Ala
    1310                 1315                 1320

Gly Cys  Phe Ala Gly Arg Glu  Glu Pro Glu Lys Ile  Ile Leu Pro
    1325                 1330                 1335

Val Gln  Gly Pro Glu Pro Ala  Ala Glu Met Pro Asp  Val Lys Ala
    1340                 1345                 1350

Glu Asp  Glu Val Asp Phe Arg  Ala Ser Ser Ile Ser  Glu Glu Val
    1355                 1360                 1365

Ala Val  Gly Ser Ile Ala Ala  Thr Leu Lys Met Lys  Gln Gly Pro
    1370                 1375                 1380

Met Thr  Gln Ala Ile Asn Arg  Glu Asn Trp Cys Thr  Ile Glu Pro
    1385                 1390                 1395

Cys Pro  Asp Ala Ala Ser Leu  Leu Ala Ser Lys Gln  Ser Pro Glu
    1400                 1405                 1410

Cys Glu  Asn Phe Leu Asp Val  Gly Leu Gly Arg Glu  Cys Thr Ser
    1415                 1420                 1425

Lys Gln  Gly Val Leu Lys Arg  Glu Ser Gly Ser Asp  Ser Asp Leu
    1430                 1435                 1440

Phe His  Ser Pro Ser Asp Asp  Met Asp Ser Ile Ile  Phe Pro Lys
    1445                 1450                 1455

Pro Glu  Glu Glu His Leu Ala  Cys Asp Ile Thr Gly  Ser Ser Ser
    1460                 1465                 1470

Ser Thr  Asp Asp Thr Ala Ser  Leu Asp Arg His Ser  Ser His Gly
    1475                 1480                 1485

Ser Asp  Val Ser Leu Ser Gln  Ile Leu Lys Pro Asn  Arg Ser Arg
    1490                 1495                 1500

Asp Arg  Gln Ser Leu Asp Gly  Phe Tyr Ser His Gly  Met Gly Ala
    1505                 1510                 1515

Glu Gly  Arg Glu Ser Glu Ser  Glu Pro Ala Asp Pro  Gly Asp Val
```

1520 1525 1530

Glu Glu Glu Glu Met Asp Ser Ile Thr Glu Val Pro Ala Asn Cys
1535 1540 1545

Ser Val Leu Arg Ser Ser Met Arg Ser Leu Ser Pro Phe Arg Arg
1550 1555 1560

His Ser Trp Gly Pro Gly Lys Asn Ala Ala Ser Asp Ala Glu Met
1565 1570 1575

Asn His Arg Ser Met Ser Trp Cys Pro Ser Gly Val Gln Tyr Ser
1580 1585 1590

Ala Gly Leu Ser Ala Asp Phe Asn Tyr Arg Ser Phe Ser Leu Glu
1595 1600 1605

Gly Leu Thr Gly Gly Ala Gly Val Gly Asn Lys Pro Ser Ser Ser
1610 1615 1620

Leu Glu Val Ser Ser Ala Asn Ala Glu Glu Leu Arg His Pro Phe
1625 1630 1635

Ser Gly Glu Glu Arg Val Asp Ser Leu Val Ser Leu Ser Glu Glu
1640 1645 1650

Asp Leu Glu Ser Asp Gln Arg Glu His Arg Met Phe Asp Gln Gln
1655 1660 1665

Ile Cys His Arg Ser Lys Gln Gln Gly Phe Asn Tyr Cys Thr Ser
1670 1675 1680

Ala Ile Ser Ser Pro Leu Thr Lys Ser Ile Ser Leu Met Thr Ile
1685 1690 1695

Ser His Pro Gly Leu Asp Asn Ser Arg Pro Phe His Ser Thr Phe
1700 1705 1710

His Asn Thr Ser Ala Asn Leu Thr Glu Ser Ile Thr Glu Glu Asn
1715 1720 1725

Tyr Asn Phe Leu Pro His Ser Pro Ser Lys Lys Asp Ser Glu Trp
1730 1735 1740

```
Lys Ser  Gly Thr Lys Val Ser  Arg Thr Phe Ser Tyr  Ile Lys Asn
    1745                1750                1755

Lys Met  Ser Ser Ser Lys Lys  Ser Lys Glu Lys Glu  Lys Glu Lys
    1760                1765                1770

Asp Lys  Ile Lys Glu Lys Glu  Lys Asp Ser Lys Asp  Lys Glu Lys
    1775                1780                1785

Asp Lys  Lys Thr Val Asn Gly  His Thr Phe Ser Ser  Ile Pro Val
    1790                1795                1800

Val Gly  Pro Ile Ser Cys Ser  Gln Cys Met Lys Pro  Phe Thr Asn
    1805                1810                1815

Lys Asp  Ala Tyr Thr Cys Ala  Asn Cys Ser Ala Phe  Val His Lys
    1820                1825                1830

Gly Cys  Arg Glu Ser Leu Ala  Ser Cys Ala Lys Val  Lys Met Lys
    1835                1840                1845

Gln Pro  Lys Gly Ser Leu Gln  Ala His Asp Thr Ser  Ser Leu Pro
    1850                1855                1860

Thr Val  Ile Met Arg Asn Lys  Pro Ser Gln Pro Lys  Glu Arg Pro
    1865                1870                1875

Arg Ser  Ala Val Leu Leu Val  Asp Glu Thr Ala Thr  Thr Pro Ile
    1880                1885                1890

Phe Ala  Asn Arg Arg Ser Gln  Gln Ser Val Ser Leu  Ser Lys Ser
    1895                1900                1905

Val Ser  Ile Gln Asn Ile Thr  Gly Val Gly Asn Asp  Glu Asn Met
    1910                1915                1920

Ser Asn  Thr Trp Lys Phe Leu  Ser His Ser Thr Asp  Ser Leu Asn
    1925                1930                1935

Lys Ile  Ser Lys Val Asn Glu  Ser Thr Glu Ser Leu  Thr Asp Glu
    1940                1945                1950
```

```
Gly Val  Gly Thr Asp Met Asn  Glu Gly Gln Leu Leu  Gly Asp Phe
    1955                1960                1965

Glu Ile  Glu Ser Lys Gln Leu  Glu Ala Glu Ser Trp  Ser Arg Ile
    1970                1975                1980

Ile Asp  Ser Lys Phe Leu Lys  Gln Gln Lys Lys Asp  Val Val Lys
    1985                1990                1995

Arg Gln  Glu Val Ile Tyr Glu  Leu Met Gln Thr Glu  Phe His His
    2000                2005                2010

Val Arg  Thr Leu Lys Ile Met  Ser Gly Val Tyr Ser  Gln Gly Met
    2015                2020                2025

Met Ala  Asp Leu Leu Phe Glu  Gln Gln Met Val Glu  Lys Leu Phe
    2030                2035                2040

Pro Cys  Leu Asp Glu Leu Ile  Ser Ile His Ser Gln  Phe Phe Gln
    2045                2050                2055

Arg Ile  Leu Glu Arg Lys Lys  Glu Ser Leu Val Asp  Lys Ser Glu
    2060                2065                2070

Lys Asn  Phe Leu Ile Lys Arg  Ile Gly Asp Val Leu  Val Asn Gln
    2075                2080                2085

Phe Ser  Gly Glu Asn Ala Glu  Arg Leu Lys Lys Thr  Tyr Gly Lys
    2090                2095                2100

Phe Cys  Gly Gln His Asn Gln  Ser Val Asn Tyr Phe  Lys Asp Leu
    2105                2110                2115

Tyr Ala  Lys Asp Lys Arg Phe  Gln Ala Phe Val Lys  Lys Lys Met
    2120                2125                2130

Ser Ser  Ser Val Val Arg Arg  Leu Gly Ile Pro Glu  Cys Ile Leu
    2135                2140                2145

Leu Val  Thr Gln Arg Ile Thr  Lys Tyr Pro Val Leu  Phe Gln Arg
    2150                2155                2160
```

Ile Leu Gln Cys Thr Lys Asp Asn Glu Val Glu Gln Glu Asp Leu
2165 2170 2175

Ala Gln Ser Leu Ser Leu Val Lys Asp Val Ile Gly Ala Val Asp
2180 2185 2190

Ser Lys Val Ala Ser Tyr Glu Lys Lys Val Arg Leu Asn Glu Ile
2195 2200 2205

Tyr Thr Lys Thr Asp Ser Lys Ser Ile Met Arg Met Lys Ser Gly
2210 2215 2220

Gln Met Phe Ala Lys Glu Asp Leu Lys Arg Lys Lys Leu Val Arg
2225 2230 2235

Asp Gly Ser Val Phe Leu Lys Asn Ala Ala Gly Arg Leu Lys Glu
2240 2245 2250

Val Gln Ala Val Leu Leu Thr Asp Ile Leu Val Phe Leu Gln Glu
2255 2260 2265

Lys Asp Gln Lys Tyr Ile Phe Ala Ser Leu Asp Gln Lys Ser Thr
2270 2275 2280

Val Ile Ser Leu Lys Lys Leu Ile Val Arg Glu Val Ala His Glu
2285 2290 2295

Glu Lys Gly Leu Phe Leu Ile Ser Met Gly Met Thr Asp Pro Glu
2300 2305 2310

Met Val Glu Val His Ala Ser Ser Lys Glu Glu Arg Asn Ser Trp
2315 2320 2325

Ile Gln Ile Ile Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu
2330 2335 2340

Asp Glu Gly Ile Pro Ser Glu Asn Glu Glu Glu Lys Lys Met Leu
2345 2350 2355

Asp Thr Arg Ala Arg Glu Leu Lys Glu Gln Leu His Gln Lys Asp
2360 2365 2370

Gln Lys Ile Leu Leu Leu Leu Glu Glu Lys Glu Met Ile Phe Arg

2375 2380 2385

Asp Met Ala Glu Cys Ser Thr Pro Leu Pro Glu Asp Cys Ser Pro
2390 2395 2400

Thr His Ser Pro Arg Val Leu Phe Arg Ser Asn Thr Glu Glu Ala
2405 2410 2415

Leu Lys Gly Gly Pro Leu Met Lys Ser Ala Ile Asn Glu Val Glu
2420 2425 2430

Ile Leu Gln Gly Leu Val Ser Gly Asn Leu Gly Gly Thr Leu Gly
2435 2440 2445

Pro Thr Val Ser Ser Pro Ile Glu Gln Asp Val Val Gly Pro Val
2450 2455 2460

Ser Leu Pro Arg Arg Ala Glu Thr Phe Gly Gly Phe Asp Ser His
2465 2470 2475

Gln Met Asn Ala Ser Lys Gly Gly Glu Lys Glu Glu Gly Asp Asp
2480 2485 2490

Gly Gln Asp Leu Arg Arg Thr Glu Ser Asp Ser Gly Leu Lys Lys
2495 2500 2505

Gly Gly Asn Ala Asn Leu Val Phe Met Leu Lys Arg Asn Ser Glu
2510 2515 2520

Gln Val Val Gln Ser Val Val His Leu Tyr Glu Leu Leu Ser Ala
2525 2530 2535

Leu Gln Gly Val Val Leu Gln Gln Asp Ser Tyr Ile Glu Asp Gln
2540 2545 2550

Lys Leu Val Leu Ser Glu Arg Ala Leu Thr Arg Ser Leu Ser Arg
2555 2560 2565

Pro Ser Ser Leu Ile Glu Gln Glu Lys Gln Arg Ser Leu Glu Lys
2570 2575 2580

Gln Arg Gln Asp Leu Ala Asn Leu Gln Lys Gln Gln Ala Gln Tyr
2585 2590 2595

```
Leu Glu  Glu Lys Arg Arg Arg  Glu Arg Glu Trp Glu  Ala Arg Glu
    2600                2605                2610

Arg Glu  Leu Arg Glu Arg Glu  Ala Leu Leu Ala Gln  Arg Glu Glu
    2615                2620                2625

Glu Val  Gln Gln Gly Gln Gln  Asp Leu Glu Lys Glu  Arg Glu Glu
    2630                2635                2640

Leu Gln  Gln Lys Lys Gly Thr  Tyr Gln Tyr Asp Leu  Glu Arg Leu
    2645                2650                2655

Arg Ala  Ala Gln Lys Gln Leu  Glu Arg Glu Gln Glu  Gln Leu Arg
    2660                2665                2670

Arg Glu  Ala Glu Arg Leu Ser  Gln Arg Gln Thr Glu  Arg Asp Leu
    2675                2680                2685

Cys Gln  Val Ser His Pro His  Thr Lys Leu Met Arg  Ile Pro Ser
    2690                2695                2700

Phe Phe  Pro Ser Pro Glu Glu  Pro Pro Ser Pro Ser  Ala Pro Ser
    2705                2710                2715

Ile Ala  Lys Ser Gly Ser Leu  Asp Ser Glu Leu Ser  Val Ser Pro
    2720                2725                2730

Lys Arg  Asn Ser Ile Ser Arg  Thr His Lys Asp Lys  Gly Pro Phe
    2735                2740                2745

His Ile  Leu Ser Ser Thr Ser  Gln Thr Asn Lys Gly  Pro Glu Gly
    2750                2755                2760

Gln Ser  Gln Ala Pro Ala Ser  Thr Ser Ala Ser Thr  Arg Leu Phe
    2765                2770                2775

Gly Leu  Thr Lys Pro Lys Glu  Lys Lys Glu Lys Lys  Lys Lys Asn
    2780                2785                2790

Lys Thr  Ser Arg Ser Gln Pro  Gly Asp Gly Pro Ala  Ser Glu Val
    2795                2800                2805
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Ser Ala Glu Gly Glu Glu Ile Phe Cys
    2810   2815

<210> 618
<211> 1434
<212> PRT
<213> Homo sapiens

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<400> 618
Met Tyr Glu Arg His Lys Arg Arg Tyr Ser Leu Cys Asp Ile Ser Lys
1   5   10   15

Val Asp Arg Thr Val Asp Val Val Leu Leu Lys Ile Asn Arg Glu Asn
            20   25   30

Trp Cys Thr Ile Glu Pro Cys Pro Asp Ala Ala Ser Leu Leu Ala Ser
        35   40   45

Lys Gln Ser Pro Glu Cys Glu Asn Phe Leu Asp Val Gly Leu Gly Arg
    50   55   60

Glu Cys Thr Ser Lys Gln Gly Val Leu Lys Arg Glu Ser Gly Ser Asp
65   70   75   80

Ser Asp Leu Phe His Ser Pro Ser Asp Asp Met Asp Ser Ile Ile Phe
                85   90   95

Pro Lys Pro Glu Glu Glu His Leu Ala Cys Asp Ile Thr Gly Ser Ser
            100   105   110

Ser Ser Thr Asp Asp Thr Ala Ser Leu Asp Arg His Ser Ser His Gly

```
        115                 120                 125

Ser Asp Val Ser Leu Ser Gln Ile Leu Lys Pro Asn Arg Ser Arg Asp
    130                 135                 140

Arg Gln Ser Leu Asp Gly Phe Tyr Ser His Gly Met Gly Ala Glu Gly
145                 150                 155                 160

Arg Glu Ser Glu Ser Glu Pro Ala Asp Pro Gly Asp Val Glu Glu Glu
                165                 170                 175

Glu Met Asp Ser Ile Thr Glu Val Pro Ala Asn Cys Ser Val Leu Arg
            180                 185                 190

Ser Ser Met Arg Ser Leu Ser Pro Phe Arg Arg His Ser Trp Gly Pro
        195                 200                 205

Gly Lys Asn Ala Ala Ser Asp Ala Glu Met Asn His Arg Ser Phe Ser
    210                 215                 220

Leu Glu Gly Leu Thr Gly Gly Ala Gly Val Gly Asn Lys Pro Ser Ser
225                 230                 235                 240

Ser Leu Glu Val Ser Ser Ala Asn Ala Glu Glu Leu Arg His Pro Phe
                245                 250                 255

Ser Gly Glu Glu Arg Val Asp Ser Leu Val Ser Leu Ser Glu Glu Asp
            260                 265                 270

Leu Glu Ser Asp Gln Arg Glu His Arg Met Phe Asp Gln Gln Ile Cys
        275                 280                 285

His Arg Ser Lys Gln Gln Gly Phe Asn Tyr Cys Thr Ser Ala Ile Ser
    290                 295                 300

Ser Pro Leu Thr Lys Ser Ile Ser Leu Met Thr Ile Ser His Pro Gly
305                 310                 315                 320

Leu Asp Asn Ser Arg Pro Phe His Ser Thr Phe His Asn Thr Ser Ala
                325                 330                 335

Asn Leu Thr Glu Ser Ile Thr Glu Glu Asn Tyr Asn Phe Leu Pro His
            340                 345                 350
```

```
Ser Pro Ser Lys Lys Asp Ser Glu Trp Lys Ser Gly Thr Lys Val Ser
        355                 360                 365

Arg Thr Phe Ser Tyr Ile Lys Asn Lys Met Ser Ser Ser Lys Lys Ser
    370                 375                 380

Lys Glu Lys Glu Lys Glu Lys Asp Lys Ile Lys Glu Lys Glu Lys Asp
385                 390                 395                 400

Ser Lys Asp Lys Glu Lys Asp Lys Lys Thr Val Asn Gly His Thr Phe
                405                 410                 415

Ser Ser Ile Pro Val Val Gly Pro Ile Ser Cys Ser Gln Cys Met Lys
            420                 425                 430

Pro Phe Thr Asn Lys Asp Ala Tyr Thr Cys Ala Asn Cys Ser Ala Phe
        435                 440                 445

Val His Lys Gly Cys Arg Glu Ser Leu Ala Ser Cys Ala Lys Val Lys
    450                 455                 460

Met Lys Pro Lys Gly Ser Leu Gln Ala His Asp Thr Ser Ser Leu Pro
465                 470                 475                 480

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

Ser Ala Val Leu Leu Val Asp Glu Thr Ala Thr Thr Pro Ile Phe Ala
            500                 505                 510

Asn Arg Arg Ser Gln Gln Ser Val Ser Leu Ser Lys Ser Val Ser Ile
        515                 520                 525

Gln Asn Ile Thr Gly Val Gly Asn Asp Glu Asn Met Ser Asn Thr Trp
    530                 535                 540

Lys Phe Leu Ser His Ser Thr Asp Ser Leu Asn Lys Ile Ser Lys Val
545                 550                 555                 560

Asn Glu Ser Thr Glu Ser Leu Thr Asp Glu Gly Val Gly Thr Asp Met
                565                 570                 575
```

```
Asn Glu Gly Gln Leu Leu Gly Asp Phe Glu Ile Glu Ser Lys Gln Leu
            580                 585                 590

Glu Ala Glu Ser Trp Ser Arg Ile Ile Asp Ser Lys Phe Leu Lys Gln
        595                 600                 605

Gln Lys Lys Asp Val Val Lys Arg Gln Glu Val Ile Tyr Glu Leu Met
    610                 615                 620

Gln Thr Glu Phe His His Val Arg Thr Leu Lys Ile Met Ser Gly Val
625                 630                 635                 640

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

Glu Lys Leu Phe Pro Cys Leu Asp Glu Leu Ile Ser Ile His Ser Gln
            660                 665                 670

Phe Phe Gln Arg Ile Leu Glu Arg Lys Lys Glu Ser Leu Val Asp Lys
        675                 680                 685

Ser Glu Lys Asn Phe Leu Ile Lys Arg Ile Gly Asp Val Leu Val Asn
    690                 695                 700

Gln Phe Ser Gly Glu Asn Ala Glu Arg Leu Lys Lys Thr Tyr Gly Lys
705                 710                 715                 720

Phe Cys Gly Gln His Asn Gln Ser Val Asn Tyr Phe Lys Asp Leu Tyr
                725                 730                 735

Ala Lys Asp Lys Arg Phe Gln Ala Phe Val Lys Lys Lys Met Ser Ser
            740                 745                 750

Ser Val Val Arg Arg Leu Gly Ile Pro Glu Cys Ile Leu Leu Val Thr
        755                 760                 765

Gln Arg Ile Thr Lys Tyr Pro Val Leu Phe Gln Arg Ile Leu Gln Cys
    770                 775                 780

Thr Lys Asp Asn Glu Val Glu Gln Glu Asp Leu Ala Gln Ser Leu Ser
785                 790                 795                 800
```

```
Leu Val Lys Asp Val Ile Gly Ala Val Asp Ser Lys Val Ala Ser Tyr
                805                 810                 815

Glu Lys Lys Val Arg Leu Asn Glu Ile Tyr Thr Lys Thr Asp Ser Lys
            820                 825                 830

Ser Ile Met Arg Met Lys Ser Gly Gln Met Phe Ala Lys Glu Asp Leu
        835                 840                 845

Lys Arg Lys Lys Leu Val Arg Asp Gly Ser Val Phe Leu Lys Asn Ala
    850                 855                 860

Ala Gly Arg Leu Lys Glu Val Gln Ala Val Leu Leu Thr Asp Ile Leu
865                 870                 875                 880

Val Phe Leu Gln Glu Lys Asp Gln Lys Tyr Ile Phe Ala Ser Leu Asp
                885                 890                 895

Gln Lys Ser Thr Val Ile Ser Leu Lys Lys Leu Ile Val Arg Glu Val
            900                 905                 910

Ala His Glu Glu Lys Gly Leu Phe Leu Ile Ser Met Gly Met Thr Asp
        915                 920                 925

Pro Glu Met Val Glu Val His Ala Ser Ser Lys Glu Glu Arg Asn Ser
    930                 935                 940

Trp Ile Gln Ile Ile Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu
945                 950                 955                 960

Asp Glu Gly Ile Pro Ser Glu Asn Glu Glu Glu Lys Lys Met Leu Asp
                965                 970                 975

Thr Arg Ala Arg Glu Leu Lys Glu Gln Leu His Gln Lys Asp Gln Lys
            980                 985                 990

Ile Leu Leu Leu Leu Glu Glu Lys  Glu Met Ile Phe Arg  Asp Met
Ala
        995                 1000                1005

Glu Cys  Ser Thr Pro Leu Pro  Glu Asp Cys Ser Pro  Thr His Ser
    1010                1015                1020
```

```
Pro Arg  Val Leu Phe Arg Ser  Asn Thr Glu Glu Ala  Leu Lys Gly
    1025                1030                1035

Gly Pro  Leu Met Lys Ser Ala  Ile Asn Glu Val Glu  Ile Leu Gln
    1040                1045                1050

Gly Leu  Val Ser Gly Asn Leu  Gly Gly Thr Leu Gly  Pro Thr Val
    1055                1060                1065

Ser Ser  Pro Ile Glu Gln Asp  Val Val Gly Pro Val  Ser Leu Pro
    1070                1075                1080

Arg Arg  Ala Glu Thr Phe Gly  Gly Phe Asp Ser His  Gln Met Asn
    1085                1090                1095

Ala Ser  Lys Gly Gly Glu Lys  Glu Glu Gly Asp Asp  Gly Gln Asp
    1100                1105                1110

Leu Arg  Arg Thr Glu Ser Asp  Ser Gly Leu Lys Lys  Gly Gly Asn
    1115                1120                1125

Ala Asn  Leu Val Phe Met Leu  Lys Arg Asn Ser Glu  Gln Val Val
    1130                1135                1140

Gln Ser  Val Val His Leu Tyr  Glu Leu Leu Ser Ala  Leu Gln Gly
    1145                1150                1155

Val Val  Leu Gln Gln Asp Ser  Tyr Ile Glu Asp Gln  Lys Leu Val
    1160                1165                1170

Leu Ser  Glu Arg Ala Leu Thr  Arg Ser Leu Ser Arg  Pro Ser Ser
    1175                1180                1185

Leu Ile  Glu Gln Glu Lys Gln  Arg Ser Leu Glu Lys  Gln Arg Gln
    1190                1195                1200

Asp Leu  Ala Asn Leu Gln Lys  Gln Gln Ala Gln Tyr  Leu Glu Glu
    1205                1210                1215

Lys Arg  Arg Arg Glu Arg Glu  Trp Glu Ala Arg Glu  Arg Glu Leu
    1220                1225                1230

Arg Glu  Arg Glu Ala Leu Leu  Ala Gln Arg Glu Glu  Glu Val Gln
```

1235 1240 1245

Gln Gly Gln Gln Asp Leu Glu Lys Glu Arg Glu Glu Leu Gln Gln
1250 1255 1260

Lys Lys Gly Thr Tyr Gln Tyr Asp Leu Glu Arg Leu Arg Ala Ala
1265 1270 1275

Gln Lys Gln Leu Glu Arg Glu Gln Glu Gln Leu Arg Arg Glu Ala
1280 1285 1290

Glu Arg Leu Ser Gln Arg Gln Thr Glu Arg Asp Leu Cys Gln Val
1295 1300 1305

Ser His Pro His Thr Lys Leu Met Arg Ile Pro Ser Phe Phe Pro
1310 1315 1320

Ser Pro Glu Glu Pro Pro Ser Pro Ser Ala Pro Ser Ile Ala Lys
1325 1330 1335

Ser Gly Ser Leu Asp Ser Glu Leu Ser Val Ser Pro Lys Arg Asn
1340 1345 1350

Ser Ile Ser Arg Thr His Lys Asp Lys Gly Pro Phe His Ile Leu
1355 1360 1365

Ser Ser Thr Ser Gln Thr Asn Lys Gly Pro Glu Gly Gln Ser Gln
1370 1375 1380

Ala Pro Ala Ser Thr Ser Ala Ser Thr Arg Leu Phe Gly Leu Thr
1385 1390 1395

Lys Pro Lys Glu Lys Lys Glu Lys Lys Lys Lys Asn Lys Thr Ser
1400 1405 1410

Arg Ser Gln Pro Gly Asp Gly Pro Ala Ser Glu Val Ser Ala Glu
1415 1420 1425

Gly Glu Glu Ile Phe Cys
1430

<210> 619
<211> 2813

<212> PRT
<213> Homo sapiens

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A kinase (PRKA) anchor prt 13; "

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<223> /note="Uniprot ID: Q12802; "

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<400> 619

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Met Lys Leu Asn Pro Gln Gln Ala Pro Leu Tyr Gly Asp Cys Val Val
1               5                  10                  15


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


Tyr Leu Val Phe Leu Gly Ser Thr Leu Arg His Cys Thr Ser Thr Arg
        35                  40                  45


Lys Val Ser Ser Asp Thr Leu Glu Thr Ile Ala Pro Gly His Asp Cys
    50                  55                  60


Cys Glu Thr Val Lys Val Gln Leu Cys Ala Ser Lys Glu Gly Leu Pro
65                  70                  75                  80


Val Phe Val Val Ala Glu Glu Asp Phe His Phe Val Gln Asp Glu Ala
                85                  90                  95


Tyr Asp Ala Ala Gln Phe Leu Ala Thr Ser Ala Gly Asn Gln Gln Ala
            100                 105                 110


Leu Asn Phe Thr Arg Phe Leu Asp Gln Ser Gly Pro Pro Ser Gly Asp
        115                 120                 125
```

```
Val Asn Ser Leu Asp Lys Lys Leu Val Leu Ala Phe Arg His Leu Lys
    130                 135                 140

Leu Pro Thr Glu Trp Asn Val Leu Gly Thr Asp Gln Ser Leu His Asp
145                 150                 155                 160

Ala Gly Pro Arg Glu Thr Leu Met His Phe Ala Val Arg Leu Gly Leu
                165                 170                 175

Leu Arg Leu Thr Trp Phe Leu Leu Gln Lys Pro Gly Gly Arg Gly Ala
            180                 185                 190

Leu Ser Ile His Asn Gln Glu Gly Ala Thr Pro Val Ser Leu Ala Leu
        195                 200                 205

Glu Arg Gly Tyr His Lys Leu His Gln Leu Leu Thr Glu Glu Asn Ala
    210                 215                 220

Gly Glu Pro Asp Ser Trp Ser Ser Leu Ser Tyr Glu Ile Pro Tyr Gly
225                 230                 235                 240

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

Ser Glu Ser Asp Ser His His Glu His Pro Phe Pro Gly Asp Gly Cys
            260                 265                 270

Thr Gly Pro Ile Phe Lys Leu Met Asn Ile Gln Gln Gln Leu Met Lys
        275                 280                 285

Thr Asn Leu Lys Gln Met Asp Ser Leu Met Pro Leu Met Met Thr Ala
    290                 295                 300

Gln Asp Pro Ser Ser Ala Pro Glu Thr Asp Gly Gln Phe Leu Pro Cys
305                 310                 315                 320

Ala Pro Glu Pro Thr Asp Pro Gln Arg Leu Ser Ser Ser Glu Glu Thr
                325                 330                 335

Glu Ser Thr Gln Cys Cys Pro Gly Ser Pro Val Ala Gln Thr Glu Ser
            340                 345                 350

Pro Cys Asp Leu Ser Ser Ile Val Glu Glu Glu Asn Thr Asp Arg Ser
```

```
        355                 360                 365

Cys Arg Lys Lys Asn Lys Gly Val Glu Arg Lys Gly Glu Glu Val Glu
    370                 375                 380

Pro Ala Pro Ile Val Asp Ser Gly Thr Val Ser Asp Gln Asp Ser Cys
385                 390                 395                 400

Leu Gln Ser Leu Pro Asp Cys Gly Val Lys Gly Thr Glu Gly Leu Ser
                405                 410                 415

Ser Cys Gly Asn Arg Asn Glu Glu Thr Gly Thr Lys Ser Ser Gly Met
            420                 425                 430

Pro Thr Asp Gln Glu Ser Leu Ser Ser Gly Asp Ala Val Leu Gln Arg
        435                 440                 445

Asp Leu Val Met Glu Pro Gly Thr Ala Gln Tyr Ser Ser Gly Gly Glu
    450                 455                 460

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

Glu Met Glu His Gly Leu Met Asn Pro Asp Ala Thr Val Trp Lys Asn
                485                 490                 495

Val Leu Gln Gly Gly Glu Ser Thr Lys Glu Arg Phe Glu Asn Ser Asn
            500                 505                 510

Ile Gly Thr Ala Gly Ala Ser Asp Val His Val Thr Ser Lys Pro Val
        515                 520                 525

Asp Lys Ile Ser Val Pro Asn Cys Ala Pro Ala Ala Ser Ser Leu Asp
    530                 535                 540

Gly Asn Lys Pro Ala Glu Ser Ser Leu Ala Phe Ser Asn Glu Glu Thr
545                 550                 555                 560

Ser Thr Glu Lys Thr Ala Glu Thr Glu Thr Ser Arg Ser Arg Glu Glu
                565                 570                 575

Ser Ala Asp Ala Pro Val Asp Gln Asn Ser Val Val Ile Pro Ala Ala
            580                 585                 590
```

```
Ala Lys Asp Lys Ile Ser Asp Gly Leu Glu Pro Tyr Thr Leu Leu Ala
        595                 600                 605

Ala Gly Ile Gly Glu Ala Met Ser Pro Ser Asp Leu Ala Leu Leu Gly
    610                 615                 620

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

His Ala Gln Ser Gln Lys Gly Lys Ser Ser Pro Ile Cys Ser Thr Thr
                645                 650                 655

Gly Asp Asp Lys Leu Cys Ala Asp Ser Ala Cys Gln Gln Asn Thr Val
            660                 665                 670

Thr Ser Ser Gly Asp Leu Val Ala Lys Leu Cys Asp Asn Ile Val Ser
        675                 680                 685

Glu Ser Glu Ser Thr Thr Ala Arg Gln Pro Ser Ser Gln Asp Pro Pro
    690                 695                 700

Asp Ala Ser His Cys Glu Asp Pro Gln Ala His Thr Val Thr Ser Asp
705                 710                 715                 720

Pro Val Arg Asp Thr Gln Glu Arg Ala Asp Phe Cys Pro Phe Lys Val
                725                 730                 735

Val Asp Asn Lys Gly Gln Arg Lys Asp Val Lys Leu Asp Lys Pro Leu
            740                 745                 750

Thr Asn Met Leu Glu Val Val Ser His Pro His Pro Val Val Pro Lys
        755                 760                 765

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

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

Ala Leu Ser Phe Val Pro Ser Gln Lys Glu Lys Gly Thr Ala Thr Pro
                805                 810                 815
```

```
Glu Leu His Thr Ala Thr Asp Tyr Arg Asp Gly Pro Asp Gly Asn Ser
            820                 825                 830

Asn Glu Pro Asp Thr Arg Pro Leu Glu Asp Arg Ala Val Gly Leu Ser
        835                 840                 845

Thr Ser Ser Thr Ala Ala Glu Leu Gln His Gly Met Gly Asn Thr Ser
    850                 855                 860

Leu Thr Gly Leu Gly Gly Glu His Glu Gly Pro Ala Pro Pro Ala Ile
865                 870                 875                 880

Pro Glu Ala Leu Asn Ile Lys Gly Asn Thr Asp Ser Ser Leu Gln Ser
                885                 890                 895

Val Gly Lys Ala Thr Leu Ala Leu Asp Ser Val Leu Thr Glu Glu Gly
            900                 905                 910

Lys Leu Leu Val Val Ser Glu Ser Ser Ala Ala Gln Glu Gln Asp Lys
        915                 920                 925

Asp Lys Ala Val Thr Cys Ser Ser Ile Lys Glu Asn Ala Leu Ser Ser
    930                 935                 940

Gly Thr Leu Gln Glu Glu Gln Arg Thr Pro Pro Pro Gly Gln Asp Thr
945                 950                 955                 960

Gln Gln Phe His Glu Lys Ser Ile Ser Ala Asp Cys Ala Lys Asp Lys
                965                 970                 975

Ala Leu Gln Leu Ser Asn Ser Pro Gly Ala Ser Ser Ala Phe Leu Lys
            980                 985                 990

Ala Glu Thr Glu His Asn Lys Glu  Val Ala Pro Gln Val  Ser Leu
Leu
        995                 1000                1005

Thr Gln  Gly Gly Ala Ala Gln  Ser Leu Val Pro Pro  Gly Ala Ser
    1010                1015                1020

Leu Ala  Thr Glu Ser Arg Gln  Glu Ala Leu Gly Ala  Glu His Asn
    1025                1030                1035
```

Ser Ser Ala Leu Leu Pro Cys Leu Leu Pro Asp Gly Ser Asp Gly
1040 1045 1050

Ser Asp Ala Leu Asn Cys Ser Gln Pro Ser Pro Leu Asp Val Gly
1055 1060 1065

Val Lys Asn Thr Gln Ser Gln Gly Lys Thr Ser Ala Cys Glu Val
1070 1075 1080

Ser Gly Asp Val Thr Val Asp Val Thr Gly Val Asn Ala Leu Gln
1085 1090 1095

Gly Met Ala Glu Pro Arg Arg Glu Asn Ile Ser His Asn Thr Gln
1100 1105 1110

Asp Ile Leu Ile Pro Asn Val Leu Leu Ser Gln Glu Lys Asn Ala
1115 1120 1125

Val Leu Gly Leu Pro Val Ala Leu Gln Asp Lys Ala Val Thr Asp
1130 1135 1140

Pro Gln Gly Val Gly Thr Pro Glu Met Ile Pro Leu Asp Trp Glu
1145 1150 1155

Lys Gly Lys Leu Glu Gly Ala Asp His Ser Cys Thr Met Gly Asp
1160 1165 1170

Ala Glu Glu Ala Gln Ile Asp Asp Glu Ala His Pro Val Leu Leu
1175 1180 1185

Gln Pro Val Ala Lys Glu Leu Pro Thr Asp Met Glu Leu Ser Ala
1190 1195 1200

His Asp Asp Gly Ala Pro Ala Gly Val Arg Glu Val Met Arg Ala
1205 1210 1215

Pro Pro Ser Gly Arg Glu Arg Ser Thr Pro Ser Leu Pro Cys Met
1220 1225 1230

Val Ser Ala Gln Asp Ala Pro Leu Pro Lys Gly Ala Asp Leu Ile
1235 1240 1245

```
Glu Glu  Ala Ala Ser Arg Ile  Val Asp Ala Val Ile  Glu Gln Val
    1250                 1255                 1260

Lys Ala  Ala Gly Ala Leu Leu  Thr Glu Gly Glu Ala  Cys His Met
    1265                 1270                 1275

Ser Leu  Ser Ser Pro Glu Leu  Gly Pro Leu Thr Lys  Gly Leu Glu
    1280                 1285                 1290

Ser Ala  Phe Thr Glu Lys Val  Ser Thr Phe Pro Pro  Gly Glu Ser
    1295                 1300                 1305

Leu Pro  Met Gly Ser Thr Pro  Glu Glu Ala Thr Gly  Ser Leu Ala
    1310                 1315                 1320

Gly Cys  Phe Ala Gly Arg Glu  Glu Pro Glu Lys Ile  Ile Leu Pro
    1325                 1330                 1335

Val Gln  Gly Pro Glu Pro Ala  Ala Glu Met Pro Asp  Val Lys Ala
    1340                 1345                 1350

Glu Asp  Glu Val Asp Phe Arg  Ala Ser Ser Ile Ser  Glu Glu Val
    1355                 1360                 1365

Ala Val  Gly Ser Ile Ala Ala  Thr Leu Lys Met Lys  Gln Gly Pro
    1370                 1375                 1380

Met Thr  Gln Ala Ile Asn Arg  Glu Asn Trp Cys Thr  Ile Glu Pro
    1385                 1390                 1395

Cys Pro  Asp Ala Ala Ser Leu  Leu Ala Ser Lys Gln  Ser Pro Glu
    1400                 1405                 1410

Cys Glu  Asn Phe Leu Asp Val  Gly Leu Gly Arg Glu  Cys Thr Ser
    1415                 1420                 1425

Lys Gln  Gly Val Leu Lys Arg  Glu Ser Gly Ser Asp  Ser Asp Leu
    1430                 1435                 1440

Phe His  Ser Pro Ser Asp Asp  Met Asp Ser Ile Ile  Phe Pro Lys
    1445                 1450                 1455

Pro Glu  Glu Glu His Leu Ala  Cys Asp Ile Thr Gly  Ser Ser Ser
```

1460 1465 1470

Ser Thr Asp Asp Thr Ala Ser Leu Asp Arg His Ser Ser His Gly
1475 1480 1485

Ser Asp Val Ser Leu Ser Gln Ile Leu Lys Pro Asn Arg Ser Arg
1490 1495 1500

Asp Arg Gln Ser Leu Asp Gly Phe Tyr Ser His Gly Met Gly Ala
1505 1510 1515

Glu Gly Arg Glu Ser Glu Ser Glu Pro Ala Asp Pro Gly Asp Val
1520 1525 1530

Glu Glu Glu Glu Met Asp Ser Ile Thr Glu Val Pro Ala Asn Cys
1535 1540 1545

Ser Val Leu Arg Ser Ser Met Arg Ser Leu Ser Pro Phe Arg Arg
1550 1555 1560

His Ser Trp Gly Pro Gly Lys Asn Ala Ala Ser Asp Ala Glu Met
1565 1570 1575

Asn His Arg Ser Ser Met Arg Val Leu Gly Asp Val Val Arg Arg
1580 1585 1590

Pro Pro Ile His Arg Arg Ser Phe Ser Leu Glu Gly Leu Thr Gly
1595 1600 1605

Gly Ala Gly Val Gly Asn Lys Pro Ser Ser Ser Leu Glu Val Ser
1610 1615 1620

Ser Ala Asn Ala Glu Glu Leu Arg His Pro Phe Ser Gly Glu Glu
1625 1630 1635

Arg Val Asp Ser Leu Val Ser Leu Ser Glu Glu Asp Leu Glu Ser
1640 1645 1650

Asp Gln Arg Glu His Arg Met Phe Asp Gln Gln Ile Cys His Arg
1655 1660 1665

Ser Lys Gln Gln Gly Phe Asn Tyr Cys Thr Ser Ala Ile Ser Ser
1670 1675 1680

```
Pro Leu  Thr Lys Ser Ile Ser  Leu Met Thr Ile Ser  His Pro Gly
    1685                1690                1695

Leu Asp  Asn Ser Arg Pro Phe  His Ser Thr Phe His  Asn Thr Ser
    1700                1705                1710

Ala Asn  Leu Thr Glu Ser Ile  Thr Glu Glu Asn Tyr  Asn Phe Leu
    1715                1720                1725

Pro His  Ser Pro Ser Lys Lys  Asp Ser Glu Trp Lys  Ser Gly Thr
    1730                1735                1740

Lys Val  Ser Arg Thr Phe Ser  Tyr Ile Lys Asn Lys  Met Ser Ser
    1745                1750                1755

Ser Lys  Lys Ser Lys Glu Lys  Glu Lys Glu Lys Asp  Lys Ile Lys
    1760                1765                1770

Glu Lys  Glu Lys Asp Ser Lys  Asp Lys Glu Lys Asp  Lys Lys Thr
    1775                1780                1785

Val Asn  Gly His Thr Phe Ser  Ser Ile Pro Val Val  Gly Pro Ile
    1790                1795                1800

Ser Cys  Ser Gln Cys Met Lys  Pro Phe Thr Asn Lys  Asp Ala Tyr
    1805                1810                1815

Thr Cys  Ala Asn Cys Ser Ala  Phe Val His Lys Gly  Cys Arg Glu
    1820                1825                1830

Ser Leu  Ala Ser Cys Ala Lys  Val Lys Met Lys Gln  Pro Lys Gly
    1835                1840                1845

Ser Leu  Gln Ala His Asp Thr  Ser Ser Leu Pro Thr  Val Ile Met
    1850                1855                1860

Arg Asn  Lys Pro Ser Gln Pro  Lys Glu Arg Pro Arg  Ser Ala Val
    1865                1870                1875

Leu Leu  Val Asp Glu Thr Ala  Thr Thr Pro Ile Phe  Ala Asn Arg
    1880                1885                1890
```

```
Arg Ser  Gln Gln Ser Val Ser  Leu Ser Lys Ser Val  Ser Ile Gln
    1895                1900                1905

Asn Ile  Thr Gly Val Gly Asn  Asp Glu Asn Met Ser  Asn Thr Trp
    1910                1915                1920

Lys Phe  Leu Ser His Ser Thr  Asp Ser Leu Asn Lys  Ile Ser Lys
    1925                1930                1935

Val Asn  Glu Ser Thr Glu Ser  Leu Thr Asp Glu Gly  Val Gly Thr
    1940                1945                1950

Asp Met  Asn Glu Gly Gln Leu  Leu Gly Asp Phe Glu  Ile Glu Ser
    1955                1960                1965

Lys Gln  Leu Glu Ala Glu Ser  Trp Ser Arg Ile Ile  Asp Ser Lys
    1970                1975                1980

Phe Leu  Lys Gln Gln Lys Lys  Asp Val Val Lys Arg  Gln Glu Val
    1985                1990                1995

Ile Tyr  Glu Leu Met Gln Thr  Glu Phe His His Val  Arg Thr Leu
    2000                2005                2010

Lys Ile  Met Ser Gly Val Tyr  Ser Gln Gly Met Met  Ala Asp Leu
    2015                2020                2025

Leu Phe  Glu Gln Gln Met Val  Glu Lys Leu Phe Pro  Cys Leu Asp
    2030                2035                2040

Glu Leu  Ile Ser Ile His Ser  Gln Phe Phe Gln Arg  Ile Leu Glu
    2045                2050                2055

Arg Lys  Lys Glu Ser Leu Val  Asp Lys Ser Glu Lys  Asn Phe Leu
    2060                2065                2070

Ile Lys  Arg Ile Gly Asp Val  Leu Val Asn Gln Phe  Ser Gly Glu
    2075                2080                2085

Asn Ala  Glu Arg Leu Lys Lys  Thr Tyr Gly Lys Phe  Cys Gly Gln
    2090                2095                2100
```

```
His Asn  Gln Ser Val Asn Tyr  Phe Lys Asp Leu Tyr  Ala Lys Asp
    2105                2110                2115

Lys Arg  Phe Gln Ala Phe Val  Lys Lys Lys Met Ser  Ser Ser Val
    2120                2125                2130

Val Arg  Arg Leu Gly Ile Pro  Glu Cys Ile Leu Leu  Val Thr Gln
    2135                2140                2145

Arg Ile  Thr Lys Tyr Pro Val  Leu Phe Gln Arg Ile  Leu Gln Cys
    2150                2155                2160

Thr Lys  Asp Asn Glu Val Glu  Gln Glu Asp Leu Ala  Gln Ser Leu
    2165                2170                2175

Ser Leu  Val Lys Asp Val Ile  Gly Ala Val Asp Ser  Lys Val Ala
    2180                2185                2190

Ser Tyr  Glu Lys Lys Val Arg  Leu Asn Glu Ile Tyr  Thr Lys Thr
    2195                2200                2205

Asp Ser  Lys Ser Ile Met Arg  Met Lys Ser Gly Gln  Met Phe Ala
    2210                2215                2220

Lys Glu  Asp Leu Lys Arg Lys  Lys Leu Val Arg Asp  Gly Ser Val
    2225                2230                2235

Phe Leu  Lys Asn Ala Ala Gly  Arg Leu Lys Glu Val  Gln Ala Val
    2240                2245                2250

Leu Leu  Thr Asp Ile Leu Val  Phe Leu Gln Glu Lys  Asp Gln Lys
    2255                2260                2265

Tyr Ile  Phe Ala Ser Leu Asp  Gln Lys Ser Thr Val  Ile Ser Leu
    2270                2275                2280

Lys Lys  Leu Ile Val Arg Glu  Val Ala His Glu Glu  Lys Gly Leu
    2285                2290                2295

Phe Leu  Ile Ser Met Gly Met  Thr Asp Pro Glu Met  Val Glu Val
    2300                2305                2310

His Ala  Ser Ser Lys Glu Glu  Arg Asn Ser Trp Ile  Gln Ile Ile
```

2315 2320 2325

Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu Asp Glu Gly Ile
2330 2335 2340

Pro Ser Glu Asn Glu Glu Glu Lys Lys Met Leu Asp Thr Arg Ala
2345 2350 2355

Arg Glu Leu Lys Glu Gln Leu His Gln Lys Asp Gln Lys Ile Leu
2360 2365 2370

Leu Leu Leu Glu Glu Lys Glu Met Ile Phe Arg Asp Met Ala Glu
2375 2380 2385

Cys Ser Thr Pro Leu Pro Glu Asp Cys Ser Pro Thr His Ser Pro
2390 2395 2400

Arg Val Leu Phe Arg Ser Asn Thr Glu Glu Ala Leu Lys Gly Gly
2405 2410 2415

Pro Leu Met Lys Ser Ala Ile Asn Glu Val Glu Ile Leu Gln Gly
2420 2425 2430

Leu Val Ser Gly Asn Leu Gly Gly Thr Leu Gly Pro Thr Val Ser
2435 2440 2445

Ser Pro Ile Glu Gln Asp Val Val Gly Pro Val Ser Leu Pro Arg
2450 2455 2460

Arg Ala Glu Thr Phe Gly Gly Phe Asp Ser His Gln Met Asn Ala
2465 2470 2475

Ser Lys Gly Gly Glu Lys Glu Glu Gly Asp Asp Gly Gln Asp Leu
2480 2485 2490

Arg Arg Thr Glu Ser Asp Ser Gly Leu Lys Lys Gly Gly Asn Ala
2495 2500 2505

Asn Leu Val Phe Met Leu Lys Arg Asn Ser Glu Gln Val Val Gln
2510 2515 2520

Ser Val Val His Leu Tyr Glu Leu Leu Ser Ala Leu Gln Gly Val
2525 2530 2535

```
Val Leu  Gln Gln Asp Ser Tyr  Ile Glu Asp Gln Lys  Leu Val Leu
    2540                2545                2550

Ser Glu  Arg Ala Leu Thr Arg  Ser Leu Ser Arg Pro  Ser Ser Leu
    2555                2560                2565

Ile Glu  Gln Glu Lys Gln Arg  Ser Leu Glu Lys Gln  Arg Gln Asp
    2570                2575                2580

Leu Ala  Asn Leu Gln Lys Gln  Gln Ala Gln Tyr Leu  Glu Glu Lys
    2585                2590                2595

Arg Arg  Arg Glu Arg Glu Trp  Glu Ala Arg Glu Arg  Glu Leu Arg
    2600                2605                2610

Glu Arg  Glu Ala Leu Leu Ala  Gln Arg Glu Glu Glu  Val Gln Gln
    2615                2620                2625

Gly Gln  Gln Asp Leu Glu Lys  Glu Arg Glu Glu Leu  Gln Gln Lys
    2630                2635                2640

Lys Gly  Thr Tyr Gln Tyr Asp  Leu Glu Arg Leu Arg  Ala Ala Gln
    2645                2650                2655

Lys Gln  Leu Glu Arg Glu Gln  Glu Gln Leu Arg Arg  Glu Ala Glu
    2660                2665                2670

Arg Leu  Ser Gln Arg Gln Thr  Glu Arg Asp Leu Cys  Gln Val Ser
    2675                2680                2685

His Pro  His Thr Lys Leu Met  Arg Ile Pro Ser Phe  Phe Pro Ser
    2690                2695                2700

Pro Glu  Glu Pro Pro Ser Pro  Ser Ala Pro Ser Ile  Ala Lys Ser
    2705                2710                2715

Gly Ser  Leu Asp Ser Glu Leu  Ser Val Ser Pro Lys  Arg Asn Ser
    2720                2725                2730

Ile Ser  Arg Thr His Lys Asp  Lys Gly Pro Phe His  Ile Leu Ser
    2735                2740                2745
```

```
Ser Thr  Ser Gln Thr Asn Lys  Gly Pro Glu Gly Gln  Ser Gln Ala
    2750                2755                2760

Pro Ala  Ser Thr Ser Ala Ser  Thr Arg Leu Phe Gly  Leu Thr Lys
    2765                2770                2775

Pro Lys  Glu Lys Lys Glu Lys  Lys Lys Lys Asn Lys  Thr Ser Arg
    2780                2785                2790

Ser Gln  Pro Gly Asp Gly Pro  Ala Ser Glu Val Ser  Ala Glu Gly
    2795                2800                2805

Glu Glu  Ile Phe Cys
    2810
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<210> 620
<211> 93
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 13; "

<220>
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<400> 620

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Met Asn Ile Gln Gln Gln Leu Met Lys Thr Asn Leu Lys Gln Met Asp
1               5                  10                  15

Ser Leu Met Pro Leu Met Met Thr Ala Gln Asp Pro Ser Ser Ala Pro
            20                  25                  30

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

Gln Arg Leu Ser Ser Ser Glu Glu Thr Glu Ser Thr Gln Cys Cys Pro
```

```
    50                  55                  60

Gly Ser Pro Val Ala Gln Thr Glu Ser Pro Cys Asp Leu Ser Ser Ile
65                  70                  75                  80

Val Glu Glu Glu Asn Thr Asp Arg Ser Cys Arg Lys Lys
                85                  90

<210> 621
<211> 146
<212> PRT
<213> Homo sapiens

<220>
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<400> 621
Met Gly Leu Arg Tyr Ser Gly Cys Leu Gly Ser His Val Glu Asn Ala
1               5                  10                  15

Gly Glu Pro Asp Ser Trp Ser Ser Leu Ser Tyr Glu Ile Pro Tyr Gly
            20                  25                  30

Asp Cys Ser Val Arg His His Arg Glu Leu Asp Ile Tyr Thr Leu Thr
        35                  40                  45

Ser Glu Ser Asp Ser His His Glu His Pro Phe Pro Gly Asp Gly Cys
    50                  55                  60

Thr Gly Pro Ile Phe Lys Leu Met Asn Ile Gln Gln Gln Leu Met Lys
65                  70                  75                  80

Thr Asn Leu Lys Gln Met Asp Ser Leu Met Pro Leu Met Met Thr Ala
                85                  90                  95
```

```
Gln Asp Pro Ser Ser Ala Pro Glu Thr Asp Gly Gln Phe Leu Pro Cys
            100                 105                 110

Ala Pro Glu Pro Thr Asp Pro Gln Arg Leu Ser Ser Ser Glu Glu Thr
        115                 120                 125

Glu Ser Thr Gln Cys Cys Pro Gly Ser Pro Val Ala Gln Thr Glu Ser
    130                 135                 140

Pro Cys
145
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<210> 622
<211> 275
<212> PRT
<213> Homo sapiens

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<400> 622

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Pro Ser Asp Asp Met Asp Ser Ile Ile Phe Pro Lys Pro Glu Glu Glu
1               5                   10                  15

His Leu Ala Cys Asp Ile Thr Gly Ser Ser Ser Ser Thr Asp Asp Thr
            20                  25                  30

Ala Ser Leu Asp Arg His Ser Ser His Gly Ser Asp Val Ser Leu Ser
        35                  40                  45

Gln Ile Leu Lys Pro Asn Arg Ser Arg Asp Arg Gln Ser Leu Asp Gly
    50                  55                  60

Phe Tyr Ser His Gly Met Gly Ala Glu Gly Arg Glu Ser Glu Ser Glu
```

65 70 75 80

Pro Ala Asp Pro Gly Asp Val Glu Glu Glu Glu Met Asp Ser Ile Thr
85 90 95

Glu Val Pro Ala Asn Cys Ser Val Leu Arg Ser Ser Met Arg Ser Leu
100 105 110

Ser Pro Phe Arg Arg His Ser Trp Gly Pro Gly Lys Asn Ala Ala Ser
115 120 125

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

Val Arg Arg Pro Pro Ile His Arg Arg Ser Met Ser Trp Cys Pro Ser
145 150 155 160

Gly Val Gln Tyr Ser Ala Gly Leu Ser Ala Asp Phe Asn Tyr Arg Ser
165 170 175

Phe Ser Leu Glu Gly Leu Thr Gly Gly Ala Gly Val Gly Asn Lys Pro
180 185 190

Ser Ser Ser Leu Glu Val Ser Ser Ala Asn Ala Glu Glu Leu Arg His
195 200 205

Pro Phe Ser Gly Glu Glu Arg Val Asp Ser Leu Val Ser Leu Ser Glu
210 215 220

Glu Asp Leu Glu Ser Asp Gln Arg Glu His Arg Met Phe Asp Gln Gln
225 230 235 240

Ile Cys His Arg Ser Lys Gln Gln Gly Phe Asn Tyr Cys Thr Ser Ala
245 250 255

Ile Ser Ser Pro Leu Thr Lys Ser Ile Ser Leu Met Thr Ile Ser His
260 265 270

Pro Gly Leu
275

<210> 623
<211> 38

<212> PRT
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<400> 623
Met Lys Leu Asn Pro Gln Gln Ala Pro Leu Tyr Gly Asp Cys Val Val
1 5 10 15

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

Tyr Leu Val Phe Leu Gly
35

<210> 624
<211> 179
<212> PRT
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<400> 624
Met Lys Leu Asn Pro Gln Gln Ala Pro Leu Tyr Gly Asp Cys Val Val
1 5 10 15

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

Tyr Leu Val Phe Leu Gly Ser Thr Leu Arg His Cys Thr Ser Thr Arg
35 40 45

Lys Val Ser Ser Asp Thr Leu Glu Thr Ile Ala Pro Gly His Asp Cys
50 55 60

Cys Glu Thr Val Lys Val Gln Leu Cys Ala Ser Lys Glu Gly Leu Pro
65 70 75 80

Val Phe Val Val Ala Glu Glu Asp Phe His Phe Val Gln Asp Glu Ala
85 90 95

Tyr Asp Ala Ala Gln Phe Leu Ala Thr Ser Ala Gly Asn Gln Gln Ala
100 105 110

Leu Asn Phe Thr Arg Phe Leu Asp Gln Ser Gly Pro Pro Ser Gly Asp
115 120 125

Val Asn Ser Leu Asp Lys Lys Leu Val Leu Ala Phe Arg His Leu Lys
130 135 140

Leu Pro Thr Glu Trp Asn Val Leu Gly Thr Asp Gln Ser Leu His Gly
145 150 155 160

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

Leu Phe Phe

<210> 625
<211> 1745
<212> PRT
<213> Homo sapiens

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<220>
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<400> 625
Met Lys Leu Asn Pro Gln Gln Ala Pro Leu Tyr Gly Asp Cys Val Val
1 5 10 15

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

Tyr Leu Val Phe Leu Gly Ser Thr Leu Arg His Cys Thr Ser Thr Arg
35 40 45

Lys Val Ser Ser Asp Thr Leu Glu Thr Ile Ala Pro Gly His Asp Cys
50 55 60

Cys Glu Thr Val Lys Val Gln Leu Cys Ala Ser Lys Glu Gly Leu Pro
65 70 75 80

Val Phe Val Val Ala Glu Glu Asp Phe His Phe Val Gln Asp Glu Ala
85 90 95

Tyr Asp Ala Ala Gln Phe Leu Ala Thr Ser Ala Gly Asn Gln Gln Ala
100 105 110

Leu Asn Phe Thr Arg Phe Leu Asp Gln Ser Gly Pro Pro Ser Gly Asp
115 120 125

Val Asn Ser Leu Asp Lys Lys Leu Val Leu Ala Phe Arg His Leu Lys
130 135 140

Leu Pro Thr Glu Trp Asn Val Leu Gly Thr Asp Gln Ser Leu His Asp
145 150 155 160

```
Ala Gly Pro Arg Glu Thr Leu Met His Phe Ala Val Arg Leu Gly Leu
                165                 170                 175

Leu Arg Leu Thr Trp Phe Leu Leu Gln Lys Pro Gly Gly Arg Gly Ala
            180                 185                 190

Leu Ser Ile His Asn Gln Glu Gly Ala Thr Pro Val Ser Leu Ala Leu
        195                 200                 205

Glu Arg Gly Tyr His Lys Leu His Gln Leu Leu Thr Glu Glu Asn Ala
    210                 215                 220

Gly Glu Pro Asp Ser Trp Ser Ser Leu Ser Tyr Glu Ile Pro Tyr Gly
225                 230                 235                 240

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

Ser Glu Ser Asp Ser His His Glu His Pro Phe Pro Gly Asp Gly Cys
            260                 265                 270

Thr Gly Pro Ile Phe Lys Leu Met Asn Ile Gln Gln Gln Leu Met Lys
        275                 280                 285

Thr Asn Leu Lys Gln Met Asp Ser Leu Met Pro Leu Met Met Thr Ala
    290                 295                 300

Gln Asp Pro Ser Ser Ala Pro Glu Thr Asp Gly Gln Phe Leu Pro Cys
305                 310                 315                 320

Ala Pro Glu Pro Thr Asp Pro Gln Arg Leu Ser Ser Ser Glu Glu Thr
                325                 330                 335

Glu Ser Thr Gln Cys Cys Pro Gly Ser Pro Val Ala Gln Thr Glu Ser
            340                 345                 350

Pro Cys Asp Leu Ser Ser Ile Val Glu Glu Glu Asn Thr Asp Arg Ser
        355                 360                 365

Cys Arg Lys Lys Asn Lys Gly Val Glu Arg Lys Gly Glu Glu Val Glu
    370                 375                 380

Pro Ala Pro Ile Val Asp Ser Gly Thr Val Ser Asp Gln Asp Ser Cys
```

385 390 395 400

Leu Gln Ser Leu Pro Asp Cys Gly Val Lys Gly Thr Glu Gly Leu Ser
405 410 415

Ser Cys Gly Asn Arg Asn Glu Glu Thr Gly Thr Lys Ser Ser Gly Met
420 425 430

Pro Thr Asp Gln Glu Ser Leu Ser Ser Gly Asp Ala Val Leu Gln Arg
435 440 445

Asp Leu Val Met Glu Pro Gly Thr Ala Gln Tyr Ser Ser Gly Gly Glu
450 455 460

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

Glu Met Glu His Gly Leu Met Asn Pro Asp Ala Thr Val Trp Lys Asn
485 490 495

Val Leu Gln Gly Gly Glu Ser Thr Lys Glu Arg Phe Glu Asn Ser Asn
500 505 510

Ile Gly Thr Ala Gly Ala Ser Asp Val His Val Thr Ser Lys Pro Val
515 520 525

Asp Lys Ile Ser Val Pro Asn Cys Ala Pro Ala Ala Ser Ser Leu Asp
530 535 540

Gly Asn Lys Pro Ala Glu Ser Ser Leu Ala Phe Ser Asn Glu Glu Thr
545 550 555 560

Ser Thr Glu Lys Thr Ala Glu Thr Glu Thr Ser Arg Ser Arg Glu Glu
565 570 575

Ser Ala Asp Ala Pro Val Asp Gln Asn Ser Val Val Ile Pro Ala Ala
580 585 590

Ala Lys Asp Lys Ile Ser Asp Gly Leu Glu Pro Tyr Thr Leu Leu Ala
595 600 605

Ala Gly Ile Gly Glu Ala Met Ser Pro Ser Asp Leu Ala Leu Leu Gly
610 615 620

```
Leu Glu Glu Asp Val Met Pro His Gln Asn Ser Glu Thr Asn Ser Ser
625                 630                 635                 640

His Ala Gln Ser Gln Lys Gly Lys Ser Ser Pro Ile Cys Ser Thr Thr
                645                 650                 655

Gly Asp Asp Lys Leu Cys Ala Asp Ser Ala Cys Gln Gln Asn Thr Val
            660                 665                 670

Thr Ser Ser Gly Asp Leu Val Ala Lys Leu Cys Asp Asn Ile Val Ser
        675                 680                 685

Glu Ser Glu Ser Thr Thr Ala Arg Gln Pro Ser Ser Gln Asp Pro Pro
    690                 695                 700

Asp Ala Ser His Cys Glu Asp Pro Gln Ala His Thr Val Thr Ser Asp
705                 710                 715                 720

Pro Val Arg Asp Thr Gln Glu Arg Ala Asp Phe Cys Pro Phe Lys Val
                725                 730                 735

Val Asp Asn Lys Gly Gln Arg Lys Asp Val Lys Leu Asp Lys Pro Leu
            740                 745                 750

Thr Asn Met Leu Glu Val Val Ser His Pro His Pro Val Val Pro Lys
        755                 760                 765

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

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

Ala Leu Ser Phe Val Pro Ser Gln Lys Glu Lys Gly Thr Ala Thr Pro
                805                 810                 815

Glu Leu His Thr Ala Thr Asp Tyr Arg Asp Gly Pro Asp Gly Asn Ser
            820                 825                 830

Asn Glu Pro Asp Thr Arg Pro Leu Glu Asp Arg Ala Val Gly Leu Ser
        835                 840                 845
```

```
Thr Ser Ser Thr Ala Ala Glu Leu Gln His Gly Met Gly Asn Thr Ser
    850                 855                 860

Leu Thr Gly Leu Gly Gly Glu His Glu Gly Pro Ala Pro Pro Ala Ile
865                 870                 875                 880

Pro Glu Ala Leu Asn Ile Lys Gly Asn Thr Asp Ser Ser Leu Gln Ser
                885                 890                 895

Val Gly Lys Ala Thr Leu Ala Leu Asp Ser Val Leu Thr Glu Glu Gly
            900                 905                 910

Lys Leu Leu Val Val Ser Glu Ser Ser Ala Ala Gln Glu Gln Asp Lys
        915                 920                 925

Asp Lys Ala Val Thr Cys Ser Ser Ile Lys Glu Asn Ala Leu Ser Ser
    930                 935                 940

Gly Thr Leu Gln Glu Glu Gln Arg Thr Pro Pro Pro Gly Gln Asp Thr
945                 950                 955                 960

Gln Gln Phe His Glu Lys Ser Ile Ser Ala Asp Cys Ala Lys Asp Lys
                965                 970                 975

Ala Leu Gln Leu Ser Asn Ser Pro Gly Ala Ser Ser Ala Phe Leu Lys
            980                 985                 990

Ala Glu Thr Glu His Asn Lys Glu  Val Ala Pro Gln Val  Ser Leu
Leu
        995                 1000                1005

Thr Gln  Gly Gly Ala Ala Gln  Ser Leu Val Pro Pro  Gly Ala Ser
    1010                1015                1020

Leu Ala  Thr Glu Ser Arg Gln  Glu Ala Leu Gly Ala  Glu His Asn
    1025                1030                1035

Ser Ser  Ala Leu Leu Pro Cys  Leu Leu Pro Asp Gly  Ser Asp Gly
    1040                1045                1050

Ser Asp  Ala Leu Asn Cys Ser  Gln Pro Ser Pro Leu  Asp Val Gly
    1055                1060                1065
```

```
Val Lys  Asn Thr Gln Ser Gln  Gly Lys Thr Ser Ala  Cys Glu Val
    1070                1075                1080

Ser Gly  Asp Val Thr Val Asp  Val Thr Gly Val Asn  Ala Leu Gln
    1085                1090                1095

Gly Met  Ala Glu Pro Arg Arg  Glu Asn Ile Ser His  Asn Thr Gln
    1100                1105                1110

Asp Ile  Leu Ile Pro Asn Val  Leu Leu Ser Gln Glu  Lys Asn Ala
    1115                1120                1125

Val Leu  Gly Leu Pro Val Ala  Leu Gln Asp Lys Ala  Val Thr Asp
    1130                1135                1140

Pro Gln  Gly Val Gly Thr Pro  Glu Met Ile Pro Leu  Asp Trp Glu
    1145                1150                1155

Lys Gly  Lys Leu Glu Gly Ala  Asp His Ser Cys Thr  Met Gly Asp
    1160                1165                1170

Ala Glu  Glu Ala Gln Ile Asp  Asp Glu Ala His Pro  Val Leu Leu
    1175                1180                1185

Gln Pro  Val Ala Lys Glu Leu  Pro Thr Asp Met Glu  Leu Ser Ala
    1190                1195                1200

His Asp  Asp Gly Ala Pro Ala  Gly Val Arg Glu Val  Met Arg Ala
    1205                1210                1215

Pro Pro  Ser Gly Arg Glu Arg  Ser Thr Pro Ser Leu  Pro Cys Met
    1220                1225                1230

Val Ser  Ala Gln Asp Ala Pro  Leu Pro Lys Gly Ala  Asp Leu Ile
    1235                1240                1245

Glu Glu  Ala Ala Ser Arg Ile  Val Asp Ala Val Ile  Glu Gln Val
    1250                1255                1260

Lys Ala  Ala Gly Ala Leu Leu  Thr Glu Gly Glu Ala  Cys His Met
    1265                1270                1275
```

```
Ser Leu  Ser Ser Pro Glu Leu  Gly Pro Leu Thr Lys  Gly Leu Glu
    1280                 1285                 1290

Ser Ala  Phe Thr Glu Lys Val  Ser Thr Phe Pro Pro  Gly Glu Ser
    1295                 1300                 1305

Leu Pro  Met Gly Ser Thr Pro  Glu Glu Ala Thr Gly  Ser Leu Ala
    1310                 1315                 1320

Gly Cys  Phe Ala Gly Arg Glu  Glu Pro Glu Lys Ile  Ile Leu Pro
    1325                 1330                 1335

Val Gln  Gly Pro Glu Pro Ala  Ala Glu Met Pro Asp  Val Lys Ala
    1340                 1345                 1350

Glu Asp  Glu Val Asp Phe Arg  Ala Ser Ser Ile Ser  Glu Glu Val
    1355                 1360                 1365

Ala Val  Gly Ser Ile Ala Ala  Thr Leu Lys Met Lys  Gln Gly Pro
    1370                 1375                 1380

Met Thr  Gln Ala Ile Asn Arg  Glu Asn Trp Cys Thr  Ile Glu Pro
    1385                 1390                 1395

Cys Pro  Asp Ala Ala Ser Leu  Leu Ala Ser Lys Gln  Ser Pro Glu
    1400                 1405                 1410

Cys Glu  Asn Phe Leu Asp Val  Gly Leu Gly Arg Glu  Cys Thr Ser
    1415                 1420                 1425

Lys Gln  Gly Val Leu Lys Arg  Glu Ser Gly Ser Asp  Ser Asp Leu
    1430                 1435                 1440

Phe His  Ser Pro Ser Asp Asp  Met Asp Ser Ile Ile  Phe Pro Lys
    1445                 1450                 1455

Pro Glu  Glu Glu His Leu Ala  Cys Asp Ile Thr Gly  Ser Ser Ser
    1460                 1465                 1470

Ser Thr  Asp Asp Thr Ala Ser  Leu Asp Arg His Ser  Ser His Gly
    1475                 1480                 1485

Ser Asp  Val Ser Leu Ser Gln  Ile Leu Lys Pro Asn  Arg Ser Arg
```

```
    1490                1495                1500

Asp Arg  Gln Ser Leu Asp Gly  Phe Tyr Ser His Gly  Met Gly Ala
    1505                1510                1515

Glu Gly  Arg Glu Ser Glu Ser  Glu Pro Ala Asp Pro  Gly Asp Val
    1520                1525                1530

Glu Glu  Glu Glu Met Asp Ser  Ile Thr Glu Val Pro  Ala Asn Cys
    1535                1540                1545

Ser Val  Leu Arg Ser Ser Met  Arg Ser Leu Ser Pro  Phe Arg Arg
    1550                1555                1560

His Ser  Trp Gly Pro Gly Lys  Asn Ala Ala Ser Asp  Ala Glu Met
    1565                1570                1575

Asn His  Arg Ser Phe Ser Leu  Glu Gly Leu Thr Gly  Gly Ala Gly
    1580                1585                1590

Val Gly  Asn Lys Pro Ser Ser  Ser Leu Glu Val Ser  Ser Ala Asn
    1595                1600                1605

Ala Glu  Glu Leu Arg His Pro  Phe Ser Gly Glu Glu  Arg Val Asp
    1610                1615                1620

Ser Leu  Val Ser Leu Ser Glu  Glu Asp Leu Glu Ser  Asp Gln Arg
    1625                1630                1635

Glu His  Arg Met Phe Asp Gln  Gln Ile Cys His Arg  Ser Lys Gln
    1640                1645                1650

Gln Gly  Phe Asn Tyr Cys Thr  Ser Ala Ile Ser Ser  Pro Leu Thr
    1655                1660                1665

Lys Ser  Ile Ser Leu Met Thr  Ile Ser His Pro Gly  Leu Asp Asn
    1670                1675                1680

Ser Arg  Pro Phe His Ser Thr  Phe His Asn Thr Ser  Ala Asn Leu
    1685                1690                1695

Thr Glu  Ser Ile Thr Glu Glu  Asn Tyr Asn Phe Leu  Pro His Ser
    1700                1705                1710
```

```
Pro Ser  Lys Lys Asp Ser Glu  Trp Lys Ser Gly Thr  Lys Val Ser
    1715                1720                1725

Arg Thr  Phe Ser Tyr Ile Lys  Asn Lys Met Ser Ser  Ser Lys Lys
    1730                1735                1740

Ser Lys
    1745
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<210> 626
<211> 1429
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AKAP13; "

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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 13; "

<220>
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<400> 626

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Met Leu Tyr Ile Asn Arg Glu Asn Trp Cys Thr Ile Glu Pro Cys Pro
1               5                  10                  15

Asp Ala Ala Ser Leu Leu Ala Ser Lys Gln Ser Pro Glu Cys Glu Asn
            20                  25                  30

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

Leu Lys Arg Glu Ser Gly Ser Asp Ser Asp Leu Phe His Ser Pro Ser
    50                  55                  60

Asp Asp Met Asp Ser Ile Ile Phe Pro Lys Pro Glu Glu Glu His Leu
65                  70                  75                  80
```

```
Ala Cys Asp Ile Thr Gly Ser Ser Ser Ser Thr Asp Asp Thr Ala Ser
                85                  90                  95

Leu Asp Arg His Ser Ser His Gly Ser Asp Val Ser Leu Ser Gln Ile
            100                 105                 110

Leu Lys Pro Asn Arg Ser Arg Asp Arg Gln Ser Leu Asp Gly Phe Tyr
        115                 120                 125

Ser His Gly Met Gly Ala Glu Gly Arg Glu Ser Glu Ser Glu Pro Ala
    130                 135                 140

Asp Pro Gly Asp Val Glu Glu Glu Glu Met Asp Ser Ile Thr Glu Val
145                 150                 155                 160

Pro Ala Asn Cys Ser Val Leu Arg Ser Ser Met Arg Ser Leu Ser Pro
                165                 170                 175

Phe Arg Arg His Ser Trp Gly Pro Gly Lys Asn Ala Ala Ser Asp Ala
            180                 185                 190

Glu Met Asn His Arg Ser Ser Met Arg Val Leu Gly Asp Val Val Arg
        195                 200                 205

Arg Pro Pro Ile His Arg Arg Ser Phe Ser Leu Glu Gly Leu Thr Gly
    210                 215                 220

Gly Ala Gly Val Gly Asn Lys Pro Ser Ser Ser Leu Glu Val Ser Ser
225                 230                 235                 240

Ala Asn Ala Glu Glu Leu Arg His Pro Phe Ser Gly Glu Glu Arg Val
                245                 250                 255

Asp Ser Leu Val Ser Leu Ser Glu Glu Asp Leu Glu Ser Asp Gln Arg
            260                 265                 270

Glu His Arg Met Phe Asp Gln Gln Ile Cys His Arg Ser Lys Gln Gln
        275                 280                 285

Gly Phe Asn Tyr Cys Thr Ser Ala Ile Ser Ser Pro Leu Thr Lys Ser
    290                 295                 300

Ile Ser Leu Met Thr Ile Ser His Pro Gly Leu Asp Asn Ser Arg Pro
```

305 310 315 320

Phe His Ser Thr Phe His Asn Thr Ser Ala Asn Leu Thr Glu Ser Ile
325 330 335

Thr Glu Glu Asn Tyr Asn Phe Leu Pro His Ser Pro Ser Lys Lys Asp
340 345 350

Ser Glu Trp Lys Ser Gly Thr Lys Val Ser Arg Thr Phe Ser Tyr Ile
355 360 365

Lys Asn Lys Met Ser Ser Ser Lys Lys Ser Lys Glu Lys Glu Lys Glu
370 375 380

Lys Asp Lys Ile Lys Glu Lys Glu Lys Asp Ser Lys Asp Lys Glu Lys
385 390 395 400

Asp Lys Lys Thr Val Asn Gly His Thr Phe Ser Ser Ile Pro Val Val
405 410 415

Gly Pro Ile Ser Cys Ser Gln Cys Met Lys Pro Phe Thr Asn Lys Asp
420 425 430

Ala Tyr Thr Cys Ala Asn Cys Ser Ala Phe Val His Lys Gly Cys Arg
435 440 445

Glu Ser Leu Ala Ser Cys Ala Lys Val Lys Met Lys Gln Pro Lys Gly
450 455 460

Ser Leu Gln Ala His Asp Thr Ser Ser Leu Pro Thr Val Ile Met Arg
465 470 475 480

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

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

Gln Ser Val Ser Leu Ser Lys Ser Val Ser Ile Gln Asn Ile Thr Gly
515 520 525

Val Gly Asn Asp Glu Asn Met Ser Asn Thr Trp Lys Phe Leu Ser His
530 535 540

Ser Thr Asp Ser Leu Asn Lys Ile Ser Lys Val Asn Glu Ser Thr Glu
545 550 555 560

Ser Leu Thr Asp Glu Gly Val Gly Thr Asp Met Asn Glu Gly Gln Leu
565 570 575

Leu Gly Asp Phe Glu Ile Glu Ser Lys Gln Leu Glu Ala Glu Ser Trp
580 585 590

Ser Arg Ile Ile Asp Ser Lys Phe Leu Lys Gln Gln Lys Lys Asp Val
595 600 605

Val Lys Arg Gln Glu Val Ile Tyr Glu Leu Met Gln Thr Glu Phe His
610 615 620

His Val Arg Thr Leu Lys Ile Met Ser Gly Val Tyr Ser Gln Gly Met
625 630 635 640

Met Ala Asp Leu Leu Phe Glu Gln Gln Met Val Glu Lys Leu Phe Pro
645 650 655

Cys Leu Asp Glu Leu Ile Ser Ile His Ser Gln Phe Phe Gln Arg Ile
660 665 670

Leu Glu Arg Lys Lys Glu Ser Leu Val Asp Lys Ser Glu Lys Asn Phe
675 680 685

Leu Ile Lys Arg Ile Gly Asp Val Leu Val Asn Gln Phe Ser Gly Glu
690 695 700

Asn Ala Glu Arg Leu Lys Lys Thr Tyr Gly Lys Phe Cys Gly Gln His
705 710 715 720

Asn Gln Ser Val Asn Tyr Phe Lys Asp Leu Tyr Ala Lys Asp Lys Arg
725 730 735

Phe Gln Ala Phe Val Lys Lys Lys Met Ser Ser Ser Val Val Arg Arg
740 745 750

Leu Gly Ile Pro Glu Cys Ile Leu Leu Val Thr Gln Arg Ile Thr Lys
755 760 765

```
Tyr Pro Val Leu Phe Gln Arg Ile Leu Gln Cys Thr Lys Asp Asn Glu
    770                 775                 780

Val Glu Gln Glu Asp Leu Ala Gln Ser Leu Ser Leu Val Lys Asp Val
785                 790                 795                 800

Ile Gly Ala Val Asp Ser Lys Val Ala Ser Tyr Glu Lys Lys Val Arg
                805                 810                 815

Leu Asn Glu Ile Tyr Thr Lys Thr Asp Ser Lys Ser Ile Met Arg Met
            820                 825                 830

Lys Ser Gly Gln Met Phe Ala Lys Glu Asp Leu Lys Arg Lys Lys Leu
        835                 840                 845

Val Arg Asp Gly Ser Val Phe Leu Lys Asn Ala Ala Gly Arg Leu Lys
    850                 855                 860

Glu Val Gln Ala Val Leu Leu Thr Asp Ile Leu Val Phe Leu Gln Glu
865                 870                 875                 880

Lys Asp Gln Lys Tyr Ile Phe Ala Ser Leu Asp Gln Lys Ser Thr Val
                885                 890                 895

Ile Ser Leu Lys Lys Leu Ile Val Arg Glu Val Ala His Glu Glu Lys
            900                 905                 910

Gly Leu Phe Leu Ile Ser Met Gly Met Thr Asp Pro Glu Met Val Glu
        915                 920                 925

Val His Ala Ser Ser Lys Glu Glu Arg Asn Ser Trp Ile Gln Ile Ile
    930                 935                 940

Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu Asp Glu Gly Ile Pro
945                 950                 955                 960

Ser Glu Asn Glu Glu Glu Lys Lys Met Leu Asp Thr Arg Ala Arg Glu
                965                 970                 975

Leu Lys Glu Gln Leu His Gln Lys Asp Gln Lys Ile Leu Leu Leu Leu
            980                 985                 990
```

```
Glu Glu Lys Glu Met Ile Phe Arg  Asp Met Ala Glu Cys  Ser Thr
Pro
        995                 1000                1005

Leu Pro  Glu Asp Cys Ser Pro  Thr His Ser Pro Arg  Val Leu Phe
    1010                1015                1020

Arg Ser  Asn Thr Glu Glu Ala  Leu Lys Gly Gly Pro  Leu Met Lys
    1025                1030                1035

Ser Ala  Ile Asn Glu Val Glu  Ile Leu Gln Gly Leu  Val Ser Gly
    1040                1045                1050

Asn Leu  Gly Gly Thr Leu Gly  Pro Thr Val Ser Ser  Pro Ile Glu
    1055                1060                1065

Gln Asp  Val Val Gly Pro Val  Ser Leu Pro Arg Arg  Ala Glu Thr
    1070                1075                1080

Phe Gly  Gly Phe Asp Ser His  Gln Met Asn Ala Ser  Lys Gly Gly
    1085                1090                1095

Glu Lys  Glu Glu Gly Asp Asp  Gly Gln Asp Leu Arg  Arg Thr Glu
    1100                1105                1110

Ser Asp  Ser Gly Leu Lys Lys  Gly Gly Asn Ala Asn  Leu Val Phe
    1115                1120                1125

Met Leu  Lys Arg Asn Ser Glu  Gln Val Val Gln Ser  Val Val His
    1130                1135                1140

Leu Tyr  Glu Leu Leu Ser Ala  Leu Gln Gly Val Val  Leu Gln Gln
    1145                1150                1155

Asp Ser  Tyr Ile Glu Asp Gln  Lys Leu Val Leu Ser  Glu Arg Ala
    1160                1165                1170

Leu Thr  Arg Ser Leu Ser Arg  Pro Ser Ser Leu Ile  Glu Gln Glu
    1175                1180                1185

Lys Gln  Arg Ser Leu Glu Lys  Gln Arg Gln Asp Leu  Ala Asn Leu
    1190                1195                1200
```

```
Gln Lys  Gln Gln Ala Gln Tyr  Leu Glu Glu Lys Arg  Arg Arg Glu
    1205                 1210                 1215

Arg Glu  Trp Glu Ala Arg Glu  Arg Glu Leu Arg Glu  Arg Glu Ala
    1220                 1225                 1230

Leu Leu  Ala Gln Arg Glu Glu  Glu Val Gln Gln Gly  Gln Gln Asp
    1235                 1240                 1245

Leu Glu  Lys Glu Arg Glu Glu  Leu Gln Gln Lys Lys  Gly Thr Tyr
    1250                 1255                 1260

Gln Tyr  Asp Leu Glu Arg Leu  Arg Ala Ala Gln Lys  Gln Leu Glu
    1265                 1270                 1275

Arg Glu  Gln Glu Gln Leu Arg  Arg Glu Ala Glu Arg  Leu Ser Gln
    1280                 1285                 1290

Arg Gln  Thr Glu Arg Asp Leu  Cys Gln Val Ser His  Pro His Thr
    1295                 1300                 1305

Lys Leu  Met Arg Ile Pro Ser  Phe Phe Pro Ser Pro  Glu Glu Pro
    1310                 1315                 1320

Pro Ser  Pro Ser Ala Pro Ser  Ile Ala Lys Ser Gly  Ser Leu Asp
    1325                 1330                 1335

Ser Glu  Leu Ser Val Ser Pro  Lys Arg Asn Ser Ile  Ser Arg Thr
    1340                 1345                 1350

His Lys  Asp Lys Gly Pro Phe  His Ile Leu Ser Ser  Thr Ser Gln
    1355                 1360                 1365

Thr Asn  Lys Gly Pro Glu Gly  Gln Ser Gln Ala Pro  Ala Ser Thr
    1370                 1375                 1380

Ser Ala  Ser Thr Arg Leu Phe  Gly Leu Thr Lys Pro  Lys Glu Lys
    1385                 1390                 1395

Lys Glu  Lys Lys Lys Lys Asn  Lys Thr Ser Arg Ser  Gln Pro Gly
    1400                 1405                 1410

Asp Gly  Pro Ala Ser Glu Val  Ser Ala Glu Gly Glu  Glu Ile Phe
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1415 1420 1425

Cys

<210> 627
<211> 166
<212> PRT
<213> Homo sapiens

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<220>
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<400> 627
Met Ser Ile Lys Trp Ala Arg Phe His Glu Val Pro His Ile Thr Val
1 5 10 15

Arg Phe Ile Gly Pro Lys His Gly Glu Glu Lys Glu Lys Glu Lys Asp
20 25 30

Lys Ile Lys Glu Lys Glu Lys Asp Ser Lys Asp Lys Glu Lys Asp Lys
35 40 45

Lys Thr Val Asn Gly His Thr Phe Ser Ser Ile Pro Val Val Gly Pro
50 55 60

Ile Ser Cys Ser Gln Cys Met Lys Pro Phe Thr Asn Lys Asp Ala Tyr
65 70 75 80

Thr Cys Ala Asn Cys Ser Ala Phe Val His Lys Gly Cys Arg Glu Ser
85 90 95

Leu Ala Ser Cys Ala Lys Val Lys Met Lys Gln Pro Lys Gly Ser Leu
100 105 110

```
Gln Ala His Asp Thr Ser Ser Leu Pro Thr Val Ile Met Arg Asn Lys
        115                 120                 125

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

Glu Thr Ala Thr Thr Pro Ile Phe Ala Asn Arg Arg Ser Gln Gln Ser
145                 150                 155                 160

Val Ser Leu Ser Lys Ser
                165
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<210> 628
<211> 967
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<400> 628

```
Met Tyr Glu Arg His Lys Arg Arg Tyr Ser Leu Cys Asp Ile Ser Lys
1               5                   10                  15

Val Asp Arg Thr Val Asp Val Val Leu Leu Lys Ile Asn Arg Glu Asn
            20                  25                  30

Trp Cys Thr Ile Glu Pro Cys Pro Asp Ala Ala Ser Leu Leu Ala Ser
        35                  40                  45

Lys Gln Ser Pro Glu Cys Glu Asn Phe Leu Asp Val Gly Leu Gly Arg
    50                  55                  60

Glu Cys Thr Ser Lys Gln Gly Val Leu Lys Arg Glu Ser Gly Ser Asp
```

65 70 75 80

Ser Asp Leu Phe His Ser Pro Ser Asp Asp Met Asp Ser Ile Ile Phe
85 90 95

Pro Lys Pro Glu Glu Glu His Leu Ala Cys Asp Ile Thr Gly Ser Ser
100 105 110

Ser Ser Thr Asp Asp Thr Ala Ser Leu Asp Arg His Ser Ser His Gly
115 120 125

Ser Asp Val Ser Leu Ser Gln Ile Leu Lys Pro Asn Arg Ser Arg Asp
130 135 140

Arg Gln Ser Leu Asp Gly Phe Tyr Ser His Gly Met Gly Ala Glu Gly
145 150 155 160

Arg Glu Ser Glu Ser Glu Pro Ala Asp Pro Gly Asp Val Glu Glu Glu
165 170 175

Glu Met Asp Ser Ile Thr Glu Val Pro Ala Asn Cys Ser Val Leu Arg
180 185 190

Ser Ser Met Arg Ser Leu Ser Pro Phe Arg Arg His Ser Trp Gly Pro
195 200 205

Gly Lys Asn Ala Ala Ser Asp Ala Glu Met Asn His Arg Ser Phe Ser
210 215 220

Leu Glu Gly Leu Thr Gly Gly Ala Gly Val Gly Asn Lys Pro Ser Ser
225 230 235 240

Ser Leu Glu Val Ser Ser Ala Asn Ala Glu Glu Leu Arg His Pro Phe
245 250 255

Ser Gly Glu Glu Arg Val Asp Ser Leu Val Ser Leu Ser Glu Glu Asp
260 265 270

Leu Glu Ser Asp Gln Arg Glu His Arg Met Phe Asp Gln Gln Ile Cys
275 280 285

His Arg Ser Lys Gln Gln Gly Phe Asn Tyr Cys Thr Ser Ala Ile Ser
290 295 300

Ser Pro Leu Thr Lys Ser Ile Ser Leu Met Thr Ile Ser His Pro Gly
305 310 315 320

Leu Asp Asn Ser Arg Pro Phe His Ser Thr Phe His Asn Thr Ser Ala
325 330 335

Asn Leu Thr Glu Ser Ile Thr Glu Glu Asn Tyr Asn Phe Leu Pro His
340 345 350

Ser Pro Ser Lys Lys Asp Ser Glu Trp Lys Ser Gly Thr Lys Val Ser
355 360 365

Arg Thr Phe Ser Tyr Ile Lys Asn Lys Met Ser Ser Ser Lys Lys Ser
370 375 380

Lys Glu Lys Glu Lys Glu Lys Asp Lys Ile Lys Glu Lys Glu Lys Asp
385 390 395 400

Ser Lys Asp Lys Glu Lys Asp Lys Lys Thr Val Asn Gly His Thr Phe
405 410 415

Ser Ser Ile Pro Val Val Gly Pro Ile Ser Cys Ser Gln Cys Met Lys
420 425 430

Pro Phe Thr Asn Lys Asp Ala Tyr Thr Cys Ala Asn Cys Ser Ala Phe
435 440 445

Val His Lys Gly Cys Arg Glu Ser Leu Ala Ser Cys Ala Lys Val Lys
450 455 460

Met Lys Pro Lys Gly Ser Leu Gln Ala His Asp Thr Ser Ser Leu Pro
465 470 475 480

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

Ser Ala Val Leu Leu Val Asp Glu Thr Ala Thr Thr Pro Ile Phe Ala
500 505 510

Asn Arg Arg Ser Gln Gln Ser Val Ser Leu Ser Lys Ser Val Ser Ile
515 520 525

```
Gln Asn Ile Thr Gly Val Gly Asn Asp Glu Asn Met Ser Asn Thr Trp
    530                 535                 540

Lys Phe Leu Ser His Ser Thr Asp Ser Leu Asn Lys Ile Ser Lys Val
545                 550                 555                 560

Asn Glu Ser Thr Glu Ser Leu Thr Asp Glu Gly Val Gly Thr Asp Met
                565                 570                 575

Asn Glu Gly Gln Leu Leu Gly Asp Phe Glu Ile Glu Ser Lys Gln Leu
            580                 585                 590

Glu Ala Glu Ser Trp Ser Arg Ile Ile Asp Ser Lys Phe Leu Lys Gln
        595                 600                 605

Gln Lys Lys Asp Val Val Lys Arg Gln Glu Val Ile Tyr Glu Leu Met
    610                 615                 620

Gln Thr Glu Phe His His Val Arg Thr Leu Lys Ile Met Ser Gly Val
625                 630                 635                 640

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

Glu Lys Leu Phe Pro Cys Leu Asp Glu Leu Ile Ser Ile His Ser Gln
            660                 665                 670

Phe Phe Gln Arg Ile Leu Glu Arg Lys Lys Glu Ser Leu Val Asp Lys
        675                 680                 685

Ser Glu Lys Asn Phe Leu Ile Lys Arg Ile Gly Asp Val Leu Val Asn
    690                 695                 700

Gln Phe Ser Gly Glu Asn Ala Glu Arg Leu Lys Lys Thr Tyr Gly Lys
705                 710                 715                 720

Phe Cys Gly Gln His Asn Gln Ser Val Asn Tyr Phe Lys Asp Leu Tyr
                725                 730                 735

Ala Lys Asp Lys Arg Phe Gln Ala Phe Val Lys Lys Lys Met Ser Ser
            740                 745                 750
```

```
Ser Val Val Arg Arg Leu Gly Ile Pro Glu Cys Ile Leu Leu Val Thr
        755                 760                 765

Gln Arg Ile Thr Lys Tyr Pro Val Leu Phe Gln Arg Ile Leu Gln Cys
    770                 775                 780

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

Leu Val Lys Asp Val Ile Gly Ala Val Asp Ser Lys Val Ala Ser Tyr
                805                 810                 815

Glu Lys Lys Val Arg Leu Asn Glu Ile Tyr Thr Lys Thr Asp Ser Lys
            820                 825                 830

Ser Ile Met Arg Met Lys Ser Gly Gln Met Phe Ala Lys Glu Asp Leu
        835                 840                 845

Lys Arg Lys Lys Leu Val Arg Asp Gly Ser Val Phe Leu Lys Asn Ala
    850                 855                 860

Ala Gly Arg Leu Lys Glu Val Gln Ala Val Leu Leu Thr Asp Ile Leu
865                 870                 875                 880

Val Phe Leu Gln Glu Lys Asp Gln Lys Tyr Ile Phe Ala Ser Leu Asp
                885                 890                 895

Gln Lys Ser Thr Val Ile Ser Leu Lys Lys Leu Ile Val Arg Glu Val
            900                 905                 910

Ala His Glu Glu Lys Gly Leu Phe Leu Ile Ser Met Gly Met Thr Asp
        915                 920                 925

Pro Glu Met Val Glu Val His Ala Ser Ser Lys Glu Glu Arg Asn Ser
    930                 935                 940

Trp Ile Gln Ile Ile Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu
945                 950                 955                 960

Asp Glu Gly Ile Pro Ser Glu
                965
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<210> 629

<211> 66
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<220>
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<400> 629
Met Ser Ser Ser Lys Lys Ser Lys Glu Lys Glu Lys Glu Lys Asp Lys
1 5 10 15

Ile Lys Glu Lys Glu Lys Asp Ser Lys Asp Lys Glu Lys Asp Lys Lys
20 25 30

Thr Val Asn Gly His Thr Phe Ser Ser Ile Pro Val Val Gly Pro Ile
35 40 45

Ser Cys Ser Gln Cys Met Lys Pro Phe Thr Asn Lys Asp Ala Tyr Thr
50 55 60

Cys Ala
65

<210> 630
<211> 98
<212> PRT
<213> Homo sapiens

<220>
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<400> 630
Met Pro Asp Val Lys Ala Glu Asp Glu Val Asp Phe Arg Ala Ser Ser
1 5 10 15

Ile Ser Glu Glu Val Ala Val Gly Ser Ile Ala Ala Thr Leu Lys Met
20 25 30

Lys Gln Gly Pro Met Thr Gln Ala Ile Asn Arg Glu Asn Trp Cys Thr
35 40 45

Ile Glu Pro Cys Pro Asp Ala Ala Ser Leu Leu Ala Ser Lys Gln Ser
50 55 60

Pro Glu Cys Glu Asn Phe Leu Asp Val Gly Leu Gly Arg Glu Cys Thr
65 70 75 80

Ser Lys Gln Gly Val Leu Lys Arg Glu Ser Gly Ser Asp Ser Asp Leu
85 90 95

Phe His

<210> 631
<211> 137
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID: Q86UN6; "

<220>
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<223> /note="ENSP ID: ENSP00000334680"

<400> 631
Met Ser Glu Thr Gln Asn Ser Thr Ser Gln Lys Ala Met Asp Glu Asp
1   5   10   15

Asn Lys Ala Ala Ser Gln Thr Met Pro Asn Thr Gln Asp Lys Asn Tyr
            20   25   30

Glu Asp Glu Leu Thr Gln Val Ala Leu Ala Leu Val Glu Asp Val Ile
        35   40   45

Asn Tyr Ala Val Lys Ile Val Glu Glu Glu Arg Asn Pro Leu Lys Asn
    50   55   60

Ile Lys Trp Met Thr His Gly Glu Phe Thr Val Glu Lys Gly Leu Lys
65   70   75   80

Gln Ile Asp Glu Tyr Phe Ser Asp Ala Pro Ile Val Val Ser Tyr Val
                85   90   95

Gly Asp His Gln Ala Leu Val His Arg Pro Gly Met Val Arg Phe Arg
            100   105   110

Glu Asn Trp Gln Lys Asn Leu Thr Asp Ala Lys Tyr Ser Phe Met Glu
        115   120   125

Ser Phe Pro Phe Leu Phe Asn Arg Val
    130   135

<210> 632
<211> 89
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID: Q86UN6; "

<220>
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<400> 632
Met Ser Glu Thr Gln Asn Ser Thr Ser Gln Lys Ala Met Asp Glu Asp
1 5 10 15

Asn Lys Ala Ala Ser Gln Thr Met Pro Asn Thr Gln Asp Lys Asn Tyr
            20 25 30

Glu Asp Glu Leu Thr Gln Val Ala Leu Ala Leu Val Glu Asp Val Ile
        35 40 45

Asn Tyr Ala Val Lys Ile Val Glu Glu Glu Arg Asn Pro Leu Lys Asn
    50 55 60

Ile Lys Trp Met Thr His Gly Glu Phe Thr Val Glu Lys Gly Leu Lys
65 70 75 80

Gln Ile Asp Glu Tyr Phe Ser Val Ser
                85

<210> 633
<211> 137
<212> PRT
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<220>
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<223> /note="ENSP ID: ENSP00000360479"

<400> 633
Met Ser Glu Thr Gln Asn Ser Thr Ser Gln Lys Ala Met Asp Glu Asp
1   5   10   15

Asn Lys Ala Ala Ser Gln Thr Met Pro Asn Thr Gln Asp Lys Asn Tyr
            20   25   30

Glu Asp Glu Leu Thr Gln Val Ala Leu Ala Leu Val Glu Asp Val Ile
        35   40   45

Asn Tyr Ala Val Lys Ile Val Glu Glu Glu Arg Asn Pro Leu Lys Asn
    50   55   60

Ile Lys Trp Met Thr His Gly Glu Phe Thr Val Glu Lys Gly Leu Lys
65   70   75   80

Gln Ile Asp Glu Tyr Phe Ser Asp Ala Pro Ile Val Val Ser Tyr Val
                85   90   95

Gly Asp His Gln Ala Leu Val His Arg Pro Gly Met Val Arg Phe Arg
            100   105   110

Glu Asn Trp Gln Lys Asn Leu Thr Asp Ala Lys Tyr Ser Phe Met Glu
        115   120   125

Ser Phe Pro Phe Leu Phe Asn Arg Val
    130   135

<210> 634
<211> 197
<212> PRT
<213> Homo sapiens

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<400> 634

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Met Ser Glu Thr Gln Asn Ser Thr Ser Gln Lys Ala Met Asp Glu Asp
1               5                  10                  15

Asn Lys Ala Ala Ser Gln Thr Met Pro Asn Thr Gln Asp Lys Asn Tyr
            20                  25                  30

Glu Asp Glu Leu Thr Gln Val Ala Leu Ala Leu Val Glu Asp Val Ile
        35                  40                  45

Asn Tyr Ala Val Lys Ile Val Glu Glu Glu Arg Asn Pro Leu Lys Asn
    50                  55                  60

Ile Lys Trp Met Thr His Gly Glu Phe Thr Val Glu Lys Gly Leu Lys
65                  70                  75                  80

Gln Ile Asp Glu Tyr Phe Ser Lys Cys Val Ser Lys Lys Cys Trp Ala
                85                  90                  95

His Gly Val Glu Phe Val Glu Arg Lys Asp Leu Ile His Ser Phe Leu
            100                 105                 110

Tyr Ile Tyr Tyr Val His Trp Ser Ile Ser Thr Ala Asp Leu Pro Val
        115                 120                 125

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

Lys Pro Pro Asp Ala Pro Ile Val Val Ser Tyr Val Gly Asp His Gln
145                 150                 155                 160

Ala Leu Val His Arg Pro Gly Met Val Arg Phe Arg Glu Asn Trp Gln
                165                 170                 175

Lys Asn Leu Thr Asp Ala Lys Tyr Ser Phe Met Glu Ser Phe Pro Phe
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180 185 190

Leu Phe Asn Arg Val
195

<210> 635
<211> 695
<212> PRT
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<223> /note="Gene Symbol: AKAP17A; "

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A kinase (PRKA) anchor prt 17A; "

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

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

Ser Val Ala Leu Pro Gln Leu Lys Gln Pro Gly Lys Ser Ile Ser Asn
35 40 45

Trp Glu Val Met Glu Arg Leu Lys Gly Met Val Gln Asn His Gln Phe
50 55 60

Ser Thr Leu Arg Ile Ser Lys Ser Thr Met Asp Phe Ile Arg Phe Glu
65 70 75 80

Gly Glu Val Glu Asn Lys Ser Leu Val Lys Ser Phe Leu Ala Cys Leu
85 90 95

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

Arg Ala Ala Glu Phe Lys Ile Asp Phe Pro Thr Arg His Asp Trp Asp
115 120 125

Ser Phe Phe Arg Asp Ala Lys Asp Met Asn Glu Thr Leu Pro Gly Glu
130 135 140

Arg Pro Asp Thr Ile His Leu Glu Gly Leu Pro Cys Lys Trp Phe Ala
145 150 155 160

Leu Lys Glu Ser Gly Ser Glu Lys Pro Ser Glu Asp Val Leu Val Lys
165 170 175

Val Phe Glu Lys Phe Gly Glu Ile Arg Asn Val Asp Ile Pro Met Leu
180 185 190

Asp Pro Tyr Arg Glu Glu Met Thr Gly Arg Asn Phe His Thr Phe Ser
195 200 205

Phe Gly Gly His Leu Asn Phe Glu Ala Tyr Val Gln Tyr Arg Glu Tyr
210 215 220

Met Gly Phe Ile Gln Ala Met Ser Ala Leu Arg Gly Met Lys Leu Met
225 230 235 240

Tyr Lys Gly Glu Asp Gly Lys Ala Val Ala Cys Asn Ile Lys Val Ser
245 250 255

Phe Asp Ser Thr Lys His Leu Ser Asp Ala Ser Ile Lys Lys Arg Gln
260 265 270

Leu Glu Arg Gln Lys Leu Gln Glu Leu Glu Gln Gln Arg Glu Glu Gln
275 280 285

Lys Arg Arg Glu Lys Glu Ala Glu Glu Arg Gln Arg Ala Glu Glu Arg
290 295 300

Lys Gln Lys Glu Leu Glu Glu Leu Glu Arg Glu Arg Lys Arg Glu Glu
305 310 315 320

```
Lys Leu Arg Lys Arg Glu Gln Lys Gln Arg Asp Arg Glu Leu Arg Arg
                325                 330                 335

Asn Gln Lys Lys Leu Glu Lys Leu Gln Ala Glu Glu Gln Lys Gln Leu
            340                 345                 350

Gln Glu Lys Ile Lys Leu Glu Glu Arg Lys Leu Leu Leu Ala Gln Arg
        355                 360                 365

Asn Leu Gln Ser Ile Arg Leu Ile Ala Glu Leu Leu Ser Arg Ala Lys
    370                 375                 380

Ala Val Lys Leu Arg Glu Gln Glu Gln Lys Glu Glu Lys Leu Arg Leu
385                 390                 395                 400

Gln Gln Gln Glu Glu Arg Arg Arg Leu Gln Glu Ala Glu Leu Arg Arg
                405                 410                 415

Val Glu Glu Glu Lys Glu Arg Ala Leu Gly Leu Gln Arg Lys Glu Arg
            420                 425                 430

Glu Leu Arg Glu Arg Leu Leu Ser Ile Leu Leu Ser Lys Lys Pro Asp
        435                 440                 445

Asp Ser His Thr His Asp Glu Leu Gly Val Ala His Ala Asp Leu Leu
    450                 455                 460

Gln Pro Val Leu Asp Ile Leu Gln Thr Val Ser Ser Gly Cys Val Ser
465                 470                 475                 480

Ala Thr Thr Leu His Pro Leu Gly Gly Gln Pro Pro Ala Gly Ala Pro
                485                 490                 495

Lys Glu Ser Pro Ala His Pro Glu Ala Asp Gly Ala Pro Lys Ser Val
            500                 505                 510

Asn Gly Ser Val Ala Glu Glu Ala Pro Cys Lys Glu Val Gln Ser Ser
        515                 520                 525

Cys Arg Val Val Pro Glu Asp Gly Ser Pro Glu Lys Arg Cys Pro Gly
    530                 535                 540

Gly Val Leu Ser Cys Ile Pro Asp Asn Asn Gln Gln Pro Lys Gly Ile
```

```
545                 550                 555                 560

Pro Ala Cys Glu Gln Asn Val Ser Arg Lys Asp Thr Arg Ser Glu Gln
                565                 570                 575

Asp Lys Cys Asn Arg Glu Pro Ser Lys Gly Arg Gly Arg Ala Thr Gly
            580                 585                 590

Asp Gly Leu Ala Asp Arg His Lys Arg Glu Arg Ser Arg Ala Arg Arg
        595                 600                 605

Ala Ser Ser Arg Glu Asp Gly Arg Pro Arg Lys Glu Arg Arg Pro His
    610                 615                 620

Lys Lys His Ala Tyr Lys Asp Asp Ser Pro Arg Arg Arg Ser Thr Ser
625                 630                 635                 640

Pro Asp His Thr Arg Ser Arg Arg Ser His Ser Lys Asp Arg His Arg
                645                 650                 655

Arg Glu Arg Ser Arg Glu Arg Arg Gly Ser Ala Ser Arg Lys His Ser
            660                 665                 670

Arg His Arg Arg Arg Ser Glu Arg Ser Arg Ser Arg Ser Pro Ser Arg
        675                 680                 685

His Arg Ser Thr Trp Asn Arg
    690                 695


<210> 636
<211> 446
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<223> /note="Gene Symbol: AKAP17A; "

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      A kinase (PRKA) anchor prt 17A; "
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<400> 636
Met Ala Ala Ala Thr Ile Val His Asp Thr Ser Glu Ala Val Glu Leu
1   5   10   15

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

Ser Val Ala Leu Pro Gln Leu Lys Gln Pro Gly Lys Ser Ile Ser Asn
        35   40   45

Trp Glu Val Met Glu Arg Leu Lys Gly Met Val Gln Asn His Gln Phe
    50   55   60

Ser Thr Leu Arg Ile Ser Lys Ser Thr Met Asp Phe Ile Arg Phe Glu
65   70   75   80

Gly Glu Val Glu Asn Lys Ser Leu Val Lys Ser Phe Leu Ala Cys Leu
                85   90   95

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

Arg Ala Ala Glu Phe Lys Ile Asp Phe Pro Thr Arg His Asp Trp Asp
        115   120   125

Ser Phe Phe Arg Asp Ala Lys Asp Met Asn Glu Thr Leu Pro Gly Glu
    130   135   140

Arg Pro Asp Thr Ile His Leu Glu Gly Leu Pro Cys Lys Trp Phe Ala
145   150   155   160

Leu Lys Glu Ser Gly Ser Glu Lys Pro Ser Glu Asp Val Leu Val Lys
                165   170   175

Val Phe Glu Lys Phe Gly Glu Ile Arg Asn Val Asp Ile Pro Met Leu
            180   185   190

Asp Pro Tyr Arg Glu Glu Met Thr Gly Arg Asn Phe His Thr Phe Ser
        195   200   205

```
Phe Gly Gly His Leu Asn Phe Glu Ala Tyr Val Gln Tyr Arg Glu Tyr
    210                 215                 220

Met Gly Phe Ile Gln Ala Met Ser Ala Leu Arg Gly Met Lys Leu Met
225                 230                 235                 240

Tyr Lys Gly Glu Asp Gly Lys Ala Val Ala Cys Asn Ile Lys Val Ser
                245                 250                 255

Phe Asp Ser Thr Lys His Leu Ser Asp Ala Ser Ile Lys Lys Arg Gln
            260                 265                 270

Leu Glu Arg Gln Lys Leu Gln Glu Leu Glu Gln Gln Arg Glu Glu Gln
        275                 280                 285

Lys Arg Arg Glu Lys Glu Ala Glu Glu Arg Gln Arg Ala Glu Glu Arg
    290                 295                 300

Lys Gln Lys Glu Leu Glu Glu Leu Glu Arg Glu Arg Lys Arg Glu Glu
305                 310                 315                 320

Lys Leu Arg Lys Arg Glu Gln Lys Gln Arg Asp Arg Glu Leu Arg Arg
                325                 330                 335

Asn Gln Lys Lys Leu Glu Lys Leu Gln Ala Glu Glu Gln Lys Gln Leu
            340                 345                 350

Gln Glu Lys Ile Lys Leu Glu Glu Arg Lys Leu Leu Leu Ala Gln Arg
        355                 360                 365

Asn Leu Gln Ser Ile Arg Leu Ile Ala Glu Leu Leu Ser Arg Ala Lys
    370                 375                 380

Val Pro Gly Gly Ser Leu Cys Ser Arg Gln Pro Arg Pro Gly Cys Pro
385                 390                 395                 400

Gln Cys Pro Pro Leu Lys Cys Gly Arg Arg His Gly Ala Val Ser Pro
                405                 410                 415

Pro Ala Ala Ala Val Ala Thr Lys Pro Ala Leu Met Pro Arg Met Thr
            420                 425                 430

Ala Pro Ser Arg Glu Gly Val Ala Leu Val Cys Arg Ser Arg
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435 440 445

<210> 637
<211> 385
<212> PRT
<213> Homo sapiens

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

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

Ser Val Ala Leu Pro Gln Leu Lys Gln Pro Gly Lys Ser Ile Ser Asn
35 40 45

Trp Glu Val Met Glu Arg Leu Lys Gly Met Val Gln Asn His Gln Phe
50 55 60

Ser Thr Leu Arg Ile Ser Lys Ser Thr Met Asp Phe Ile Arg Phe Glu
65 70 75 80

Gly Glu Val Glu Asn Lys Ser Leu Val Lys Ser Phe Leu Ala Cys Leu
85 90 95

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

```
Arg Ala Ala Glu Phe Lys Ile Asp Phe Pro Thr Arg His Asp Trp Asp
        115                 120                 125

Ser Phe Phe Arg Asp Ala Lys Asp Met Asn Glu Thr Leu Pro Gly Glu
    130                 135                 140

Arg Pro Asp Thr Ile His Leu Glu Gly Leu Pro Cys Lys Trp Phe Ala
145                 150                 155                 160

Leu Lys Glu Ser Gly Ser Glu Lys Pro Ser Glu Asp Val Leu Val Lys
                165                 170                 175

Val Phe Glu Lys Phe Gly Glu Ile Arg Asn Val Asp Ile Pro Met Leu
            180                 185                 190

Asp Pro Tyr Arg Glu Glu Met Thr Gly Arg Asn Phe His Thr Phe Ser
        195                 200                 205

Phe Gly Gly His Leu Asn Phe Glu Ala Tyr Val Gln Tyr Arg Glu Tyr
    210                 215                 220

Met Gly Phe Ile Gln Ala Met Ser Ala Leu Arg Gly Met Lys Leu Met
225                 230                 235                 240

Tyr Lys Gly Glu Asp Gly Lys Ala Val Ala Cys Asn Ile Lys Val Ser
                245                 250                 255

Phe Asp Ser Thr Lys His Leu Ser Asp Ala Ser Ile Lys Lys Arg Gln
            260                 265                 270

Leu Glu Arg Gln Lys Leu Gln Glu Leu Glu Gln Gln Arg Glu Glu Gln
        275                 280                 285

Lys Arg Arg Glu Lys Glu Ala Glu Glu Arg Gln Arg Ala Glu Glu Arg
    290                 295                 300

Lys Gln Lys Glu Leu Glu Glu Leu Glu Arg Glu Arg Lys Arg Glu Glu
305                 310                 315                 320

Lys Leu Arg Lys Arg Glu Gln Lys Gln Arg Asp Arg Glu Leu Arg Arg
                325                 330                 335
```

```
Asn Gln Lys Lys Leu Glu Lys Leu Gln Ala Glu Glu Gln Lys Gln Leu
            340                 345                 350

Gln Glu Lys Ile Lys Leu Glu Glu Arg Lys Leu Leu Leu Ala Gln Arg
        355                 360                 365

Asn Leu Gln Ser Ile Arg Leu Ile Ala Glu Leu Leu Ser Arg Ala Lys
    370                 375                 380

Leu
385
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<210> 638
<211> 859
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 108; "

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID: Q9Y2D5; "

<220>
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<223> /note="ENSP ID: ENSP00000259318"

<400> 638

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Met Glu Ile Glu Val Ser Val Ala Glu Cys Lys Ser Val Pro Gly Ile
1               5                   10                  15

Thr Ser Thr Pro His Pro Met Asp His Pro Ser Ala Phe Tyr Ser Pro
            20                  25                  30

Pro His Asn Gly Leu Leu Thr Asp His His Glu Ser Leu Asp Asn Asp
        35                  40                  45

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

```
Cys Asp Ser Ala Val Asp Gly Thr Tyr Asn Gly Thr Ser Ser Pro Glu
65                  70                  75                  80

Pro Gly Ala Val Val Leu Val Gly Gly Leu Ser Pro Pro Val His Glu
                85                  90                  95

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

Pro His Ile Glu Leu Ser Asn Ser Ser Pro Asp Pro Met Ala Glu Ala
        115                 120                 125

Glu Arg Thr Asn Gly His Ser Pro Ser Gln Pro Arg Asp Ala Leu Gly
    130                 135                 140

Asp Ser Leu Gln Val Pro Val Ser Pro Ser Ser Thr Thr Ser Ser Arg
145                 150                 155                 160

Cys Ser Ser Arg Asp Gly Glu Phe Thr Leu Thr Thr Leu Lys Lys Glu
                165                 170                 175

Ala Lys Phe Glu Leu Arg Ala Phe His Glu Asp Lys Lys Pro Ser Lys
            180                 185                 190

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

Val Arg Pro Ser Glu Glu Met Leu Glu Leu Glu Lys Glu Arg Arg Glu
    210                 215                 220

Leu Ile Arg Ser Gln Ala Val Lys Lys Asn Pro Gly Ile Ala Ala Lys
225                 230                 235                 240

Trp Trp Asn Pro Pro Gln Glu Lys Thr Ile Glu Glu Gln Leu Asp Glu
                245                 250                 255

Glu His Leu Glu Ser His Lys Lys Tyr Lys Glu Arg Lys Glu Arg Arg
            260                 265                 270

Ala Gln Gln Glu Gln Leu Leu Leu Gln Lys Gln Leu Gln Gln Gln Gln
        275                 280                 285
```

```
Gln Gln Pro Pro Ser Gln Leu Cys Thr Ala Pro Ala Ser Ser His Glu
    290                 295                 300

Arg Ala Ser Met Ile Asp Lys Ala Lys Glu Asp Ile Val Thr Glu Gln
305                 310                 315                 320

Ile Asp Phe Ser Ala Ala Arg Lys Gln Phe Gln Leu Met Glu Asn Ser
                325                 330                 335

Arg Gln Ala Val Ala Lys Gly Gln Ser Thr Pro Arg Leu Phe Ser Ile
            340                 345                 350

Lys Pro Phe Tyr Arg Pro Leu Gly Ser Val Asn Ser Asp Lys Pro Leu
        355                 360                 365

Thr Asn Pro Arg Pro Pro Ser Val Gly Gly Pro Pro Glu Asp Ser Gly
    370                 375                 380

Ala Ser Ala Ala Lys Gly Gln Lys Ser Pro Gly Ala Leu Glu Thr Pro
385                 390                 395                 400

Ser Ala Ala Gly Ser Gln Gly Asn Thr Ala Ser Gln Gly Lys Glu Gly
                405                 410                 415

Pro Tyr Ser Glu Pro Ser Lys Arg Gly Pro Leu Ser Lys Leu Trp Ala
            420                 425                 430

Glu Asp Gly Glu Phe Thr Ser Ala Arg Ala Val Leu Thr Val Val Lys
        435                 440                 445

Asp Asp Asp His Gly Ile Leu Asp Gln Phe Ser Arg Ser Val Asn Val
    450                 455                 460

Ser Leu Thr Gln Glu Glu Leu Asp Ser Gly Leu Asp Glu Leu Ser Val
465                 470                 475                 480

Arg Ser Gln Asp Thr Thr Val Leu Glu Thr Leu Ser Asn Asp Phe Ser
                485                 490                 495

Met Asp Asn Ile Ser Asp Ser Gly Ala Ser Asn Glu Thr Thr Asn Ala
            500                 505                 510
```

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

Thr Asp Asn Pro Ser Glu Gly Arg Gly Glu Gly Val Ser Lys Ser Phe
    530                 535                 540

Ser Asp His Gly Phe Tyr Ser Pro Ser Ser Thr Leu Gly Asp Ser Pro
545                 550                 555                 560

Leu Val Asp Asp Pro Leu Glu Tyr Gln Ala Gly Leu Leu Val Gln Asn
                565                 570                 575

Ala Ile Gln Gln Ala Ile Ala Glu Gln Val Asp Lys Ala Val Ser Lys
            580                 585                 590

Thr Ser Arg Asp Gly Ala Glu Gln Gln Gly Pro Glu Ala Thr Val Glu
        595                 600                 605

Glu Ala Glu Ala Ala Ala Phe Gly Ser Glu Lys Pro Gln Ser Met Phe
    610                 615                 620

Glu Pro Pro Gln Val Ser Ser Pro Val Gln Glu Lys Arg Asp Val Leu
625                 630                 635                 640

Pro Lys Ile Leu Pro Ala Glu Asp Arg Ala Leu Arg Glu Arg Gly Pro
                645                 650                 655

Pro Gln Pro Leu Pro Ala Val Gln Pro Ser Gly Pro Ile Asn Met Glu
            660                 665                 670

Glu Thr Arg Pro Glu Gly Ser Tyr Phe Ser Lys Tyr Ser Glu Ala Ala
        675                 680                 685

Glu Leu Arg Ser Thr Ala Ser Leu Leu Ala Thr Gln Glu Ser Asp Val
    690                 695                 700

Met Val Gly Pro Phe Lys Leu Arg Ser Arg Lys Gln Arg Thr Leu Ser
705                 710                 715                 720

Met Ile Glu Glu Glu Ile Arg Ala Ala Gln Glu Arg Glu Glu Glu Leu
                725                 730                 735

Lys Arg Gln Arg Gln Val Leu Gln Ser Thr Gln Ser Pro Arg Thr Lys
```

```
            740                 745                 750

Asn Ala Pro Ser Leu Pro Ser Arg Thr Cys Tyr Lys Thr Ala Pro Gly
        755                 760                 765

Lys Ile Glu Lys Val Lys Pro Pro Pro Ser Pro Thr Thr Glu Gly Pro
    770                 775                 780

Ser Leu Gln Pro Asp Leu Ala Pro Glu Glu Ala Ala Gly Thr Gln Arg
785                 790                 795                 800

Pro Lys Asn Leu Met Gln Thr Leu Met Glu Asp Tyr Glu Thr His Lys
                805                 810                 815

Ser Lys Arg Arg Glu Arg Met Asp Asp Ser Ser Val Leu Glu Ala Thr
            820                 825                 830

Arg Val Asn Arg Arg Lys Ser Ala Leu Ala Leu Arg Trp Glu Ala Gly
        835                 840                 845

Ile Tyr Ala Asn Gln Glu Glu Glu Asp Asn Glu
    850                 855


<210> 639
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<212> PRT
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<223> /note="Uniprot ID:  Q9Y2D5; "

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<400> 639
Met Arg Trp Pro Gln Pro Gly Ala Ala Ala Arg Leu Pro Pro Glu Ser
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Pro Gly Pro Pro Glu Ser Pro Gly Pro Pro Glu Arg Glu Ala Ala Ala
20 25 30

Ala Arg Arg Trp Thr Gly Ala Glu Pro Gln Asp Cys Ala Pro Gly Ser
35 40 45

Gly Arg Pro Glu Lys Pro Pro Gln Leu Ser Glu Asp Asp Ile Trp Leu
50 55 60

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

Ser Ser Leu Ser Pro Asp His Lys Asn Met Glu Ile Glu Val Ser Val
85 90 95

Ala Glu Cys Lys Ser Val Pro Gly Ile Thr Ser Thr Pro His Pro Met
100 105 110

Asp His Pro Ser Ala Phe Tyr Ser Pro Pro His Asn Gly Leu Leu Thr
115 120 125

Asp His His Glu Ser Leu Asp Asn Asp Val Ala Arg Glu Ile Arg Tyr
130 135 140

Leu Asp Glu Val Leu Glu Ala Asn Cys Cys Asp Ser Ala Val Asp Gly
145 150 155 160

Thr Tyr Asn Gly Thr Ser Ser Pro Glu Pro Gly Ala Val Val Leu Val
165 170 175

Gly Gly Leu Ser Pro Pro Val His Glu Ala Thr Gln Pro Glu Pro Thr
180 185 190

Glu Arg Thr Ala Ser Arg Gln Ala Pro Pro His Ile Glu Leu Ser Asn
195 200 205

Ser Ser Pro Asp Pro Met Ala Glu Ala Glu Arg Thr Asn Gly His Ser
210 215 220

```
Pro Ser Gln Pro Arg Asp Ala Leu Gly Asp Ser Leu Gln Val Pro Val
225                 230                 235                 240

Ser Pro Ser Ser Thr Thr Ser Ser Arg Cys Ser Ser Arg Asp Gly Glu
                245                 250                 255

Phe Thr Leu Thr Thr Leu Lys Lys Glu Ala Lys Phe Glu Leu Arg Ala
            260                 265                 270

Phe His Glu Asp Lys Lys Pro Ser Lys Leu Phe Glu Asp Asp Glu His
        275                 280                 285

Glu Lys Glu Gln Tyr Cys Ile Arg Lys Val Arg Pro Ser Glu Glu Met
    290                 295                 300

Leu Glu Leu Glu Lys Glu Arg Arg Glu Leu Ile Arg Ser Gln Ala Val
305                 310                 315                 320

Lys Lys Asn Pro Gly Ile Ala Ala Lys Trp Trp Asn Pro Pro Gln Glu
                325                 330                 335

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

Lys Tyr Lys Glu Arg Lys Glu Arg Arg Ala Gln Gln Glu Gln Leu Leu
        355                 360                 365

Leu Gln Lys Gln Leu Gln Gln Gln Gln Gln Gln Pro Pro Ser Gln Leu
    370                 375                 380

Cys Thr Ala Pro Ala Ser Ser His Glu Arg Ala Ser Met Ile Asp Lys
385                 390                 395                 400

Ala Lys Glu Asp Ile Val Thr Glu Gln Ile Asp Phe Ser Ala Ala Arg
                405                 410                 415

Lys Gln Phe Gln Leu Met Glu Asn Ser Arg Gln Ala Val Ala Lys Gly
            420                 425                 430

Gln Ser Thr Pro Arg Leu Phe Ser Ile Lys Pro Phe Tyr Arg Pro Leu
        435                 440                 445

Gly Ser Val Asn Ser Asp Lys Pro Leu Thr Asn Pro Arg Pro Pro Ser
```

```
    450                 455                 460

Val Gly Gly Pro Pro Glu Asp Ser Gly Ala Ser Ala Ala Lys Gly Gln
465                 470                 475                 480

Lys Ser Pro Gly Ala Leu Glu Thr Pro Ser Ala Ala Gly Ser Gln Gly
                485                 490                 495

Asn Thr Ala Ser Gln Gly Lys Glu Gly Pro Tyr Ser Glu Pro Ser Lys
            500                 505                 510

Arg Gly Pro Leu Ser Lys Leu Trp Ala Glu Asp Gly Glu Phe Thr Ser
        515                 520                 525

Ala Arg Ala Val Leu Thr Val Val Lys Asp Asp Asp His Gly Ile Leu
    530                 535                 540

Asp Gln Phe Ser Arg Ser Val Asn Val Ser Leu Thr Gln Glu Glu Leu
545                 550                 555                 560

Asp Ser Gly Leu Asp Glu Leu Ser Val Arg Ser Gln Asp Thr Thr Val
                565                 570                 575

Leu Glu Thr Leu Ser Asn Asp Phe Ser Met Asp Asn Ile Ser Asp Ser
            580                 585                 590

Gly Ala Ser Asn Glu Thr Thr Asn Ala Leu Gln Glu Asn Ser Leu Ala
        595                 600                 605

Asp Phe Ser Leu Pro Gln Thr Pro Gln Thr Asp Asn Pro Ser Glu Gly
    610                 615                 620

Arg Gly Glu Gly Val Ser Lys Ser Phe Ser Asp His Gly Phe Tyr Ser
625                 630                 635                 640

Pro Ser Ser Thr Leu Gly Asp Ser Pro Leu Val Asp Asp Pro Leu Glu
                645                 650                 655

Tyr Gln Ala Gly Leu Leu Val Gln Asn Ala Ile Gln Gln Ala Ile Ala
            660                 665                 670

Glu Gln Val Asp Lys Ala Val Ser Lys Thr Ser Arg Asp Gly Ala Glu
        675                 680                 685
```

```
Gln Gln Gly Pro Glu Ala Thr Val Glu Glu Ala Glu Ala Ala Ala Phe
    690                 695                 700

Gly Ser Glu Lys Pro Gln Ser Met Phe Glu Pro Pro Gln Val Ser Ser
705                 710                 715                 720

Pro Val Gln Glu Lys Arg Asp Val Leu Pro Lys Ile Leu Pro Ala Glu
                725                 730                 735

Asp Arg Ala Leu Arg Glu Arg Gly Pro Pro Gln Pro Leu Pro Ala Val
            740                 745                 750

Gln Pro Ser Gly Pro Ile Asn Met Glu Glu Thr Arg Pro Glu Gly Ser
        755                 760                 765

Tyr Phe Ser Lys Tyr Ser Glu Ala Ala Glu Leu Arg Ser Thr Ala Ser
    770                 775                 780

Leu Leu Ala Thr Gln Glu Ser Asp Val Met Val Gly Pro Phe Lys Leu
785                 790                 795                 800

Arg Ser Arg Lys Gln Arg Thr Leu Ser Met Ile Glu Glu Glu Ile Arg
                805                 810                 815

Ala Ala Gln Glu Arg Glu Glu Glu Leu Lys Arg Gln Arg Gln Val Leu
            820                 825                 830

Gln Ser Thr Gln Ser Pro Arg Thr Lys Asn Ala Pro Ser Leu Pro Ser
        835                 840                 845

Arg Thr Cys Tyr Lys Thr Ala Pro Gly Lys Ile Glu Lys Val Lys Pro
    850                 855                 860

Pro Pro Ser Pro Thr Thr Glu Gly Pro Ser Leu Gln Pro Asp Leu Ala
865                 870                 875                 880

Pro Glu Glu Ala Ala Gly Thr Gln Arg Pro Lys Asn Leu Met Gln Thr
                885                 890                 895

Leu Met Glu Asp Tyr Glu Thr His Lys Ser Lys Arg Arg Glu Arg Met
            900                 905                 910
```

Asp Asp Ser Ser Val Leu Glu Ala Thr Arg Val Asn Arg Arg Lys Ser
915 920 925

Ala Leu Ala Leu Arg Trp Glu Ala Gly Ile Tyr Ala Asn Gln Glu Glu
930 935 940

Glu Asp Asn Glu
945

<210> 640
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<220>
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<400> 640
Met Arg Trp Pro Gln Pro Gly Ala Ala Ala Arg Leu Pro Pro Glu Ser
1 5 10 15

Pro Gly Pro Pro Glu Ser Pro Gly Pro Pro Glu Arg Glu Ala Ala Ala
20 25 30

Ala Arg Arg Trp Thr Gly Ala Glu Pro Gln Asp Cys Ala Pro Gly Ser
35 40 45

Gly Arg Pro Glu Lys Pro Pro Gln Leu Ser Glu Asp Asp Ile Trp Leu
50 55 60

Lys Ser Glu Gly Asp Asn Tyr Ser Ala Thr Leu Leu Glu Pro Ala Ala

65 70 75 80

Ser Ser Leu Ser Pro Asp His Lys Asn Met Glu Ile Glu Val Ser Val
85 90 95

Ala Glu Cys Lys Ser Val Pro Gly Ile Thr Ser Thr Pro His Pro Met
100 105 110

Asp His Pro Ser Ala Phe Tyr Ser Pro Pro His Asn Gly Leu Leu Thr
115 120 125

Asp His His Glu Ser Leu Asp Asn Asp Val Ala Arg Glu Ile Arg Tyr
130 135 140

Leu Asp Glu Val Leu Glu Ala Asn Cys Cys Asp Ser Ala Val Asp Gly
145 150 155 160

Thr Tyr Asn Gly Thr Ser Ser Pro Glu Pro Gly Ala Val Val Leu Val
165 170 175

Gly Gly Leu Ser Pro Pro Val His Glu Ala Thr Gln Pro Glu Pro Thr
180 185 190

Glu Arg Thr Ala Ser Arg Gln Ala Pro Pro His Ile Glu Leu Ser Asn
195 200 205

Ser Ser Pro Asp Pro Met Ala Glu Ala Glu Arg Thr Asn Gly His Ser
210 215 220

Pro Ser Gln Pro Arg Asp Ala Leu Gly Asp Ser Leu Gln Val Pro Val
225 230 235 240

Ser Pro Ser Ser Thr Thr Ser Ser Arg Cys Ser Ser Arg Asp Gly Glu
245 250 255

Phe Thr Leu Thr Thr Leu Lys Lys Glu Ala Lys Phe Glu Leu Arg Ala
260 265 270

Phe His Glu Asp Lys Lys Pro Ser Lys Leu Phe Glu Asp Asp Glu His
275 280 285

Glu Lys Glu Gln Tyr Cys Ile Arg Lys Val Arg Pro Ser Glu Glu Met
290 295 300

```
Leu Glu Leu Glu Lys Glu Arg Arg Glu Leu Ile Arg Ser Gln Ala Val
305                 310                 315                 320

Lys Lys Asn Pro Gly Ile Ala Ala Lys Trp Trp Asn Pro Pro Gln Glu
                325                 330                 335

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

Lys Tyr Lys Glu Arg Lys Glu Arg Arg Ala Gln Gln Glu Gln Leu Leu
        355                 360                 365

Leu Gln Lys Gln Leu Gln Gln Gln Gln Gln Gln Pro Pro Ser Gln Leu
    370                 375                 380

Cys Thr Ala Pro Ala Ser Ser His Glu Arg Ala Ser Met Ile Asp Lys
385                 390                 395                 400

Ala Lys Glu Asp Ile Val Thr Glu Gln Ile Asp Phe Ser Ala Ala Arg
                405                 410                 415

Lys Gln Phe Gln Leu Met Glu Asn Ser Arg Gln Ala Val Ala Lys Gly
            420                 425                 430

Gln Ser Thr Pro Arg Leu Phe Ser Ile Lys Pro Phe Tyr Arg Pro Leu
        435                 440                 445

Gly Ser Val Asn Ser Asp Lys Pro Leu Thr Asn Pro Arg Pro Pro Ser
    450                 455                 460

Val Gly Gly Pro Pro Glu Asp Ser Gly Ala Ser Ala Ala Lys Gly Gln
465                 470                 475                 480

Lys Ser Pro Gly Ala Leu Glu Thr Pro Ser Ala Ala Gly Ser Gln Gly
                485                 490                 495

Asn Thr Ala Ser Gln Gly Lys Glu Gly Pro Tyr Ser Glu Pro Ser Lys
            500                 505                 510

Arg Gly Pro Leu Ser Lys Leu Trp Ala Glu Asp Gly Glu Phe Thr Ser
        515                 520                 525
```

```
Ala Arg Ala Val Leu Thr Val Val Lys Asp Asp Asp His Gly Ile Leu
    530                 535                 540

Asp Gln Phe Ser Arg Ser Val Asn Val Ser Leu Thr Gln Glu Glu Leu
545                 550                 555                 560

Asp Ser Gly Leu Asp Glu Leu Ser Val Arg Ser Gln Asp Thr Thr Val
                565                 570                 575

Leu Glu Thr Leu Ser Asn Asp Phe Ser Met Asp Asn Ile Ser Asp Ser
            580                 585                 590

Gly Ala Ser Asn Glu Thr Thr Asn Ala Leu Gln Glu Asn Ser Leu Ala
        595                 600                 605

Asp Phe Ser Leu Pro Gln Thr Pro Gln Thr Asp Asn Pro Ser Glu Gly
    610                 615                 620

Arg Gly Glu Gly Val Ser Lys Ser Phe Ser Asp His Gly Phe Tyr Ser
625                 630                 635                 640

Pro Ser Ser Thr Leu Gly Asp Ser Pro Leu Val Asp Asp Pro Leu Glu
                645                 650                 655

Tyr Gln Ala Gly Leu Leu Val Gln Asn Ala Ile Gln Gln Ala Ile Ala
            660                 665                 670

Glu Gln Val Asp Lys Ala Val Ser Lys Thr Ser Arg Asp Gly Ala Glu
        675                 680                 685

Gln Gln Gly Pro Glu Ala Thr Val Glu Glu Ala Glu Ala Ala Ala Phe
    690                 695                 700

Gly Ser Glu Lys Pro Gln Ser Met Phe Glu Pro Pro Gln Val Ser Ser
705                 710                 715                 720

Pro Val Gln Glu Lys Arg Asp Val Leu Pro Lys Ile Leu Pro Ala Glu
                725                 730                 735

Asp Arg Ala Leu Arg Glu Arg Gly Pro Pro Gln Pro Leu Pro Ala Val
            740                 745                 750
```

Gln Pro Ser Gly Pro Ile Asn Met Glu Glu Thr Arg Pro Glu Gly Ser
        755   760   765

Tyr Phe Ser Lys Tyr Ser Glu Ala Ala Glu Leu Arg Ser Thr Ala Ser
    770   775   780

Leu Leu Ala Thr Gln Glu Ser Asp Val Met Val Gly Pro Phe Lys Leu
785   790   795   800

Arg Ser Arg Lys Gln Arg Thr Leu Ser Met Ile Glu Glu Glu Ile Arg
                805   810   815

Ala Ala Gln Glu Arg Glu Glu Glu Leu Lys Arg Gln Arg Gln Val Leu
            820   825   830

Gln Ser Thr Gln Ser Pro Arg Thr Lys Asn Ala Pro Ser Leu Pro Ser
        835   840   845

Arg Thr Cys Tyr Lys Thr Ala Pro Gly Lys Ile Glu Lys Val Lys Pro
    850   855   860

Pro Pro Ser Pro Thr Thr Glu Gly Pro Ser Leu Gln Pro Asp Leu Ala
865   870   875   880

Pro Glu Glu Ala Ala Gly Thr Gln Arg Pro Lys Asn Leu Met Gln Thr
                885   890   895

Leu Met Glu Asp Tyr Glu Thr His Lys Ser Lys Arg Arg Glu Arg Met
            900   905   910

Asp Asp Ser Ser Tyr Thr Ser Lys Leu Leu Ser Cys Lys Val Thr Ser
        915   920   925

Glu Val Leu Glu Ala Thr Arg Val Asn Arg Arg Lys Ser Ala Leu Ala
    930   935   940

Leu Arg Trp Glu Ala Gly Ile Tyr Ala Asn Gln Glu Glu Glu Asp Asn
945   950   955   960

Glu

<210> 641

<211> 778
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 108; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP2; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 2; "

<220>
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<223> /note="ENSP ID: ENSP00000419268"

<400> 641

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

```
Glu Ala Thr Gln Pro Glu Pro Thr Glu Arg Thr Ala Ser Arg Gln Ala
145                 150                 155                 160

Pro Pro His Ile Glu Leu Ser Asn Ser Ser Pro Asp Pro Met Ala Glu
                165                 170                 175

Ala Glu Arg Thr Asn Gly His Ser Pro Ser Gln Pro Arg Asp Ala Leu
            180                 185                 190

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

Arg Cys Ser Ser Arg Asp Gly Glu Phe Thr Leu Thr Thr Leu Lys Lys
    210                 215                 220

Glu Ala Lys Phe Glu Leu Arg Ala Phe His Glu Asp Lys Lys Pro Ser
225                 230                 235                 240

Lys Leu Phe Glu Asp Asp Glu His Glu Lys Glu Gln Tyr Cys Ile Arg
                245                 250                 255

Lys Val Arg Pro Ser Glu Glu Met Leu Glu Leu Glu Lys Glu Arg Arg
            260                 265                 270

Glu Leu Ile Arg Ser Gln Ala Val Lys Lys Asn Pro Gly Ile Ala Ala
        275                 280                 285

Lys Trp Trp Asn Pro Pro Gln Glu Lys Thr Ile Glu Glu Gln Leu Asp
    290                 295                 300

Glu Glu His Leu Glu Ser His Lys Lys Tyr Lys Glu Arg Lys Glu Arg
305                 310                 315                 320

Arg Ala Gln Gln Glu Gln Leu Leu Leu Gln Lys Gln Leu Gln Gln Gln
                325                 330                 335

Gln Gln Gln Pro Pro Ser Gln Leu Cys Thr Ala Pro Ala Ser Ser His
            340                 345                 350

Glu Arg Ala Ser Met Ile Asp Lys Ala Lys Glu Asp Ile Val Thr Glu
        355                 360                 365
```

```
Gln Ile Asp Phe Ser Ala Ala Arg Lys Gln Phe Gln Leu Met Glu Asn
    370                 375                 380

Ser Arg Gln Ala Val Ala Lys Gly Gln Ser Thr Pro Arg Leu Phe Ser
385                 390                 395                 400

Ile Lys Pro Phe Tyr Arg Pro Leu Gly Ser Val Asn Ser Asp Lys Pro
                405                 410                 415

Leu Thr Asn Pro Arg Pro Pro Ser Val Gly Gly Pro Pro Glu Asp Ser
            420                 425                 430

Gly Ala Ser Ala Ala Lys Gly Gln Lys Ser Pro Gly Ala Leu Glu Thr
        435                 440                 445

Pro Ser Ala Ala Gly Ser Gln Gly Asn Thr Ala Ser Gln Gly Lys Glu
    450                 455                 460

Gly Pro Tyr Ser Glu Pro Ser Lys Arg Gly Pro Leu Ser Lys Leu Trp
465                 470                 475                 480

Ala Glu Asp Gly Glu Phe Thr Ser Ala Arg Ala Val Leu Thr Val Val
                485                 490                 495

Lys Asp Asp Asp His Gly Ile Leu Asp Gln Phe Ser Arg Ser Val Asn
            500                 505                 510

Val Ser Leu Thr Gln Glu Glu Leu Asp Ser Gly Leu Asp Glu Leu Ser
        515                 520                 525

Val Arg Ser Gln Asp Thr Thr Val Leu Glu Thr Leu Ser Asn Asp Phe
    530                 535                 540

Ser Met Asp Asn Ile Ser Asp Ser Gly Ala Ser Asn Glu Thr Thr Asn
545                 550                 555                 560

Ala Leu Gln Glu Asn Ser Leu Ala Asp Phe Ser Leu Pro Gln Thr Pro
                565                 570                 575

Gln Thr Asp Asn Pro Ser Glu Gly Arg Gly Glu Gly Val Ser Lys Ser
            580                 585                 590

Phe Ser Asp His Gly Phe Tyr Ser Pro Ser Ser Thr Leu Gly Asp Ser
```

595 600 605

Pro Leu Val Asp Asp Pro Leu Glu Tyr Gln Ala Gly Leu Leu Val Gln
610 615 620

Asn Ala Ile Gln Gln Ala Ile Ala Glu Gln Val Asp Lys Ala Val Ser
625 630 635 640

Lys Thr Ser Arg Asp Gly Ala Glu Gln Gln Gly Pro Glu Ala Thr Val
645 650 655

Glu Glu Ala Glu Ala Ala Ala Phe Gly Ser Glu Lys Pro Gln Ser Met
660 665 670

Phe Glu Pro Pro Gln Val Ser Ser Pro Val Gln Glu Lys Arg Asp Val
675 680 685

Leu Pro Lys Ile Leu Pro Ala Glu Asp Arg Ala Leu Arg Glu Arg Gly
690 695 700

Pro Pro Gln Pro Leu Pro Ala Val Gln Pro Ser Gly Pro Ile Asn Met
705 710 715 720

Glu Glu Thr Arg Pro Glu Gly Ser Tyr Phe Ser Lys Tyr Ser Glu Ala
725 730 735

Ala Glu Leu Arg Ser Thr Ala Ser Leu Leu Ala Thr Gln Glu Ser Asp
740 745 750

Val Met Val Gly Pro Phe Lys Leu Arg Ser Arg Lys Gln Arg Thr Leu
755 760 765

Ser Met Ile Glu Glu Glu Ile Arg Ala Ala
770 775

<210> 642
<211> 54
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 108; "

<220>

<221> source
<223> /note="Gene Symbol: AKAP2; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 2; "

<220>
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<223> /note="ENSP ID: ENSP00000419364"

<400> 642
Met Arg Trp Pro Gln Pro Gly Ala Ala Ala Arg Leu Pro Pro Glu Ser
1 5 10 15

Pro Gly Pro Pro Glu Ser Pro Gly Pro Pro Glu Arg Glu Ala Ala Ala
20 25 30

Ala Arg Arg Trp Thr Gly Ala Glu Pro Gln Asp Cys Ala Pro Gly Ser
35 40 45

Gly Arg Pro Glu Gly Lys
50

<210> 643
<211> 853
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 109; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP3; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 3; "

<220>
<221> source
<223> /note="Uniprot ID: O75969; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000228850"

<400> 643
Met Ser Glu Lys Val Asp Trp Leu Gln Ser Gln Asn Gly Val Cys Lys

```
1               5                   10                  15

Val Asp Val Tyr Ser Pro Gly Asp Asn Gln Ala Gln Asp Trp Lys Met
            20                  25                  30

Asp Thr Ser Thr Asp Pro Val Arg Val Leu Ser Trp Leu Arg Arg Asp
        35                  40                  45

Leu Glu Lys Ser Thr Ala Glu Phe Gln Asp Val Arg Phe Lys Pro Gly
    50                  55                  60

Glu Ser Phe Gly Gly Glu Thr Ser Asn Ser Gly Asp Pro His Lys Gly
65                  70                  75                  80

Phe Ser Val Asp Tyr Tyr Asn Thr Thr Thr Lys Gly Thr Pro Glu Arg
                85                  90                  95

Leu His Phe Glu Met Thr His Lys Glu Ile Pro Cys Gln Gly Pro Arg
            100                 105                 110

Ala Gln Leu Gly Asn Gly Ser Ser Val Asp Glu Val Ser Phe Tyr Ala
        115                 120                 125

Asn Arg Leu Thr Asn Leu Val Ile Ala Met Ala Arg Lys Glu Ile Asn
    130                 135                 140

Glu Lys Ile Asp Gly Ser Glu Asn Lys Cys Val Tyr Gln Ser Leu Tyr
145                 150                 155                 160

Met Gly Asn Glu Pro Thr Pro Thr Lys Ser Leu Ser Lys Ile Ala Ser
                165                 170                 175

Glu Leu Val Asn Glu Thr Val Ser Ala Cys Ser Arg Asn Ala Ala Pro
            180                 185                 190

Asp Lys Ala Pro Gly Ser Gly Asp Arg Val Ser Gly Ser Ser Gln Ser
        195                 200                 205

Pro Pro Asn Leu Lys Tyr Lys Ser Thr Leu Lys Ile Lys Glu Ser Thr
    210                 215                 220

Lys Glu Arg Gln Gly Pro Asp Asp Lys Pro Pro Ser Lys Lys Ser Phe
225                 230                 235                 240
```

```
Phe Tyr Lys Glu Val Phe Glu Ser Arg Asn Gly Asp Tyr Ala Arg Glu
                245                 250                 255

Gly Gly Arg Phe Phe Pro Arg Glu Arg Lys Arg Phe Arg Gly Gln Glu
            260                 265                 270

Arg Pro Asp Asp Phe Thr Ala Ser Val Ser Glu Gly Ile Met Thr Tyr
        275                 280                 285

Ala Asn Ser Val Val Ser Asp Met Met Val Ser Ile Met Lys Thr Leu
    290                 295                 300

Lys Ile Gln Val Lys Asp Thr Thr Ile Ala Thr Ile Leu Leu Lys Lys
305                 310                 315                 320

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

Phe Leu Arg Asn Leu His Ser Val Thr Gly Thr Leu Met Thr Asp Thr
            340                 345                 350

Gln Phe Val Ser Ala Val Lys Arg Thr Val Phe Ser His Gly Ser Gln
        355                 360                 365

Lys Ala Thr Asp Ile Met Asp Ala Met Leu Arg Lys Leu Tyr Asn Val
    370                 375                 380

Met Phe Ala Lys Lys Val Pro Glu His Val Arg Lys Ala Gln Asp Lys
385                 390                 395                 400

Ala Glu Ser Tyr Ser Leu Ile Ser Met Lys Gly Met Gly Asp Pro Lys
                405                 410                 415

Asn Arg Asn Val Asn Phe Ala Met Lys Ser Glu Thr Lys Leu Arg Glu
            420                 425                 430

Lys Met Tyr Ser Glu Pro Lys Ser Glu Glu Glu Thr Cys Ala Lys Thr
        435                 440                 445

Leu Gly Glu His Ile Ile Lys Glu Gly Leu Thr Leu Trp His Lys Thr
    450                 455                 460
```

```
Gln Gln Lys Glu Cys Lys Ser Leu Gly Phe Gln His Ala Ala Phe Glu
465                 470                 475                 480

Ala Pro Asn Thr Gln Arg Lys Pro Ala Ser Asp Ile Ser Phe Glu Tyr
                485                 490                 495

Pro Glu Asp Ile Gly Asn Leu Ser Leu Pro Pro Tyr Pro Pro Glu Lys
            500                 505                 510

Pro Glu Asn Phe Met Tyr Asp Ser Asp Ser Trp Ala Glu Asp Leu Ile
        515                 520                 525

Val Ser Ala Leu Leu Leu Ile Gln Tyr His Leu Ala Gln Gly Gly Arg
    530                 535                 540

Arg Asp Ala Arg Ser Phe Val Glu Ala Ala Gly Thr Thr Asn Phe Pro
545                 550                 555                 560

Ala Asn Glu Pro Pro Val Ala Pro Asp Glu Ser Cys Leu Lys Ser Ala
                565                 570                 575

Pro Ile Val Gly Asp Gln Glu Gln Ala Glu Lys Lys Asp Leu Arg Ser
            580                 585                 590

Val Phe Phe Asn Phe Ile Arg Asn Leu Leu Ser Glu Thr Ile Phe Lys
        595                 600                 605

Arg Asp Gln Ser Pro Glu Pro Lys Val Pro Glu Gln Pro Val Lys Glu
    610                 615                 620

Asp Arg Lys Leu Cys Glu Arg Pro Leu Ala Ser Ser Pro Pro Arg Leu
625                 630                 635                 640

Tyr Glu Asp Asp Glu Thr Pro Gly Ala Leu Ser Gly Leu Thr Lys Met
                645                 650                 655

Ala Val Ser Gln Ile Asp Gly His Met Ser Gly Gln Met Val Glu His
            660                 665                 670

Leu Met Asn Ser Val Met Lys Leu Cys Val Ile Ile Ala Lys Ser Cys
        675                 680                 685
```

```
Asp Ala Ser Leu Ala Glu Leu Gly Asp Asp Lys Ser Gly Asp Ala Ser
    690                 695                 700

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

Lys Gly Thr Gly Ser Ala Glu Ala Val Leu Gln Asn Ala Tyr Gln Ala
                725                 730                 735

Ile His Asn Glu Met Arg Gly Thr Ser Gly Gln Pro Pro Glu Gly Cys
            740                 745                 750

Ala Ala Pro Thr Val Ile Val Ser Asn His Asn Leu Thr Asp Thr Val
        755                 760                 765

Gln Asn Lys Gln Leu Gln Ala Val Leu Gln Trp Val Ala Ala Ser Glu
    770                 775                 780

Leu Asn Val Pro Ile Leu Tyr Phe Ala Gly Asp Asp Glu Gly Ile Gln
785                 790                 795                 800

Glu Lys Leu Leu Gln Leu Ser Ala Ala Ala Val Asp Lys Gly Cys Ser
                805                 810                 815

Val Gly Glu Val Leu Gln Ser Val Leu Arg Tyr Glu Lys Glu Arg Gln
            820                 825                 830

Leu Asn Glu Ala Val Gly Asn Val Thr Pro Leu Gln Leu Leu Asp Trp
        835                 840                 845

Leu Met Val Asn Leu
    850


<210> 644
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 109; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP3; "
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<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 3; "

<220>
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<223> /note="ENSP ID: ENSP00000439382"

<400> 644
Met Ser Glu Lys Val Asp Trp Leu Gln Ser Gln Asn Gly Val Cys Lys
1 5 10 15

Val Asp Val Tyr Ser Pro Gly Asp Asn Gln Ala Gln Asp Trp Lys Met
20 25 30

Asp Thr Ser Thr Asp Pro Val Arg Val Leu Ser Trp Leu Arg Arg Asp
35 40 45

Leu Glu Lys Ser Thr Ala Glu Phe Gln Asp Val Arg Phe Lys Pro Gly
50 55 60

Glu Ser Phe Gly Gly Glu Thr Ser Asn Ser Gly Asp Pro His Lys Gly
65 70 75 80

Phe Ser Val Asp Tyr Tyr Asn Thr Thr Thr Lys Gly Thr Pro Glu Arg
85 90 95

<210> 645
<211> 853
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 109; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP3; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 3; "

<220>
<221> source
<223> /note="Uniprot ID: O75969; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000440994"

<400> 645
Met Ser Glu Lys Val Asp Trp Leu Gln Ser Gln Asn Gly Val Cys Lys
1 5 10 15

Val Asp Val Tyr Ser Pro Gly Asp Asn Gln Ala Gln Asp Trp Lys Met
20 25 30

Asp Thr Ser Thr Asp Pro Val Arg Val Leu Ser Trp Leu Arg Arg Asp
35 40 45

Leu Glu Lys Ser Thr Ala Glu Phe Gln Asp Val Arg Phe Lys Pro Gly
50 55 60

Glu Ser Phe Gly Gly Glu Thr Ser Asn Ser Gly Asp Pro His Lys Gly
65 70 75 80

Phe Ser Val Asp Tyr Tyr Asn Thr Thr Thr Lys Gly Thr Pro Glu Arg
85 90 95

Leu His Phe Glu Met Thr His Lys Glu Ile Pro Cys Gln Gly Pro Arg
100 105 110

Ala Gln Leu Gly Asn Gly Ser Ser Val Asp Glu Val Ser Phe Tyr Ala
115 120 125

Asn Arg Leu Thr Asn Leu Val Ile Ala Met Ala Arg Lys Glu Ile Asn
130 135 140

Glu Lys Ile Asp Gly Ser Glu Asn Lys Cys Val Tyr Gln Ser Leu Tyr
145 150 155 160

Met Gly Asn Glu Pro Thr Pro Thr Lys Ser Leu Ser Lys Ile Ala Ser
165 170 175

Glu Leu Val Asn Glu Thr Val Ser Ala Cys Ser Arg Asn Ala Ala Pro
180 185 190

Asp Lys Ala Pro Gly Ser Gly Asp Arg Val Ser Gly Ser Ser Gln Ser
195 200 205

Pro Pro Asn Leu Lys Tyr Lys Ser Thr Leu Lys Ile Lys Glu Ser Thr

```
    210                 215                 220

Lys Glu Arg Gln Gly Pro Asp Asp Lys Pro Pro Ser Lys Lys Ser Phe
225                 230                 235                 240

Phe Tyr Lys Glu Val Phe Glu Ser Arg Asn Gly Asp Tyr Ala Arg Glu
                245                 250                 255

Gly Gly Arg Phe Phe Pro Arg Glu Arg Lys Arg Phe Arg Gly Gln Glu
            260                 265                 270

Arg Pro Asp Asp Phe Thr Ala Ser Val Ser Glu Gly Ile Met Thr Tyr
        275                 280                 285

Ala Asn Ser Val Val Ser Asp Met Met Val Ser Ile Met Lys Thr Leu
    290                 295                 300

Lys Ile Gln Val Lys Asp Thr Thr Ile Ala Thr Ile Leu Leu Lys Lys
305                 310                 315                 320

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

Phe Leu Arg Asn Leu His Ser Val Thr Gly Thr Leu Met Thr Asp Thr
            340                 345                 350

Gln Phe Val Ser Ala Val Lys Arg Thr Val Phe Ser His Gly Ser Gln
        355                 360                 365

Lys Ala Thr Asp Ile Met Asp Ala Met Leu Arg Lys Leu Tyr Asn Val
    370                 375                 380

Met Phe Ala Lys Lys Val Pro Glu His Val Arg Lys Ala Gln Asp Lys
385                 390                 395                 400

Ala Glu Ser Tyr Ser Leu Ile Ser Met Lys Gly Met Gly Asp Pro Lys
                405                 410                 415

Asn Arg Asn Val Asn Phe Ala Met Lys Ser Glu Thr Lys Leu Arg Glu
            420                 425                 430

Lys Met Tyr Ser Glu Pro Lys Ser Glu Glu Glu Thr Cys Ala Lys Thr
        435                 440                 445
```

```
Leu Gly Glu His Ile Ile Lys Glu Gly Leu Thr Leu Trp His Lys Thr
    450                 455                 460

Gln Gln Lys Glu Cys Lys Ser Leu Gly Phe Gln His Ala Ala Phe Glu
465                 470                 475                 480

Ala Pro Asn Thr Gln Arg Lys Pro Ala Ser Asp Ile Ser Phe Glu Tyr
                485                 490                 495

Pro Glu Asp Ile Gly Asn Leu Ser Leu Pro Pro Tyr Pro Pro Glu Lys
            500                 505                 510

Pro Glu Asn Phe Met Tyr Asp Ser Asp Ser Trp Ala Glu Asp Leu Ile
        515                 520                 525

Val Ser Ala Leu Leu Leu Ile Gln Tyr His Leu Ala Gln Gly Gly Arg
    530                 535                 540

Arg Asp Ala Arg Ser Phe Val Glu Ala Ala Gly Thr Thr Asn Phe Pro
545                 550                 555                 560

Ala Asn Glu Pro Pro Val Ala Pro Asp Glu Ser Cys Leu Lys Ser Ala
                565                 570                 575

Pro Ile Val Gly Asp Gln Glu Gln Ala Glu Lys Lys Asp Leu Arg Ser
            580                 585                 590

Val Phe Phe Asn Phe Ile Arg Asn Leu Leu Ser Glu Thr Ile Phe Lys
        595                 600                 605

Arg Asp Gln Ser Pro Glu Pro Lys Val Pro Glu Gln Pro Val Lys Glu
    610                 615                 620

Asp Arg Lys Leu Cys Glu Arg Pro Leu Ala Ser Ser Pro Pro Arg Leu
625                 630                 635                 640

Tyr Glu Asp Asp Glu Thr Pro Gly Ala Leu Ser Gly Leu Thr Lys Met
                645                 650                 655

Ala Val Ser Gln Ile Asp Gly His Met Ser Gly Gln Met Val Glu His
            660                 665                 670
```

```
Leu Met Asn Ser Val Met Lys Leu Cys Val Ile Ile Ala Lys Ser Cys
        675                 680                 685

Asp Ala Ser Leu Ala Glu Leu Gly Asp Asp Lys Ser Gly Asp Ala Ser
    690                 695                 700

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

Lys Gly Thr Gly Ser Ala Glu Ala Val Leu Gln Asn Ala Tyr Gln Ala
                725                 730                 735

Ile His Asn Glu Met Arg Gly Thr Ser Gly Gln Pro Pro Glu Gly Cys
            740                 745                 750

Ala Ala Pro Thr Val Ile Val Ser Asn His Asn Leu Thr Asp Thr Val
        755                 760                 765

Gln Asn Lys Gln Leu Gln Ala Val Leu Gln Trp Val Ala Ala Ser Glu
    770                 775                 780

Leu Asn Val Pro Ile Leu Tyr Phe Ala Gly Asp Asp Glu Gly Ile Gln
785                 790                 795                 800

Glu Lys Leu Leu Gln Leu Ser Ala Ala Ala Val Asp Lys Gly Cys Ser
                805                 810                 815

Val Gly Glu Val Leu Gln Ser Val Leu Arg Tyr Glu Lys Glu Arg Gln
            820                 825                 830

Leu Asn Glu Ala Val Gly Asn Val Thr Pro Leu Gln Leu Leu Asp Trp
        835                 840                 845

Leu Met Val Asn Leu
    850


<210> 646
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 109; "
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<220>
<221> source
<223> /note="Gene Symbol: AKAP3; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442376"

<400> 646

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Met Ser Glu Lys Val Asp Trp Leu Gln Ser Gln Asn Gly Val Cys Lys
1               5                  10                  15

Val Asp Val Tyr Ser Pro Gly Asp Asn Gln Ala Gln Asp Trp Lys Met
            20                  25                  30

Asp Thr Ser Thr Asp Pro Val Arg Val Leu Ser Trp Leu Arg Arg Asp
        35                  40                  45

Leu Glu Lys Ser Thr Ala Glu Phe Gln Asp Val Arg Phe Lys Pro Gly
    50                  55                  60

Glu Ser Phe Gly Gly Glu Thr Ser Asn Ser Gly Asp Pro His Lys Gly
65                  70                  75                  80

Phe Ser Val Asp Tyr Tyr Asn Thr Thr Thr Lys Gly Thr Pro Glu Arg
                85                  90                  95

Leu His Phe Glu Met Thr His Lys Glu Ile Pro Cys Gln Gly Pro Arg
            100                 105                 110

Ala Gln Leu Gly Asn Gly Ser Ser Val Asp Glu Val Ser Phe Tyr Ala
        115                 120                 125

Asn Arg Leu Thr Asn Leu Val Ile Ala Met Ala Arg Lys Glu Ile Asn
    130                 135                 140

Glu Lys Ile Asp Gly Ser Glu Asn Lys Cys Val Tyr Gln Ser Leu Tyr
145                 150                 155                 160

Met
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<210> 647
<211> 854
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 110; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP4; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q5JQC9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000351327"

<400> 647
Met Met Ala Tyr Ser Asp Thr Thr Met Met Ser Asp Asp Ile Asp Trp
1   5   10   15

Leu Arg Ser His Arg Gly Val Cys Lys Val Asp Leu Tyr Asn Pro Glu
            20   25   30

Gly Gln Gln Asp Gln Asp Arg Lys Val Ile Cys Phe Val Asp Val Ser
        35   40   45

Thr Leu Asn Val Glu Asp Lys Asp Tyr Lys Asp Ala Ala Ser Ser Ser
    50   55   60

Ser Glu Gly Asn Leu Asn Leu Gly Ser Leu Glu Glu Lys Glu Ile Ile
65   70   75   80

Val Ile Lys Asp Thr Glu Lys Lys Asp Gln Ser Lys Thr Glu Gly Ser
                85   90   95

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

```
Trp Leu Leu Ser Asp Leu Gln Lys Tyr Ala Leu Gly Phe Gln His Ala
        115                 120                 125

Leu Ser Pro Ser Thr Ser Thr Cys Lys His Lys Val Gly Asp Thr Glu
    130                 135                 140

Gly Glu Tyr His Arg Ala Ser Ser Glu Asn Cys Tyr Ser Val Tyr Ala
145                 150                 155                 160

Asp Gln Val Asn Ile Asp Tyr Leu Met Asn Arg Pro Gln Asn Leu Arg
                165                 170                 175

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

Ala Pro Pro Ala Lys Pro Pro Ser Thr Gln Arg Ala Val Ile Ser Pro
        195                 200                 205

Asp Gly Glu Cys Ser Ile Asp Asp Leu Ser Phe Tyr Val Asn Arg Leu
    210                 215                 220

Ser Ser Leu Val Ile Gln Met Ala His Lys Glu Ile Lys Glu Lys Leu
225                 230                 235                 240

Glu Gly Lys Ser Lys Cys Leu His His Ser Ile Cys Pro Ser Pro Gly
                245                 250                 255

Asn Lys Glu Arg Ile Ser Pro Arg Thr Pro Ala Ser Lys Ile Ala Ser
            260                 265                 270

Glu Met Ala Tyr Glu Ala Val Glu Leu Thr Ala Ala Glu Met Arg Gly
        275                 280                 285

Thr Gly Glu Glu Ser Arg Glu Gly Gly Gln Lys Ser Phe Leu Tyr Ser
    290                 295                 300

Glu Leu Ser Asn Lys Ser Lys Ser Gly Asp Lys Gln Met Ser Gln Arg
305                 310                 315                 320

Glu Ser Lys Glu Phe Ala Asp Ser Ile Ser Lys Gly Leu Met Val Tyr
                325                 330                 335

Ala Asn Gln Val Ala Ser Asp Met Met Val Ser Leu Met Lys Thr Leu
```

```
            340                 345                 350

Lys Val His Ser Ser Gly Lys Pro Ile Pro Ala Ser Val Val Leu Lys
        355                 360                 365

Arg Val Leu Leu Arg His Thr Lys Glu Ile Val Ser Asp Leu Ile Asp
    370                 375                 380

Ser Cys Met Lys Asn Leu His Asn Ile Thr Gly Val Leu Met Thr Asp
385                 390                 395                 400

Ser Asp Phe Val Ser Ala Val Lys Arg Asn Leu Phe Asn Gln Trp Lys
                405                 410                 415

Gln Asn Ala Thr Asp Ile Met Glu Ala Met Leu Lys Arg Leu Val Ser
            420                 425                 430

Ala Leu Ile Gly Glu Glu Lys Glu Thr Lys Ser Gln Ser Leu Ser Tyr
        435                 440                 445

Ala Ser Leu Lys Ala Gly Ser His Asp Pro Lys Cys Arg Asn Gln Ser
    450                 455                 460

Leu Glu Phe Ser Thr Met Lys Ala Glu Met Lys Glu Arg Asp Lys Gly
465                 470                 475                 480

Lys Met Lys Ser Asp Pro Cys Lys Ser Leu Thr Ser Ala Glu Lys Val
                485                 490                 495

Gly Glu His Ile Leu Lys Glu Gly Leu Thr Ile Trp Asn Gln Lys Gln
            500                 505                 510

Gly Asn Ser Cys Lys Val Ala Thr Lys Ala Cys Ser Asn Lys Asp Glu
        515                 520                 525

Lys Gly Glu Lys Ile Asn Ala Ser Thr Asp Ser Leu Ala Lys Asp Leu
    530                 535                 540

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

Lys Gly Lys Asp Thr Cys Glu Glu Asp Cys Pro Gly Ser Thr Met Gly
                565                 570                 575
```

```
Tyr Met Ala Gln Ser Thr Gln Tyr Glu Lys Cys Gly Gly Gly Gln Ser
            580                 585                 590

Ala Lys Ala Leu Ser Val Lys Gln Leu Glu Ser His Arg Ala Pro Gly
        595                 600                 605

Pro Ser Thr Cys Gln Lys Glu Asn Gln His Leu Asp Ser Gln Lys Met
    610                 615                 620

Asp Met Ser Asn Ile Val Leu Met Leu Ile Gln Lys Leu Leu Asn Glu
625                 630                 635                 640

Asn Pro Phe Lys Cys Glu Asp Pro Cys Glu Gly Glu Asn Lys Cys Ser
                645                 650                 655

Glu Pro Arg Ala Ser Lys Ala Ala Ser Met Ser Asn Arg Ser Asp Lys
            660                 665                 670

Ala Glu Glu Gln Cys Gln Glu His Gln Glu Leu Asp Cys Thr Ser Gly
        675                 680                 685

Met Lys Gln Ala Asn Gly Gln Phe Ile Asp Lys Leu Val Glu Ser Val
    690                 695                 700

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

Leu Ala Glu Leu Glu Glu Gln Ala Ala Ser Ala Asn Lys Pro Asn Phe
                725                 730                 735

Arg Gly Thr Arg Cys Ile His Ser Gly Ala Met Pro Gln Asn Tyr Gln
            740                 745                 750

Asp Ser Leu Gly His Glu Val Ile Val Asn Asn Gln Cys Ser Thr Asn
        755                 760                 765

Ser Leu Gln Lys Gln Leu Gln Ala Val Leu Gln Trp Ile Ala Ala Ser
    770                 775                 780

Gln Phe Asn Val Pro Met Leu Tyr Phe Met Gly Asp Lys Asp Gly Gln
785                 790                 795                 800
```

Leu Glu Lys Leu Pro Gln Val Ser Ala Lys Ala Ala Glu Lys Gly Tyr
805 810 815

Ser Val Gly Gly Leu Leu Gln Glu Val Met Lys Phe Ala Lys Glu Arg
820 825 830

Gln Pro Asp Glu Ala Val Gly Lys Val Ala Arg Lys Gln Leu Leu Asp
835 840 845

Trp Leu Leu Ala Asn Leu
850

<210> 648
<211> 845
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 110; "

<220>
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<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 4; "

<220>
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<220>
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<400> 648
Met Ser Asp Asp Ile Asp Trp Leu Arg Ser His Arg Gly Val Cys Lys
1 5 10 15

Val Asp Leu Tyr Asn Pro Glu Gly Gln Gln Asp Gln Asp Arg Lys Val
20 25 30

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

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

```
    50                  55                  60

Leu Glu Glu Lys Glu Ile Ile Val Ile Lys Asp Thr Glu Lys Lys Asp
65                  70                  75                  80

Gln Ser Lys Thr Glu Gly Ser Val Cys Leu Phe Lys Gln Ala Pro Ser
                85                  90                  95

Asp Pro Val Ser Val Leu Asn Trp Leu Leu Ser Asp Leu Gln Lys Tyr
            100                 105                 110

Ala Leu Gly Phe Gln His Ala Leu Ser Pro Ser Thr Ser Thr Cys Lys
        115                 120                 125

His Lys Val Gly Asp Thr Glu Gly Glu Tyr His Arg Ala Ser Ser Glu
    130                 135                 140

Asn Cys Tyr Ser Val Tyr Ala Asp Gln Val Asn Ile Asp Tyr Leu Met
145                 150                 155                 160

Asn Arg Pro Gln Asn Leu Arg Leu Glu Met Thr Ala Ala Lys Asn Thr
                165                 170                 175

Asn Asn Asn Gln Ser Pro Ser Ala Pro Pro Ala Lys Pro Pro Ser Thr
            180                 185                 190

Gln Arg Ala Val Ile Ser Pro Asp Gly Glu Cys Ser Ile Asp Asp Leu
        195                 200                 205

Ser Phe Tyr Val Asn Arg Leu Ser Ser Leu Val Ile Gln Met Ala His
    210                 215                 220

Lys Glu Ile Lys Glu Lys Leu Glu Gly Lys Ser Lys Cys Leu His His
225                 230                 235                 240

Ser Ile Cys Pro Ser Pro Gly Asn Lys Glu Arg Ile Ser Pro Arg Thr
                245                 250                 255

Pro Ala Ser Lys Ile Ala Ser Glu Met Ala Tyr Glu Ala Val Glu Leu
            260                 265                 270

Thr Ala Ala Glu Met Arg Gly Thr Gly Glu Glu Ser Arg Glu Gly Gly
        275                 280                 285
```

Gln Lys Ser Phe Leu Tyr Ser Glu Leu Ser Asn Lys Ser Lys Ser Gly
290 295 300

Asp Lys Gln Met Ser Gln Arg Glu Ser Lys Glu Phe Ala Asp Ser Ile
305 310 315 320

Ser Lys Gly Leu Met Val Tyr Ala Asn Gln Val Ala Ser Asp Met Met
325 330 335

Val Ser Leu Met Lys Thr Leu Lys Val His Ser Ser Gly Lys Pro Ile
340 345 350

Pro Ala Ser Val Val Leu Lys Arg Val Leu Leu Arg His Thr Lys Glu
355 360 365

Ile Val Ser Asp Leu Ile Asp Ser Cys Met Lys Asn Leu His Asn Ile
370 375 380

Thr Gly Val Leu Met Thr Asp Ser Asp Phe Val Ser Ala Val Lys Arg
385 390 395 400

Asn Leu Phe Asn Gln Trp Lys Gln Asn Ala Thr Asp Ile Met Glu Ala
405 410 415

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

Lys Ser Gln Ser Leu Ser Tyr Ala Ser Leu Lys Ala Gly Ser His Asp
435 440 445

Pro Lys Cys Arg Asn Gln Ser Leu Glu Phe Ser Thr Met Lys Ala Glu
450 455 460

Met Lys Glu Arg Asp Lys Gly Lys Met Lys Ser Asp Pro Cys Lys Ser
465 470 475 480

Leu Thr Ser Ala Glu Lys Val Gly Glu His Ile Leu Lys Glu Gly Leu
485 490 495

Thr Ile Trp Asn Gln Lys Gln Gly Asn Ser Cys Lys Val Ala Thr Lys
500 505 510

```
Ala Cys Ser Asn Lys Asp Glu Lys Gly Glu Lys Ile Asn Ala Ser Thr
        515                 520                 525

Asp Ser Leu Ala Lys Asp Leu Ile Val Ser Ala Leu Lys Leu Ile Gln
    530                 535                 540

Tyr His Leu Thr Gln Gln Thr Lys Gly Lys Asp Thr Cys Glu Glu Asp
545                 550                 555                 560

Cys Pro Gly Ser Thr Met Gly Tyr Met Ala Gln Ser Thr Gln Tyr Glu
                565                 570                 575

Lys Cys Gly Gly Gly Gln Ser Ala Lys Ala Leu Ser Val Lys Gln Leu
            580                 585                 590

Glu Ser His Arg Ala Pro Gly Pro Ser Thr Cys Gln Lys Glu Asn Gln
        595                 600                 605

His Leu Asp Ser Gln Lys Met Asp Met Ser Asn Ile Val Leu Met Leu
    610                 615                 620

Ile Gln Lys Leu Leu Asn Glu Asn Pro Phe Lys Cys Glu Asp Pro Cys
625                 630                 635                 640

Glu Gly Glu Asn Lys Cys Ser Glu Pro Arg Ala Ser Lys Ala Ala Ser
                645                 650                 655

Met Ser Asn Arg Ser Asp Lys Ala Glu Glu Gln Cys Gln Glu His Gln
            660                 665                 670

Glu Leu Asp Cys Thr Ser Gly Met Lys Gln Ala Asn Gly Gln Phe Ile
        675                 680                 685

Asp Lys Leu Val Glu Ser Val Met Lys Leu Cys Leu Ile Met Ala Lys
    690                 695                 700

Tyr Ser Asn Asp Gly Ala Ala Leu Ala Glu Leu Glu Glu Gln Ala Ala
705                 710                 715                 720

Ser Ala Asn Lys Pro Asn Phe Arg Gly Thr Arg Cys Ile His Ser Gly
                725                 730                 735
```

```
Ala Met Pro Gln Asn Tyr Gln Asp Ser Leu Gly His Glu Val Ile Val
            740                 745                 750

Asn Asn Gln Cys Ser Thr Asn Ser Leu Gln Lys Gln Leu Gln Ala Val
        755                 760                 765

Leu Gln Trp Ile Ala Ala Ser Gln Phe Asn Val Pro Met Leu Tyr Phe
    770                 775                 780

Met Gly Asp Lys Asp Gly Gln Leu Glu Lys Leu Pro Gln Val Ser Ala
785                 790                 795                 800

Lys Ala Ala Glu Lys Gly Tyr Ser Val Gly Gly Leu Leu Gln Glu Val
                805                 810                 815

Met Lys Phe Ala Lys Glu Arg Gln Pro Asp Glu Ala Val Gly Lys Val
            820                 825                 830

Ala Arg Lys Gln Leu Leu Asp Trp Leu Leu Ala Asn Leu
        835                 840                 845


<210> 649
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<212> PRT
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<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000402403"

<400> 649
Met Ser Asp Asp Ile Asp Trp Leu Arg Ser His Arg Gly Val Cys Lys
1               5                   10                  15

Val Asp Leu Tyr Asn Pro Glu Gly Gln Gln Asp Gln Asp Arg Lys Val
            20                  25                  30
```

```
Ile Cys Phe Val Asp Val Ser Thr Leu Asn Val Glu Asp Lys Asp Tyr
        35                  40                  45

Lys Asp Ala Ala Ser Ser Ser Ser Glu Gly Asn Leu Asn Leu Gly Ser
    50                  55                  60

Leu Glu Glu Lys Glu Ile Ile Val Ile Lys Asp Thr Glu Lys Lys Asp
65                  70                  75                  80

Gln Ser Lys Thr Glu Gly Ser Val Cys Leu Phe Lys Gln Ala Pro Ser
                85                  90                  95

Asp Pro Val Ser Val Leu Asn Trp Leu Leu Ser Asp Leu Gln Lys Tyr
            100                 105                 110

Ala Leu Gly Phe Gln His Ala Leu Ser Pro Ser Thr Ser Thr Cys Lys
        115                 120                 125

His Lys Val Gly Asp Thr Glu Gly Glu Tyr His Arg Ala Ser Ser Glu
    130                 135                 140

Asn Cys Tyr Ser Val Tyr Ala Asp Gln Val Asn Ile Asp Tyr Leu Met
145                 150                 155                 160

Asn Arg Pro Gln Asn Leu Arg Leu Glu Met Thr Ala Ala Lys Asn Thr
                165                 170                 175

Asn Asn Asn Gln Asn Thr Cys Glu Glu Asp Cys Pro Gly Ser Thr Met
            180                 185                 190

Gly Tyr Met Ala Gln Ser Thr Gln Tyr Glu Lys Cys Gly Gly Gly Gln
        195                 200                 205

Ser Ala Lys Ala Leu
    210


<210> 650
<211> 254
<212> PRT
<213> Homo sapiens

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<223> /note="Payload ID: 110; "

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A kinase (PRKA) anchor prt 4; "

<220>
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<223> /note="ENSP ID: ENSP00000412279"

<400> 650
Met Ser Asp Asp Ile Asp Trp Leu Arg Ser His Arg Gly Val Cys Lys
1 5 10 15

Val Asp Leu Tyr Asn Pro Glu Gly Gln Gln Asp Gln Asp Arg Lys Val
20 25 30

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

Lys Asp Ala Ala Ser Ser Ser Ser Glu Gly Asn Leu Asn Leu Gly Ser
50 55 60

Leu Glu Glu Lys Glu Ile Ile Val Ile Lys Asp Thr Glu Lys Lys Asp
65 70 75 80

Gln Ser Lys Thr Glu Gly Ser Val Cys Leu Phe Lys Gln Ala Pro Ser
85 90 95

Asp Pro Val Ser Val Leu Asn Trp Leu Leu Ser Asp Leu Gln Lys Tyr
100 105 110

Ala Leu Gly Phe Gln His Ala Leu Ser Pro Ser Thr Ser Thr Cys Lys
115 120 125

His Lys Val Gly Asp Thr Glu Gly Glu Tyr His Arg Ala Ser Ser Glu
130 135 140

Asn Cys Tyr Ser Val Tyr Ala Asp Gln Val Asn Ile Asp Tyr Leu Met
145 150 155 160

Asn Arg Pro Gln Asn Leu Arg Leu Glu Met Thr Ala Ala Lys Asn Thr

```
                165                 170                 175

Asn Asn Asn Gln Ser Pro Ser Ala Pro Pro Ala Lys Pro Pro Ser Thr
            180                 185                 190

Gln Arg Ala Val Ile Ser Pro Asp Gly Glu Cys Ser Ile Asp Asp Leu
        195                 200                 205

Ser Phe Tyr Val Asn Arg Leu Ser Ser Leu Val Ile Gln Met Ala His
    210                 215                 220

Lys Glu Ile Lys Glu Lys Leu Glu Gly Lys Ser Lys Cys Leu His His
225                 230                 235                 240

Ser Ile Cys Pro Ser Pro Gly Asn Lys Glu Arg Ile Ser Pro
                245                 250


<210> 651
<211> 427
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000315615"

<400> 651
Met Glu Thr Thr Ile Ser Glu Ile His Val Glu Asn Lys Asp Glu Lys
1               5                   10                  15

Arg Ser Ala Glu Gly Ser Pro Gly Ala Glu Arg Gln Lys Glu Lys Ala
            20                  25                  30
```

```
Ser Met Leu Cys Phe Lys Arg Arg Lys Lys Ala Ala Lys Ala Leu Lys
        35                  40                  45

Pro Lys Ala Gly Ser Glu Ala Ala Asp Val Ala Arg Lys Cys Pro Gln
    50                  55                  60

Glu Ala Gly Ala Ser Asp Gln Pro Glu Pro Thr Arg Gly Ala Trp Ala
65                  70                  75                  80

Ser Leu Lys Arg Leu Val Thr Arg Arg Lys Arg Ser Glu Ser Ser Lys
                85                  90                  95

Gln Gln Lys Pro Leu Glu Gly Glu Met Gln Pro Ala Ile Asn Ala Glu
            100                 105                 110

Asp Ala Asp Leu Ser Lys Lys Lys Ala Lys Ser Arg Leu Lys Ile Pro
        115                 120                 125

Cys Ile Lys Phe Pro Arg Gly Pro Lys Arg Ser Asn His Ser Lys Ile
    130                 135                 140

Ile Glu Asp Ser Asp Cys Ser Ile Lys Val Gln Glu Glu Ala Glu Ile
145                 150                 155                 160

Leu Asp Ile Gln Thr Gln Thr Pro Leu Asn Asp Gln Ala Thr Lys Ala
                165                 170                 175

Lys Ser Thr Gln Asp Leu Ser Glu Gly Ile Ser Arg Lys Asp Gly Asp
            180                 185                 190

Glu Val Cys Glu Ser Asn Val Ser Asn Ser Thr Thr Ser Gly Glu Lys
        195                 200                 205

Val Ile Ser Val Glu Leu Gly Leu Asp Asn Gly His Ser Ala Ile Gln
    210                 215                 220

Thr Gly Thr Leu Ile Leu Glu Glu Ile Glu Thr Ile Lys Glu Lys Gln
225                 230                 235                 240

Asp Val Gln Pro Gln Gln Ala Ser Pro Leu Glu Thr Ser Glu Thr Asp
                245                 250                 255
```

```
His Gln Gln Pro Val Leu Ser Asp Val Pro Pro Leu Pro Ala Ile Pro
            260                 265                 270

Asp Gln Gln Ile Val Glu Glu Ala Ser Asn Ser Thr Leu Glu Ser Ala
        275                 280                 285

Pro Asn Gly Lys Asp Tyr Glu Ser Thr Glu Ile Val Ala Glu Glu Thr
    290                 295                 300

Lys Pro Lys Asp Thr Glu Leu Ser Gln Glu Ser Asp Phe Lys Glu Asn
305                 310                 315                 320

Gly Ile Thr Glu Glu Lys Ser Lys Ser Glu Glu Ser Lys Arg Met Glu
                325                 330                 335

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

Thr Lys Ser Lys Asn Val Pro Lys Gln Phe Leu Ile Ser Ala Glu Asn
        355                 360                 365

Glu Gln Val Gly Val Phe Ala Asn Asp Asn Gly Phe Glu Asp Arg Thr
    370                 375                 380

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

Lys Asn Ala Ile Gln Leu Ser Ile Glu Gln Leu Val Asn Glu Met Ala
                405                 410                 415

Ser Asp Asp Asn Lys Ile Asn Asn Leu Leu Gln
            420                 425


<210> 652
<211> 427
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: AKAP5; "
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<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 5; "

<220>
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<223> /note="Uniprot ID: P24588; "

<220>
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<400> 652
Met Glu Thr Thr Ile Ser Glu Ile His Val Glu Asn Lys Asp Glu Lys
1   5   10   15

Arg Ser Ala Glu Gly Ser Pro Gly Ala Glu Arg Gln Lys Glu Lys Ala
            20   25   30

Ser Met Leu Cys Phe Lys Arg Arg Lys Lys Ala Ala Lys Ala Leu Lys
        35   40   45

Pro Lys Ala Gly Ser Glu Ala Ala Asp Val Ala Arg Lys Cys Pro Gln
    50   55   60

Glu Ala Gly Ala Ser Asp Gln Pro Glu Pro Thr Arg Gly Ala Trp Ala
65   70   75   80

Ser Leu Lys Arg Leu Val Thr Arg Arg Lys Arg Ser Glu Ser Ser Lys
                85   90   95

Gln Gln Lys Pro Leu Glu Gly Glu Met Gln Pro Ala Ile Asn Ala Glu
            100   105   110

Asp Ala Asp Leu Ser Lys Lys Lys Ala Lys Ser Arg Leu Lys Ile Pro
        115   120   125

Cys Ile Lys Phe Pro Arg Gly Pro Lys Arg Ser Asn His Ser Lys Ile
    130   135   140

Ile Glu Asp Ser Asp Cys Ser Ile Lys Val Gln Glu Glu Ala Glu Ile
145   150   155   160

Leu Asp Ile Gln Thr Gln Thr Pro Leu Asn Asp Gln Ala Thr Lys Ala
                165   170   175

```
Lys Ser Thr Gln Asp Leu Ser Glu Gly Ile Ser Arg Lys Asp Gly Asp
            180                 185                 190

Glu Val Cys Glu Ser Asn Val Ser Asn Ser Thr Thr Ser Gly Glu Lys
        195                 200                 205

Val Ile Ser Val Glu Leu Gly Leu Asp Asn Gly His Ser Ala Ile Gln
    210                 215                 220

Thr Gly Thr Leu Ile Leu Glu Glu Ile Glu Thr Ile Lys Glu Lys Gln
225                 230                 235                 240

Asp Val Gln Pro Gln Gln Ala Ser Pro Leu Glu Thr Ser Glu Thr Asp
                245                 250                 255

His Gln Gln Pro Val Leu Ser Asp Val Pro Pro Leu Pro Ala Ile Pro
            260                 265                 270

Asp Gln Gln Ile Val Glu Glu Ala Ser Asn Ser Thr Leu Glu Ser Ala
        275                 280                 285

Pro Asn Gly Lys Asp Tyr Glu Ser Thr Glu Ile Val Ala Glu Glu Thr
    290                 295                 300

Lys Pro Lys Asp Thr Glu Leu Ser Gln Glu Ser Asp Phe Lys Glu Asn
305                 310                 315                 320

Gly Ile Thr Glu Glu Lys Ser Lys Ser Glu Glu Ser Lys Arg Met Glu
                325                 330                 335

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

Thr Lys Ser Lys Asn Val Pro Lys Gln Phe Leu Ile Ser Ala Glu Asn
        355                 360                 365

Glu Gln Val Gly Val Phe Ala Asn Asp Asn Gly Phe Glu Asp Arg Thr
    370                 375                 380

Ser Glu Gln Tyr Glu Thr Leu Leu Ile Glu Thr Ala Ser Ser Leu Val
385                 390                 395                 400
```

```
Lys Asn Ala Ile Gln Leu Ser Ile Glu Gln Leu Val Asn Glu Met Ala
                405                 410                 415


Ser Asp Asp Asn Lys Ile Asn Asn Leu Leu Gln
            420                 425


<210> 653
<211> 2319
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<400> 653
Met Leu Thr Met Ser Val Thr Leu Ser Pro Leu Arg Ser Gln Asp Leu
1               5                   10                  15


Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro
            20                  25                  30


Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser
        35                  40                  45


Asp Gln Gln Tyr Glu Lys Pro Pro Pro Leu His Thr Gly Ala Asp Trp
    50                  55                  60


Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr
65                  70                  75                  80


Ser Glu Arg Val Arg Asp Leu Thr Tyr Ser Val Gln Gln Asp Ser Asp
                85                  90                  95
```

```
Ser Lys His Val Asp Val His Leu Val Gln Leu Lys Asp Ile Cys Glu
            100                 105                 110

Asp Ile Ser Asp His Val Glu Gln Ile His Ala Leu Leu Glu Thr Glu
        115                 120                 125

Phe Ser Leu Lys Leu Leu Ser Tyr Ser Val Asn Val Ile Val Asp Ile
    130                 135                 140

His Ala Val Gln Leu Leu Trp His Gln Leu Arg Val Ser Val Leu Val
145                 150                 155                 160

Leu Arg Glu Arg Ile Leu Gln Gly Leu Gln Asp Ala Asn Gly Asn Tyr
                165                 170                 175

Thr Arg Gln Thr Asp Ile Leu Gln Ala Phe Ser Glu Glu Thr Lys Glu
            180                 185                 190

Gly Arg Leu Asp Ser Leu Thr Glu Val Asp Asp Ser Gly Gln Leu Thr
        195                 200                 205

Ile Lys Cys Ser Gln Asn Tyr Leu Ser Leu Asp Cys Gly Ile Thr Ala
    210                 215                 220

Phe Glu Leu Ser Asp Tyr Ser Pro Ser Glu Asp Leu Leu Ser Gly Leu
225                 230                 235                 240

Gly Asp Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp
                245                 250                 255

Ser Tyr Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val
            260                 265                 270

Gly Leu Leu Thr Val Ala Ala Asp Ser Ile Ser Thr Asn Gly Ser Glu
        275                 280                 285

Ala Val Thr Glu Glu Val Ser Gln Val Ser Leu Ser Val Asp Asp Lys
    290                 295                 300

Gly Gly Cys Glu Glu Asp Asn Ala Ser Ala Val Glu Glu Gln Pro Gly
305                 310                 315                 320
```

```
Leu Thr Leu Gly Val Ser Ser Ser Ser Gly Glu Ala Leu Thr Asn Ala
                325                 330                 335

Ala Gln Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser
            340                 345                 350

His His Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr
        355                 360                 365

Pro Lys Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro
    370                 375                 380

Thr Gln Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr
385                 390                 395                 400

Phe Lys Asn Asp Leu Lys Gly Asn Gly Gly Lys Arg Gln Met Val Asp
                405                 410                 415

Leu Lys Pro Glu Met Ser Arg Ser Thr Pro Ser Leu Val Asp Pro Pro
            420                 425                 430

Asp Arg Ser Lys Leu Cys Leu Val Leu Gln Ser Ser Tyr Pro Asn Ser
        435                 440                 445

Pro Ser Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn
    450                 455                 460

Gly Asn Leu Glu Asn Thr Val Lys Phe His Ile Lys Glu Ile Ser Ser
465                 470                 475                 480

Ser Leu Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys
                485                 490                 495

Lys Pro His Lys Thr Ser Glu Glu Val Pro Pro Cys Arg Thr Pro Lys
            500                 505                 510

Arg Gly Thr Gly Ser Gly Lys Gln Ala Lys Asn Thr Lys Ser Ser Ala
        515                 520                 525

Val Pro Asn Gly Glu Leu Ser Tyr Thr Ser Lys Ala Ile Glu Gly Pro
    530                 535                 540
```

```
Gln Thr Asn Ser Ala Ser Thr Ser Ser Leu Glu Pro Cys Asn Gln Arg
545                 550                 555                 560

Ser Trp Asn Ala Lys Leu Gln Leu Gln Ser Glu Thr Ser Ser Ser Pro
                565                 570                 575

Ala Phe Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met
            580                 585                 590

Ser Pro Val Pro Leu Leu Ser Lys His Lys Ser Lys Lys Gly Gln Ala
        595                 600                 605

Ser Ser Pro Ser His Val Thr Arg Asn Gly Glu Val Val Glu Ala Trp
    610                 615                 620

Tyr Gly Ser Asp Glu Tyr Leu Ala Leu Pro Ser His Leu Lys Gln Thr
625                 630                 635                 640

Glu Val Leu Ala Leu Lys Leu Glu Asn Leu Thr Lys Leu Leu Pro Gln
                645                 650                 655

Lys Pro Arg Gly Glu Thr Ile Gln Asn Ile Asp Asp Trp Glu Leu Ser
            660                 665                 670

Glu Met Asn Ser Asp Ser Glu Ile Tyr Pro Thr Tyr His Val Lys Lys
        675                 680                 685

Lys His Thr Arg Leu Gly Arg Val Ser Pro Ser Ser Ser Ser Asp Ile
    690                 695                 700

Ala Ser Ser Leu Gly Glu Ser Ile Glu Ser Gly Pro Leu Ser Asp Ile
705                 710                 715                 720

Leu Ser Asp Glu Glu Ser Ser Met Pro Leu Ala Gly Met Lys Lys Tyr
                725                 730                 735

Ala Asp Glu Lys Ser Glu Arg Ala Ser Ser Ser Glu Lys Asn Glu Ser
            740                 745                 750

His Ser Ala Thr Lys Ser Ala Leu Ile Gln Lys Leu Met Gln Asp Ile
        755                 760                 765

Gln His Gln Asp Asn Tyr Glu Ala Ile Trp Glu Lys Ile Glu Gly Phe
```

770 775 780

Val Asn Lys Leu Asp Glu Phe Ile Gln Trp Leu Asn Glu Ala Met Glu
785 790 795 800

Thr Thr Glu Asn Trp Thr Pro Pro Lys Ala Glu Met Asp Asp Leu Lys
805 810 815

Leu Tyr Leu Glu Thr His Leu Ser Phe Lys Leu Asn Val Asp Ser His
820 825 830

Cys Ala Leu Lys Glu Ala Val Glu Glu Glu Gly His Gln Leu Leu Glu
835 840 845

Leu Ile Ala Ser His Lys Ala Gly Leu Lys Asp Met Leu Arg Met Ile
850 855 860

Ala Ser Gln Trp Lys Glu Leu Gln Arg Gln Ile Lys Arg Gln His Ser
865 870 875 880

Trp Ile Leu Arg Ala Leu Asp Thr Ile Lys Ala Glu Ile Leu Ala Thr
885 890 895

Asp Val Ser Val Glu Asp Glu Glu Gly Thr Gly Ser Pro Lys Ala Glu
900 905 910

Val Gln Leu Cys Tyr Leu Glu Ala Gln Arg Asp Ala Val Glu Gln Met
915 920 925

Ser Leu Lys Leu Tyr Ser Glu Gln Tyr Thr Ser Ser Ser Lys Arg Lys
930 935 940

Glu Glu Phe Ala Asp Met Ser Lys Val His Ser Val Gly Ser Asn Gly
945 950 955 960

Leu Leu Asp Phe Asp Ser Glu Tyr Gln Glu Leu Trp Asp Trp Leu Ile
965 970 975

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu
980 985 990

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser
Ile

995 1000 1005

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu
1010 1015 1020

Lys Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val
1025 1030 1035

Asp Ser Ile Asn Glu Lys Trp Glu Leu Leu Gly Lys Thr Leu Gly
1040 1045 1050

Glu Lys Ile Gln Asp Thr Met Ala Gly His Ser Gly Ser Ser Pro
1055 1060 1065

Arg Asp Leu Leu Ser Pro Glu Ser Gly Ser Leu Val Arg Gln Leu
1070 1075 1080

Glu Val Arg Ile Lys Glu Leu Lys Gly Trp Leu Arg Asp Thr Glu
1085 1090 1095

Leu Phe Ile Phe Asn Ser Cys Leu Arg Gln Glu Lys Glu Gly Thr
1100 1105 1110

Met Asn Thr Glu Lys Gln Leu Gln Tyr Phe Lys Ser Leu Cys Arg
1115 1120 1125

Glu Ile Lys Gln Arg Arg Arg Gly Val Ala Ser Ile Leu Arg Leu
1130 1135 1140

Cys Gln His Leu Leu Asp Asp Arg Glu Thr Cys Asn Leu Asn Ala
1145 1150 1155

Asp His Gln Pro Met Gln Leu Ile Ile Val Asn Leu Glu Arg Arg
1160 1165 1170

Trp Glu Ala Ile Val Met Gln Ala Val Gln Trp Gln Thr Arg Leu
1175 1180 1185

Gln Lys Lys Met Gly Lys Glu Ser Glu Thr Leu Asn Val Ile Asp
1190 1195 1200

Pro Gly Leu Met Asp Leu Asn Gly Met Ser Glu Asp Ala Leu Glu
1205 1210 1215

```
Trp Asp  Glu Met Asp Ile Ser  Asn Lys Leu Ile Ser  Leu Asn Glu
    1220                1225                1230

Glu Ser  Asn Asp Leu Asp Gln  Glu Leu Gln Pro Val  Ile Pro Ser
    1235                1240                1245

Leu Lys  Leu Gly Glu Thr Ser  Asn Glu Asp Pro Gly  Tyr Asp Glu
    1250                1255                1260

Glu Ala  Asp Asn His Gly Gly  Ser Gln Tyr Ala Ser  Asn Ile Thr
    1265                1270                1275

Ala Pro  Ser Ser Pro His Ile  Tyr Gln Val Tyr Ser  Leu His Asn
    1280                1285                1290

Val Glu  Leu Tyr Glu Asp Asn  His Met Pro Phe Leu  Lys Asn Asn
    1295                1300                1305

Pro Lys  Val Thr Gly Met Thr  Gln Pro Asn Val Leu  Thr Lys Ser
    1310                1315                1320

Leu Ser  Lys Asp Ser Ser Phe  Ser Ser Thr Lys Ser  Leu Pro Asp
    1325                1330                1335

Leu Leu  Gly Gly Ser Asn Leu  Val Lys Pro Cys Ala  Cys His Gly
    1340                1345                1350

Gly Asp  Met Ser Gln Asn Ser  Gly Ser Glu Ser Gly  Ile Val Ser
    1355                1360                1365

Glu Gly  Asp Thr Glu Thr Thr  Thr Asn Ser Glu Met  Cys Leu Leu
    1370                1375                1380

Asn Ala  Val Asp Gly Ser Pro  Ser Asn Leu Glu Thr  Glu His Leu
    1385                1390                1395

Asp Pro  Gln Met Gly Asp Ala  Val Asn Val Leu Lys  Gln Lys Phe
    1400                1405                1410

Thr Asp  Glu Gly Glu Ser Ile  Lys Leu Pro Asn Ser  Ser Gln Ser
    1415                1420                1425
```

Ser Ile Ser Pro Val Gly Cys Val Asn Gly Lys Val Gly Asp Leu
1430 1435 1440

Asn Ser Ile Thr Lys His Thr Pro Asp Cys Leu Gly Glu Glu Leu
1445 1450 1455

Gln Gly Lys His Asp Val Phe Thr Phe Tyr Asp Tyr Ser Tyr Leu
1460 1465 1470

Gln Gly Ser Lys Leu Lys Leu Pro Met Ile Met Lys Gln Ser Gln
1475 1480 1485

Ser Glu Lys Ala His Val Glu Asp Pro Leu Leu Arg Gly Phe Tyr
1490 1495 1500

Phe Asp Lys Lys Ser Cys Lys Ser Lys His Gln Thr Thr Glu Leu
1505 1510 1515

Gln Pro Asp Val Pro Pro His Glu Arg Ile Leu Ala Ser Ala Ser
1520 1525 1530

His Glu Met Asp Arg Ile Ser Tyr Lys Ser Gly Asn Ile Glu Lys
1535 1540 1545

Thr Phe Thr Gly Met Gln Asn Ala Lys Gln Leu Ser Leu Leu Ser
1550 1555 1560

His Ser Ser Ser Ile Glu Ser Leu Ser Pro Gly Gly Asp Leu Phe
1565 1570 1575

Gly Leu Gly Ile Phe Lys Asn Gly Ser Asp Ser Leu Gln Arg Ser
1580 1585 1590

Thr Ser Leu Glu Ser Trp Leu Thr Ser Tyr Lys Ser Asn Glu Asp
1595 1600 1605

Leu Phe Ser Cys His Ser Ser Gly Asp Ile Ser Val Ser Ser Gly
1610 1615 1620

Ser Val Gly Glu Leu Ser Lys Arg Thr Leu Asp Leu Leu Asn Arg
1625 1630 1635

```
Leu Glu  Asn Ile Gln Ser Pro  Ser Glu Gln Lys Ile  Lys Arg Ser
    1640                 1645                 1650

Val Ser  Asp Ile Thr Leu Gln  Ser Ser Ser Gln Lys  Met Ser Phe
    1655                 1660                 1665

Thr Gly  Gln Met Ser Leu Asp  Ile Ala Ser Ser Ile  Asn Glu Asp
    1670                 1675                 1680

Ser Ala  Ala Ser Leu Thr Glu  Leu Ser Ser Ser Asp  Glu Leu Ser
    1685                 1690                 1695

Leu Cys  Ser Glu Asp Ile Val  Leu His Lys Asn Lys  Ile Pro Glu
    1700                 1705                 1710

Ser Asn  Ala Ser Phe Arg Lys  Arg Leu Thr Arg Ser  Val Ala Asp
    1715                 1720                 1725

Glu Ser  Asp Val Asn Val Ser  Met Ile Val Asn Val  Ser Cys Thr
    1730                 1735                 1740

Ser Ala  Cys Thr Asp Asp Glu  Asp Asp Ser Asp Leu  Leu Ser Ser
    1745                 1750                 1755

Ser Thr  Leu Thr Leu Thr Glu  Glu Glu Leu Cys Ile  Lys Asp Glu
    1760                 1765                 1770

Asp Asp  Asp Ser Ser Ile Ala  Thr Asp Asp Glu Ile  Tyr Glu Asp
    1775                 1780                 1785

Cys Thr  Leu Met Ser Gly Leu  Asp Tyr Ile Lys Asn  Glu Leu Gln
    1790                 1795                 1800

Thr Trp  Ile Arg Pro Lys Leu  Ser Leu Thr Arg Asp  Lys Lys Arg
    1805                 1810                 1815

Cys Asn  Val Ser Asp Glu Met  Lys Gly Ser Lys Asp  Ile Ser Ser
    1820                 1825                 1830

Ser Glu  Met Thr Asn Pro Ser  Asp Thr Leu Asn Ile  Glu Thr Leu
    1835                 1840                 1845

Leu Asn  Gly Ser Val Lys Arg  Val Ser Glu Asn Asn  Gly Asn Gly
```

1850 1855 1860

Lys Asn Ser Ser His Thr His Glu Leu Gly Thr Lys Arg Glu Asn
1865 1870 1875

Lys Lys Thr Ile Phe Lys Val Asn Lys Asp Pro Tyr Val Ala Asp
1880 1885 1890

Met Glu Asn Gly Asn Ile Glu Gly Ile Pro Glu Arg Gln Lys Gly
1895 1900 1905

Lys Pro Asn Val Thr Ser Lys Val Ser Glu Asn Leu Gly Ser His
1910 1915 1920

Gly Lys Glu Ile Ser Glu Ser Glu His Cys Lys Cys Lys Ala Leu
1925 1930 1935

Met Asp Ser Leu Asp Asp Ser Asn Thr Ala Gly Lys Glu Phe Val
1940 1945 1950

Ser Gln Asp Val Arg His Leu Pro Lys Lys Cys Pro Asn His His
1955 1960 1965

His Phe Glu Asn Gln Ser Thr Ala Ser Thr Pro Thr Glu Lys Ser
1970 1975 1980

Phe Ser Glu Leu Ala Leu Glu Thr Arg Phe Asn Asn Arg Gln Asp
1985 1990 1995

Ser Asp Ala Leu Lys Ser Ser Asp Asp Ala Pro Ser Met Ala Gly
2000 2005 2010

Lys Ser Ala Gly Cys Cys Leu Ala Leu Glu Gln Asn Gly Thr Glu
2015 2020 2025

Glu Asn Ala Ser Ile Ser Asn Ile Ser Cys Cys Asn Cys Glu Pro
2030 2035 2040

Asp Val Phe His Gln Lys Asp Ala Glu Asp Cys Ser Val His Asn
2045 2050 2055

Phe Val Lys Glu Ile Ile Asp Met Ala Ser Thr Ala Leu Lys Ser
2060 2065 2070

```
Lys Ser  Gln Pro Glu Asn Glu  Val Ala Ala Pro Thr  Ser Leu Thr
    2075                 2080                 2085

Gln Ile  Lys Glu Lys Val Leu  Glu His Ser His Arg  Pro Ile Gln
    2090                 2095                 2100

Leu Arg  Lys Gly Asp Phe Tyr  Ser Tyr Leu Ser Leu  Ser Ser His
    2105                 2110                 2115

Asp Ser  Asp Cys Gly Glu Val  Thr Asn Tyr Ile Glu  Glu Lys Ser
    2120                 2125                 2130

Ser Thr  Pro Leu Pro Leu Asp  Thr Thr Asp Ser Gly  Leu Asp Asp
    2135                 2140                 2145

Lys Glu  Asp Ile Glu Cys Phe  Phe Glu Ala Cys Val  Glu Gly Asp
    2150                 2155                 2160

Ser Asp  Gly Glu Glu Pro Cys  Phe Ser Ser Ala Pro  Pro Asn Glu
    2165                 2170                 2175

Ser Ala  Val Pro Ser Glu Ala  Ala Met Pro Leu Gln  Ala Thr Ala
    2180                 2185                 2190

Cys Ser  Ser Glu Phe Ser Asp  Ser Ser Leu Ser Ala  Asp Asp Ala
    2195                 2200                 2205

Asp Thr  Val Ala Leu Ser Ser  Pro Ser Ser Gln Glu  Arg Ala Glu
    2210                 2215                 2220

Val Gly  Lys Glu Val Asn Gly  Leu Pro Gln Thr Ser  Ser Gly Cys
    2225                 2230                 2235

Ala Glu  Asn Leu Glu Phe Thr  Pro Ser Lys Leu Asp  Ser Glu Lys
    2240                 2245                 2250

Glu Ser  Ser Gly Lys Pro Gly  Glu Ser Gly Met Pro  Glu Glu His
    2255                 2260                 2265

Asn Ala  Ala Ser Ala Lys Ser  Lys Val Gln Asp Leu  Ser Leu Lys
    2270                 2275                 2280
```

```
Ala Asn  Gln Pro Thr Asp Lys  Ala Ala Leu His Pro  Ser Pro Lys
    2285                 2290                 2295

Thr Leu  Thr Cys Glu Glu Asn  Leu Leu Asn Leu His  Glu Lys Arg
    2300                 2305                 2310

His Arg  Asn Met His Arg
    2315
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<210> 654
<211> 1075
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 112; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP6; "

<220>
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A kinase (PRKA) anchor prt 6; "

<220>
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<400> 654

```
Met Leu Thr Met Ser Val Thr Leu Ser Pro Leu Arg Ser Gln Asp Leu
1               5                  10                  15

Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro
            20                  25                  30

Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser
        35                  40                  45

Asp Gln Gln Tyr Glu Lys Pro Pro Pro Leu His Thr Gly Ala Asp Trp
    50                  55                  60

Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr
```

65 70 75 80

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

Ser Lys His Val Asp Val His Leu Val Gln Leu Lys Asp Ile Cys Glu
100 105 110

Asp Ile Ser Asp His Val Glu Gln Ile His Ala Leu Leu Glu Thr Glu
115 120 125

Phe Ser Leu Lys Leu Leu Ser Tyr Ser Val Asn Val Ile Val Asp Ile
130 135 140

His Ala Val Gln Leu Leu Trp His Gln Leu Arg Val Ser Val Leu Val
145 150 155 160

Leu Arg Glu Arg Ile Leu Gln Gly Leu Gln Asp Ala Asn Gly Asn Tyr
165 170 175

Thr Arg Gln Thr Asp Ile Leu Gln Ala Phe Ser Glu Glu Thr Lys Glu
180 185 190

Gly Arg Leu Asp Ser Leu Thr Glu Val Asp Asp Ser Gly Gln Leu Thr
195 200 205

Ile Lys Cys Ser Gln Asn Tyr Leu Ser Leu Asp Cys Gly Ile Thr Ala
210 215 220

Phe Glu Leu Ser Asp Tyr Ser Pro Ser Glu Asp Leu Leu Ser Gly Leu
225 230 235 240

Gly Asp Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp
245 250 255

Ser Tyr Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val
260 265 270

Gly Leu Leu Thr Val Ala Ala Asp Ser Ile Ser Thr Asn Gly Ser Glu
275 280 285

Ala Val Thr Glu Glu Val Ser Gln Val Ser Leu Ser Val Asp Asp Lys
290 295 300

```
Gly Gly Cys Glu Glu Asp Asn Ala Ser Ala Val Glu Glu Gln Pro Gly
305                 310                 315                 320

Leu Thr Leu Gly Val Ser Ser Ser Ser Gly Glu Ala Leu Thr Asn Ala
                325                 330                 335

Ala Gln Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser
            340                 345                 350

His His Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr
        355                 360                 365

Pro Lys Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro
    370                 375                 380

Thr Gln Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr
385                 390                 395                 400

Phe Lys Asn Asp Leu Lys Gly Asn Gly Gly Lys Arg Gln Met Val Asp
                405                 410                 415

Leu Lys Pro Glu Met Ser Arg Ser Thr Pro Ser Leu Val Asp Pro Pro
            420                 425                 430

Asp Arg Ser Lys Leu Cys Leu Val Leu Gln Ser Ser Tyr Pro Asn Ser
        435                 440                 445

Pro Ser Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn
    450                 455                 460

Gly Asn Leu Glu Asn Thr Val Lys Phe His Ile Lys Glu Ile Ser Ser
465                 470                 475                 480

Ser Leu Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys
                485                 490                 495

Lys Pro His Lys Thr Ser Glu Glu Val Pro Pro Cys Arg Thr Pro Lys
            500                 505                 510

Arg Gly Thr Gly Ser Gly Lys Gln Ala Lys Asn Thr Lys Ser Ser Ala
        515                 520                 525
```

```
Val Pro Asn Gly Glu Leu Ser Tyr Thr Ser Lys Ala Ile Glu Gly Pro
    530                 535                 540

Gln Thr Asn Ser Ala Ser Thr Ser Ser Leu Glu Pro Cys Asn Gln Arg
545                 550                 555                 560

Ser Trp Asn Ala Lys Leu Gln Leu Gln Ser Glu Thr Ser Ser Ser Pro
                565                 570                 575

Ala Phe Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met
            580                 585                 590

Ser Pro Val Pro Leu Leu Ser Lys His Lys Ser Lys Lys Gly Gln Ala
        595                 600                 605

Ser Ser Pro Ser His Val Thr Arg Asn Gly Glu Val Val Glu Ala Trp
    610                 615                 620

Tyr Gly Ser Asp Glu Tyr Leu Ala Leu Pro Ser His Leu Lys Gln Thr
625                 630                 635                 640

Glu Val Leu Ala Leu Lys Leu Glu Asn Leu Thr Lys Leu Leu Pro Gln
                645                 650                 655

Lys Pro Arg Gly Glu Thr Ile Gln Asn Ile Asp Asp Trp Glu Leu Ser
            660                 665                 670

Glu Met Asn Ser Asp Ser Glu Ile Tyr Pro Thr Tyr His Val Lys Lys
        675                 680                 685

Lys His Thr Arg Leu Gly Arg Val Ser Pro Ser Ser Ser Ser Asp Ile
    690                 695                 700

Ala Ser Ser Leu Gly Glu Ser Ile Glu Ser Gly Pro Leu Ser Asp Ile
705                 710                 715                 720

Leu Ser Asp Glu Glu Ser Ser Met Pro Leu Ala Gly Met Lys Lys Tyr
                725                 730                 735

Ala Asp Glu Lys Ser Glu Arg Ala Ser Ser Ser Glu Lys Asn Glu Ser
            740                 745                 750
```

```
His Ser Ala Thr Lys Ser Ala Leu Ile Gln Lys Leu Met Gln Asp Ile
        755                 760                 765

Gln His Gln Asp Asn Tyr Glu Ala Ile Trp Glu Lys Ile Glu Gly Phe
    770                 775                 780

Val Asn Lys Leu Asp Glu Phe Ile Gln Trp Leu Asn Glu Ala Met Glu
785                 790                 795                 800

Thr Thr Glu Asn Trp Thr Pro Pro Lys Ala Glu Met Asp Asp Leu Lys
                805                 810                 815

Leu Tyr Leu Glu Thr His Leu Ser Phe Lys Leu Asn Val Asp Ser His
            820                 825                 830

Cys Ala Leu Lys Glu Ala Val Glu Glu Glu Gly His Gln Leu Leu Glu
        835                 840                 845

Leu Ile Ala Ser His Lys Ala Gly Leu Lys Asp Met Leu Arg Met Ile
    850                 855                 860

Ala Ser Gln Trp Lys Glu Leu Gln Arg Gln Ile Lys Arg Gln His Ser
865                 870                 875                 880

Trp Ile Leu Arg Ala Leu Asp Thr Ile Lys Ala Glu Ile Leu Ala Thr
                885                 890                 895

Asp Val Ser Val Glu Asp Glu Glu Gly Thr Gly Ser Pro Lys Ala Glu
            900                 905                 910

Val Gln Leu Cys Tyr Leu Glu Ala Gln Arg Asp Ala Val Glu Gln Met
        915                 920                 925

Ser Leu Lys Leu Tyr Ser Glu Gln Tyr Thr Ser Ser Ser Lys Arg Lys
    930                 935                 940

Glu Glu Phe Ala Asp Met Ser Lys Val His Ser Val Gly Ser Asn Gly
945                 950                 955                 960

Leu Leu Asp Phe Asp Ser Glu Tyr Gln Glu Leu Trp Asp Trp Leu Ile
                965                 970                 975

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu
```

```
            980                 985                 990

Glu Gln Gln Gln His Leu Tyr Lys  Arg Tyr Ser Val Glu  Met Ser
Ile
        995                 1000                1005

Arg His  Leu Lys Lys Thr Glu  Leu Leu Ser Lys Val  Glu Ala Leu
    1010                1015                1020

Lys Lys  Gly Gly Val Leu Leu  Pro Asn Asp Leu Leu  Glu Lys Val
    1025                1030                1035

Asp Ser  Ile Asn Glu Lys Trp  Glu Leu Leu Gly Val  Phe Ala Phe
    1040                1045                1050

Leu Leu  Leu Phe Val Gly Tyr  Val Tyr Ile Phe Cys  Val Val Lys
    1055                1060                1065

Tyr Ser  Val Arg Phe Leu Ile
    1070                1075


<210> 655
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 112; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP6; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451146"

<400> 655
Met Leu Thr Met Ser Val Thr Leu Ser Pro Leu Arg Ser Gln Asp Leu
1               5                   10                  15

Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro
            20                  25                  30
```

```
Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser
        35                  40                  45

Asp Gln Gln Tyr Glu Lys Pro Pro Pro Leu His Thr Gly Ala Asp Trp
    50                  55                  60

Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr
65                  70                  75                  80

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

Ser Lys His Val Asp Val His Leu Val Gln Leu Lys
            100                 105


<210> 656
<211> 356
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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      A kinase (PRKA) anchor prt 6; "

<220>
<221> source
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<400> 656
Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp Ser Tyr
1               5                   10                  15

Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val Gly Leu
            20                  25                  30

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

```
Thr Glu Glu Val Ser Gln Val Ser Leu Ser Val Asp Asp Lys Gly Gly
    50                  55                  60

Cys Glu Glu Asp Asn Ala Ser Ala Val Glu Glu Gln Pro Gly Leu Thr
65                  70                  75                  80

Leu Gly Val Ser Ser Ser Ser Gly Glu Ala Leu Thr Asn Ala Ala Gln
                85                  90                  95

Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser His His
            100                 105                 110

Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr Pro Lys
        115                 120                 125

Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro Thr Gln
    130                 135                 140

Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr Phe Lys
145                 150                 155                 160

Asn Asp Leu Lys Gly Asn Gly Gly Lys Arg Gln Met Val Asp Leu Lys
                165                 170                 175

Pro Glu Met Ser Arg Ser Thr Pro Ser Leu Val Asp Pro Pro Asp Arg
            180                 185                 190

Ser Lys Leu Cys Leu Val Leu Gln Ser Ser Tyr Pro Asn Ser Pro Ser
        195                 200                 205

Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn Gly Asn
    210                 215                 220

Leu Glu Asn Thr Val Lys Phe His Ile Lys Glu Ile Ser Ser Ser Leu
225                 230                 235                 240

Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys Lys Pro
                245                 250                 255

His Lys Thr Ser Glu Glu Val Pro Pro Cys Arg Thr Pro Lys Arg Gly
            260                 265                 270

Thr Gly Ser Gly Lys Gln Ala Lys Asn Thr Lys Ser Ser Ala Val Pro
```

```
        275                 280                 285

Asn Gly Glu Leu Ser Tyr Thr Ser Lys Ala Ile Glu Gly Pro Gln Thr
    290                 295                 300

Asn Ser Ala Ser Thr Ser Ser Leu Glu Pro Cys Asn Gln Arg Ser Trp
305                 310                 315                 320

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

Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met Ser Pro
            340                 345                 350

Val Pro Leu Leu
        355


<210> 657
<211> 25
<212> PRT
<213> Homo sapiens

<220>
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      A kinase (PRKA) anchor prt 6; "

<220>
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<223> /note="ENSP ID: ENSP00000451246"

<400> 657
Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp Ser Tyr
1               5                   10                  15

Ser Glu Met Glu Lys Glu Phe Pro Glu
            20                  25


<210> 658
<211> 1245
<212> PRT
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<213> Homo sapiens

<220>
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A kinase (PRKA) anchor prt 6; "

<220>
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<400> 658

```
Met Leu Thr Met Ser Val Thr Leu Ser Pro Leu Arg Ser Gln Asp Leu
1               5                  10                  15

Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro
            20                  25                  30

Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser
        35                  40                  45

Asp Gln Gln Tyr Glu Lys Pro Pro Pro Leu His Thr Gly Ala Asp Trp
    50                  55                  60

Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr
65                  70                  75                  80

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

Ser Lys His Val Asp Val His Leu Val Gln Leu Lys Asp Ile Cys Glu
            100                 105                 110

Asp Ile Ser Asp His Val Glu Gln Ile His Ala Leu Leu Glu Thr Glu
        115                 120                 125

Phe Ser Leu Lys Leu Leu Ser Tyr Ser Val Asn Val Ile Val Asp Ile
    130                 135                 140

His Ala Val Gln Leu Leu Trp His Gln Leu Arg Val Ser Val Leu Val
```

145 150 155 160

Leu Arg Glu Arg Ile Leu Gln Gly Leu Gln Asp Ala Asn Gly Asn Tyr
165 170 175

Thr Arg Gln Thr Asp Ile Leu Gln Ala Phe Ser Glu Glu Thr Lys Glu
180 185 190

Gly Arg Leu Asp Ser Leu Thr Glu Val Asp Asp Ser Gly Gln Leu Thr
195 200 205

Ile Lys Cys Ser Gln Asn Tyr Leu Ser Leu Asp Cys Gly Ile Thr Ala
210 215 220

Phe Glu Leu Ser Asp Tyr Ser Pro Ser Glu Asp Leu Leu Ser Gly Leu
225 230 235 240

Gly Asp Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp
245 250 255

Ser Tyr Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val
260 265 270

Gly Leu Leu Thr Val Ala Ala Asp Ser Ile Ser Thr Asn Gly Ser Glu
275 280 285

Ala Val Thr Glu Glu Val Ser Gln Val Ser Leu Ser Val Asp Asp Lys
290 295 300

Gly Gly Cys Glu Glu Asp Asn Ala Ser Ala Val Glu Glu Gln Pro Gly
305 310 315 320

Leu Thr Leu Gly Val Ser Ser Ser Ser Gly Glu Ala Leu Thr Asn Ala
325 330 335

Ala Gln Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser
340 345 350

His His Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr
355 360 365

Pro Lys Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro
370 375 380

```
Thr Gln Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr
385                 390                 395                 400

Phe Lys Asn Asp Leu Lys Gly Asn Gly Gly Lys Arg Gln Met Val Asp
                405                 410                 415

Leu Lys Pro Glu Met Ser Arg Ser Thr Pro Ser Leu Val Asp Pro Pro
            420                 425                 430

Asp Arg Ser Lys Leu Cys Leu Val Leu Gln Ser Ser Tyr Pro Asn Ser
        435                 440                 445

Pro Ser Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn
    450                 455                 460

Gly Asn Leu Glu Asn Thr Val Lys Phe His Ile Lys Glu Ile Ser Ser
465                 470                 475                 480

Ser Leu Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys
                485                 490                 495

Lys Pro His Lys Thr Ser Glu Glu Val Pro Pro Cys Arg Thr Pro Lys
            500                 505                 510

Arg Gly Thr Gly Ser Gly Lys Gln Ala Lys Asn Thr Lys Ser Ser Ala
        515                 520                 525

Val Pro Asn Gly Glu Leu Ser Tyr Thr Ser Lys Ala Ile Glu Gly Pro
    530                 535                 540

Gln Thr Asn Ser Ala Ser Thr Ser Ser Leu Glu Pro Cys Asn Gln Arg
545                 550                 555                 560

Ser Trp Asn Ala Lys Leu Gln Leu Gln Ser Glu Thr Ser Ser Ser Pro
                565                 570                 575

Ala Phe Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met
            580                 585                 590

Ser Pro Val Pro Leu Leu Ser Lys His Lys Ser Lys Lys Gly Gln Ala
        595                 600                 605
```

```
Ser Ser Pro Ser His Val Thr Arg Asn Gly Glu Val Val Glu Ala Trp
    610                 615                 620

Tyr Gly Ser Asp Glu Tyr Leu Ala Leu Pro Ser His Leu Lys Gln Thr
625                 630                 635                 640

Glu Val Leu Ala Leu Lys Leu Glu Asn Leu Thr Lys Leu Leu Pro Gln
                645                 650                 655

Lys Pro Arg Gly Glu Thr Ile Gln Asn Ile Asp Asp Trp Glu Leu Ser
            660                 665                 670

Glu Met Asn Ser Asp Ser Glu Ile Tyr Pro Thr Tyr His Val Lys Lys
        675                 680                 685

Lys His Thr Arg Leu Gly Arg Val Ser Pro Ser Ser Ser Ser Asp Ile
    690                 695                 700

Ala Ser Ser Leu Gly Glu Ser Ile Glu Ser Gly Pro Leu Ser Asp Ile
705                 710                 715                 720

Leu Ser Asp Glu Glu Ser Ser Met Pro Leu Ala Gly Met Lys Lys Tyr
                725                 730                 735

Ala Asp Glu Lys Ser Glu Arg Ala Ser Ser Ser Glu Lys Asn Glu Ser
            740                 745                 750

His Ser Ala Thr Lys Ser Ala Leu Ile Gln Lys Leu Met Gln Asp Ile
        755                 760                 765

Gln His Gln Asp Asn Tyr Glu Ala Ile Trp Glu Lys Ile Glu Gly Phe
    770                 775                 780

Val Asn Lys Leu Asp Glu Phe Ile Gln Trp Leu Asn Glu Ala Met Glu
785                 790                 795                 800

Thr Thr Glu Asn Trp Thr Pro Pro Lys Ala Glu Met Asp Asp Leu Lys
                805                 810                 815

Leu Tyr Leu Glu Thr His Leu Ser Phe Lys Leu Asn Val Asp Ser His
            820                 825                 830
```

```
Cys Ala Leu Lys Glu Ala Val Glu Glu Glu Gly His Gln Leu Leu Glu
        835                 840                 845

Leu Ile Ala Ser His Lys Ala Gly Leu Lys Asp Met Leu Arg Met Ile
    850                 855                 860

Ala Ser Gln Trp Lys Glu Leu Gln Arg Gln Ile Lys Arg Gln His Ser
865                 870                 875                 880

Trp Ile Leu Arg Ala Leu Asp Thr Ile Lys Ala Glu Ile Leu Ala Thr
                885                 890                 895

Asp Val Ser Val Glu Asp Glu Glu Gly Thr Gly Ser Pro Lys Ala Glu
            900                 905                 910

Val Gln Leu Cys Tyr Leu Glu Ala Gln Arg Asp Ala Val Glu Gln Met
        915                 920                 925

Ser Leu Lys Leu Tyr Ser Glu Gln Tyr Thr Ser Ser Ser Lys Arg Lys
    930                 935                 940

Glu Glu Phe Ala Asp Met Ser Lys Val His Ser Val Gly Ser Asn Gly
945                 950                 955                 960

Leu Leu Asp Phe Asp Ser Glu Tyr Gln Glu Leu Trp Asp Trp Leu Ile
                965                 970                 975

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu
            980                 985                 990

Glu Gln Gln Gln His Leu Tyr Lys  Arg Tyr Ser Val Glu  Met Ser
Ile
        995                 1000                1005

Arg His  Leu Lys Lys Thr Glu  Leu Leu Ser Lys Val  Glu Ala Leu
    1010                1015                1020

Lys Lys  Gly Gly Val Leu Leu  Pro Asn Asp Leu Leu  Glu Lys Val
    1025                1030                1035

Asp Ser  Ile Asn Glu Lys Trp  Glu Leu Leu Gly Lys  Thr Leu Gly
    1040                1045                1050
```

```
Glu Lys  Ile Gln Asp Thr Met  Ala Gly His Ser Gly  Ser Ser Pro
    1055                1060                1065

Arg Asp  Leu Leu Ser Pro Glu  Ser Gly Ser Leu Val  Arg Gln Leu
    1070                1075                1080

Glu Val  Arg Ile Lys Glu Leu  Lys Gly Trp Leu Arg  Asp Thr Glu
    1085                1090                1095

Leu Phe  Ile Phe Asn Ser Cys  Leu Arg Gln Glu Lys  Glu Gly Thr
    1100                1105                1110

Met Asn  Thr Glu Lys Gln Leu  Gln Tyr Phe Lys Ser  Leu Cys Arg
    1115                1120                1125

Glu Ile  Lys Gln Arg Arg Arg  Gly Val Ala Ser Ile  Leu Arg Leu
    1130                1135                1140

Cys Gln  His Leu Leu Asp Asp  Arg Glu Thr Cys Asn  Leu Asn Ala
    1145                1150                1155

Asp His  Gln Pro Met Gln Leu  Ile Ile Val Asn Leu  Glu Arg Arg
    1160                1165                1170

Trp Glu  Ala Ile Val Met Gln  Ala Val Gln Trp Gln  Thr Arg Leu
    1175                1180                1185

Gln Lys  Lys Met Gly Lys Glu  Ser Ile Arg Leu Ala  Ala Thr Gln
    1190                1195                1200

Gly Trp  Pro His Pro Pro Ala  Leu Gly Trp Pro Leu  Val Pro Ser
    1205                1210                1215

Arg Leu  Ser Leu Pro Phe Ile  Thr Leu Thr Ser Pro  Lys Met Asn
    1220                1225                1230

Leu Pro  Ser Lys Cys Val Phe  Ser Thr Gln Ala Leu
    1235                1240                1245
```

<210> 659
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 112; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP6; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452109"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 659
Xaa Asn Thr Glu Lys Gln Leu Gln Tyr Phe Lys Ser Leu Cys Arg Glu
1 5 10 15

Ile Lys Gln Arg Arg Arg Gly Val Ala Ser Ile Leu Arg Leu Cys Gln
20 25 30

His Leu Leu Asp Asp Arg Glu Thr Cys Asn Leu Asn Ala Asp His Gln
35 40 45

Pro Met Gln Leu Ile Ile Val Asn Leu Glu Arg Arg Trp Glu Ala Ile
50 55 60

Val Met Gln Ala Val Gln Trp Gln Thr Arg Leu Gln Lys Lys Met Gly
65 70 75 80

Lys Glu Ser Val Ser Asp Ala Phe Phe Lys His Asn Cys Leu Ser Phe
85 90 95

Ser Gln Thr Lys Asn Asn Ser Phe Arg Leu Gly Asn Gly Val His Leu
100 105 110

Ile Asn Gly Phe Thr Asn
115

<210> 660

<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 112; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP6; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452204"

<400> 660
Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp Ser Tyr
1 5 10 15

Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val Gly Leu
20 25 30

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

<210> 661
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP7; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000263050"

<400> 661

```
Met Leu Lys Lys Lys Gln Ser Asn Gly Tyr Tyr His Cys Glu Ser Ser
1               5                   10                  15

Ile Val Ile Gly Glu Lys Asn Gly Gly Glu Pro Asp Asp Ala Glu Leu
            20                  25                  30

Val Arg Leu Ser Lys Arg Leu Val Glu Asn Ala Val Leu Lys Ala Val
        35                  40                  45

Gln Gln Tyr Leu Glu Glu Thr Gln Asn Lys Asn Lys Pro Gly Glu Gly
    50                  55                  60

Ser Ser Val Lys Thr Glu Ala Ala Asp Gln Asn Gly Asn Asp Asn Glu
65                  70                  75                  80

Asn Asn Arg Lys
```

<210> 662
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
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<223> /note="Gene Symbol: AKAP7; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="Uniprot ID: O43687; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000345149"

<400> 662

```
Met Gly Gln Leu Cys Cys Phe Pro Phe Ser Arg Asp Glu Gly Lys Ile
1               5                   10                  15

Ser Glu Lys Asn Gly Gly Glu Pro Asp Asp Ala Glu Leu Val Arg Leu
            20                  25                  30
```

Ser Lys Arg Leu Val Glu Asn Ala Val Leu Lys Ala Val Gln Gln Tyr
35 40 45

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

Lys Thr Glu Ala Ala Asp Gln Asn Gly Asn Asp Asn Glu Asn Asn Arg
65 70 75 80

Lys

<210> 663
<211> 348
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP7; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="Uniprot ID: Q9P0M2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405252"

<400> 663
Met Glu Arg Pro Glu Ala Gly Gly Ile Asn Ser Asn Glu Cys Glu Asn
1 5 10 15

Val Ser Arg Lys Lys Lys Met Ser Glu Glu Phe Glu Ala Asn Thr Met
20 25 30

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

```
Cys Gly Ile Thr Asp Glu Pro Gln Ile Asn Leu Lys Arg Ser Gln Glu
    50                  55                  60

Asn Glu Trp Val Lys Ser Asp Gln Val Lys Lys Arg Lys Lys Lys Arg
65                  70                  75                  80

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

Glu Ile Ile Lys Gly Ile Lys Ile Leu Gln Asn Ala Ile Ile Gln Gln
            100                 105                 110

Asp Glu Arg Leu Ala Lys Ala Met Val Ser Asp Gly Ser Phe His Ile
        115                 120                 125

Thr Leu Leu Val Met Gln Leu Leu Asn Glu Asp Glu Val Asn Ile Gly
    130                 135                 140

Ile Asp Ala Leu Leu Glu Leu Lys Pro Phe Ile Glu Glu Leu Leu Gln
145                 150                 155                 160

Gly Lys His Leu Thr Leu Pro Phe Gln Gly Ile Gly Thr Phe Gly Asn
                165                 170                 175

Gln Val Gly Phe Val Lys Leu Ala Glu Gly Asp His Val Asn Ser Leu
            180                 185                 190

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

Leu Val Gly Glu Ser Arg Ser Phe Lys Pro His Leu Thr Phe Met Lys
    210                 215                 220

Leu Ser Lys Ser Pro Trp Leu Arg Lys Asn Gly Val Lys Lys Ile Asp
225                 230                 235                 240

Pro Asp Leu Tyr Glu Lys Phe Ile Ser His Arg Phe Gly Glu Glu Ile
                245                 250                 255

Leu Tyr Arg Ile Asp Leu Cys Ser Met Leu Lys Lys Lys Gln Ser Asn
            260                 265                 270

Gly Tyr Tyr His Cys Glu Ser Ser Ile Val Ile Gly Glu Lys Asn Gly
```

```
        275                 280                 285

Gly Glu Pro Asp Asp Ala Glu Leu Val Arg Leu Ser Lys Arg Leu Val
    290                 295                 300

Glu Asn Ala Val Leu Lys Ala Val Gln Gln Tyr Leu Glu Glu Thr Gln
305                 310                 315                 320

Asn Lys Asn Lys Pro Gly Glu Gly Ser Ser Val Lys Thr Glu Ala Ala
                325                 330                 335

Asp Gln Asn Gly Asn Asp Asn Glu Asn Asn Arg Lys
            340                 345


<210> 664
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP7; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="Uniprot ID:  O43687; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418208"

<400> 664
Met Gly Gln Leu Cys Cys Phe Pro Phe Ser Arg Asp Glu Gly Lys Ile
1               5                   10                  15

Ser Glu Leu Glu Ser Ser Ser Ser Ala Val Leu Gln Arg Tyr Ser Lys
            20                  25                  30

Asp Ile Pro Ser Trp Ser Ser Gly Glu Lys Asn Gly Gly Glu Pro Asp
        35                  40                  45
```

```
Asp Ala Glu Leu Val Arg Leu Ser Lys Arg Leu Val Glu Asn Ala Val
    50                  55                  60

Leu Lys Ala Val Gln Gln Tyr Leu Glu Glu Thr Gln Asn Lys Asn Lys
65                  70                  75                  80

Pro Gly Glu Gly Ser Ser Val Lys Thr Glu Ala Ala Asp Gln Asn Gly
                85                  90                  95

Asn Asp Asn Glu Asn Asn Arg Lys
            100


<210> 665
<211> 350
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP7; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000441048"

<400> 665
Met Glu Arg Pro Glu Ala Gly Ile Asn Ser Asn Glu Cys Glu Asn Val
1               5                  10                  15

Ser Arg Lys Lys Lys Met Ser Glu Glu Phe Glu Ala Asn Thr Met Asp
            20                  25                  30

Ser Leu Val Asp Met Pro Phe Ala Thr Val Asp Ile Gln Asp Asp Cys
        35                  40                  45

Gly Ile Thr Asp Glu Pro Gln Ile Asn Leu Lys Arg Ser Gln Glu Asn
    50                  55                  60

Glu Trp Val Lys Ser Asp Gln Val Lys Lys Arg Lys Lys Lys Arg Lys
```

65 70 75 80

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

Ile Ile Lys Gly Ile Lys Ile Leu Gln Asn Ala Ile Ile Gln Gln Asp
100 105 110

Glu Arg Leu Ala Lys Ala Met Val Ser Asp Gly Ser Phe His Ile Thr
115 120 125

Leu Leu Val Met Gln Leu Leu Asn Glu Asp Glu Val Asn Ile Gly Ile
130 135 140

Asp Ala Leu Leu Glu Leu Lys Pro Phe Ile Glu Glu Leu Leu Gln Gly
145 150 155 160

Lys His Leu Thr Leu Pro Phe Gln Gly Ile Gly Thr Phe Gly Asn Gln
165 170 175

Val Gly Phe Val Lys Leu Ala Glu Gly Asp His Val Asn Ser Leu Leu
180 185 190

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

Val Gly Glu Ser Arg Ser Phe Lys Pro His Leu Thr Phe Met Lys Leu
210 215 220

Ser Lys Ser Pro Trp Leu Arg Lys Asn Gly Val Lys Lys Ile Asp Pro
225 230 235 240

Asp Leu Tyr Glu Lys Phe Ile Ser His Arg Phe Gly Glu Glu Ile Leu
245 250 255

Tyr Arg Ile Asp Leu Cys Ser Met Leu Lys Lys Lys Gln Ser Asn Gly
260 265 270

Tyr Tyr His Cys Glu Ser Ser Ile Val Ile Gly Lys Lys Pro Ile Gly
275 280 285

Ile Arg Asp Leu Ile Asn Glu Ala Leu His Arg Glu Thr Met Gly Leu
290 295 300

```
Lys Ser Lys Val Lys Gln Ile Lys Glu Leu Leu Leu Lys Pro Glu Thr
305                 310                 315                 320


Gln Ala Arg Ile Arg Arg Glu Leu Phe Glu Gly Arg Leu Ile Asn Asn
                325                 330                 335


Ser Asn Ser Ala Asn Asp Val Asp Phe Ser Thr Thr Leu Thr
            340                 345                 350


<210> 666
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP7; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445486"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 666
Xaa Thr Asp Glu Pro Gln Ile Asn Leu Lys Arg Ser Gln Glu Asn Glu
1               5                   10                  15


Trp Val Lys Ser Asp Gln Val Lys Lys Arg Lys Lys Lys Arg Lys Asp
            20                  25                  30


Tyr Gln Pro Asn Tyr Phe Leu Ser Ile Pro Ile Thr Asn Lys Glu Arg
        35                  40                  45


Ser Arg Cys
    50
```

<210> 667
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 113; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP7; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446022"

<400> 667
Met Leu Lys Lys Lys Gln Ser Asn Gly Tyr Tyr His Cys Glu Ser Ser
1 5 10 15

Ile Val Ile Gly Lys Lys Pro Ile Gly Ile Arg Asp Leu Ile Asn Glu
20 25 30

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

Lys Glu Leu Leu Leu Lys Pro Glu Thr Gln Ala Arg Ile Arg Arg Glu
50 55 60

Leu Phe Glu Gly Arg Leu Ile Asn Asn Ser Asn Ser Ala Asn Asp Val
65 70 75 80

Asp Phe Ser Thr Thr Leu Thr
85

<210> 668
<211> 692
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 114; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 8; "

<220>
<221> source
<223> /note="Uniprot ID: O43823; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000269701"

<400> 668
Met Asp Gln Gly Tyr Gly Gly Tyr Gly Ala Trp Ser Ala Gly Pro Ala
1   5   10   15

Asn Thr Gln Gly Ala Tyr Gly Thr Gly Val Ala Ser Trp Gln Gly Tyr
            20   25   30

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

Ala Thr Tyr Ser Tyr Gly Pro Ala Ser Trp Glu Ala Ala Lys Ala Asn
    50   55   60

Asp Gly Gly Leu Ala Ala Gly Ala Pro Ala Met His Met Ala Ser Tyr
65   70   75   80

Gly Pro Glu Pro Cys Thr Asp Asn Ser Asp Ser Leu Ile Ala Lys Ile
                85   90   95

Asn Gln Arg Leu Asp Met Met Ser Lys Glu Gly Gly Arg Gly Gly Ser
            100   105   110

Gly Gly Gly Gly Glu Gly Ile Gln Asp Arg Glu Ser Ser Phe Arg Phe
        115   120   125

Gln Pro Phe Glu Ser Tyr Asp Ser Arg Pro Cys Leu Pro Glu His Asn
    130   135   140

Pro Tyr Arg Pro Ser Tyr Ser Tyr Asp Tyr Glu Phe Asp Leu Gly Ser
145   150   155   160

```
Asp Arg Asn Gly Ser Phe Gly Gly Gln Tyr Ser Glu Cys Arg Asp Pro
                165                 170                 175

Ala Arg Glu Arg Gly Ser Leu Asp Gly Phe Met Arg Gly Arg Gly Gln
            180                 185                 190

Gly Arg Phe Gln Asp Arg Ser Asn Pro Gly Thr Phe Met Arg Ser Asp
        195                 200                 205

Pro Phe Val Pro Pro Ala Ala Ser Ser Glu Pro Leu Ser Thr Pro Trp
    210                 215                 220

Asn Glu Leu Asn Tyr Val Gly Gly Arg Gly Leu Gly Gly Pro Ser Pro
225                 230                 235                 240

Ser Arg Pro Pro Pro Ser Leu Phe Ser Gln Ser Met Ala Pro Asp Tyr
                245                 250                 255

Gly Val Met Gly Met Gln Gly Ala Gly Gly Tyr Asp Ser Thr Met Pro
            260                 265                 270

Tyr Gly Cys Gly Arg Ser Gln Pro Arg Met Arg Asp Arg Asp Arg Pro
        275                 280                 285

Lys Arg Arg Gly Phe Asp Arg Phe Gly Pro Asp Gly Thr Gly Arg Lys
    290                 295                 300

Arg Lys Gln Phe Gln Leu Tyr Glu Glu Pro Asp Thr Lys Leu Ala Arg
305                 310                 315                 320

Val Asp Ser Glu Gly Asp Phe Ser Glu Asn Asp Asp Ala Ala Gly Asp
                325                 330                 335

Phe Arg Ser Gly Asp Glu Glu Phe Lys Gly Glu Asp Glu Leu Cys Asp
            340                 345                 350

Ser Gly Arg Gln Arg Gly Glu Lys Glu Asp Glu Asp Glu Asp Val Lys
        355                 360                 365

Lys Arg Arg Glu Lys Gln Arg Arg Arg Asp Arg Thr Arg Asp Arg Ala
    370                 375                 380
```

```
Ala Asp Arg Ile Gln Phe Ala Cys Ser Val Cys Lys Phe Arg Ser Phe
385                 390                 395                 400

Asp Asp Glu Glu Ile Gln Lys His Leu Gln Ser Lys Phe His Lys Glu
                405                 410                 415

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

Leu Gln Glu Tyr Ile Val Asn Arg Asn Lys Lys Ile Glu Lys Arg Arg
        435                 440                 445

Gln Glu Leu Met Glu Lys Glu Thr Ala Lys Pro Lys Pro Asp Pro Phe
    450                 455                 460

Lys Gly Ile Gly Gln Glu His Phe Phe Lys Lys Ile Glu Ala Ala His
465                 470                 475                 480

Cys Leu Ala Cys Asp Met Leu Ile Pro Ala Gln Pro Gln Leu Leu Gln
                485                 490                 495

Arg His Leu His Ser Val Asp His Asn His Asn Arg Arg Leu Ala Ala
            500                 505                 510

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

Asn Arg His Ile Val Lys Met Leu Glu Lys Tyr Leu Lys Gly Glu Asp
    530                 535                 540

Pro Phe Thr Ser Glu Thr Val Asp Pro Glu Met Glu Gly Asp Asp Asn
545                 550                 555                 560

Leu Gly Gly Glu Asp Lys Lys Glu Thr Pro Glu Glu Val Ala Ala Asp
                565                 570                 575

Val Leu Ala Glu Val Ile Thr Ala Ala Val Arg Ala Val Asp Gly Glu
            580                 585                 590

Gly Ala Pro Ala Pro Glu Ser Ser Gly Glu Pro Ala Glu Asp Glu Gly
        595                 600                 605
```

```
Pro Thr Asp Thr Ala Glu Ala Gly Ser Asp Pro Gln Ala Glu Gln Leu
    610                 615                 620

Leu Glu Glu Gln Val Pro Cys Gly Thr Ala His Glu Lys Gly Val Pro
625                 630                 635                 640

Lys Ala Arg Ser Glu Ala Ala Glu Ala Gly Asn Gly Ala Glu Thr Met
                645                 650                 655

Ala Ala Glu Ala Glu Ser Ala Gln Thr Arg Val Ala Pro Ala Pro Ala
            660                 665                 670

Ala Ala Asp Ala Glu Val Glu Gln Thr Asp Ala Glu Ser Lys Asp Ala
        675                 680                 685

Val Pro Thr Glu
    690


<210> 669
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 114; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468902"

<400> 669
Met Asp Gln Gly Tyr Gly Gly Tyr Gly Ala Trp Ser Ala Gly Pro Ala
1               5                   10                  15

Asn Thr Gln Gly Ala Tyr Gly Thr Gly Val Ala Ser Trp Gln Ala Pro
            20                  25                  30

Ser Ala Ser Ser Arg Ser Ser Pro Met Thr Pro Gly Pro Ala Cys Arg
        35                  40                  45
```

```
Ser Thr Thr Pro Thr Ala Pro Ala Thr Ala Thr Thr Met Ser Ser Thr
    50                  55                  60

Trp Gly Pro Thr Ala Met Ala Ala Leu Gly Gly Ser Thr Val Asn Ala
65                  70                  75                  80

Glu Thr Gln Pro Gly Ser Gly Ala Pro Leu Met Ala Ser Cys Gly Ala
                85                  90                  95

Gly Ala Arg Ala Ala Ser Arg Thr Gly Ala Thr Leu Ala Pro Ser Cys
            100                 105                 110

Ala Ala Thr Pro Ser Cys Pro Pro Leu Arg Pro Leu Ser Pro Cys Pro
        115                 120                 125

Arg Pro Gly Thr Ser
    130


<210> 670
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 114; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469908"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 670
Xaa Arg Gly Arg Gly Gln Gly Arg Phe Gln Asp Arg Ser Asn Pro Gly
1               5                   10                  15
```

```
Thr Phe Met Arg Ser Asp Pro Phe Val Pro Pro Ala Ala Ser Ser Glu
            20                  25                  30

Pro Leu Ser Thr Pro Trp Asn Glu Leu Asn Tyr Val Gly Gly Arg Gly
        35                  40                  45

Leu Gly Gly Pro Ser Pro Ser Arg Pro Pro Pro Ser Leu Phe Ser Gln
    50                  55                  60

Ser Met Ala Pro Asp Tyr Gly Val Met Gly Met Gln Gly Ala Gly Gly
65                  70                  75                  80

Tyr Asp Ser Thr Met Pro Tyr Gly Cys Gly Arg Ser Gln Pro Arg Met
                85                  90                  95

Arg Asp Arg Asp Arg Pro Lys Arg Arg Gly Phe Asp Arg Phe Gly Pro
            100                 105                 110

Asp Gly Thr Gly Arg Lys Arg Lys Gln Phe Gln Leu Tyr Glu Glu Pro
        115                 120                 125

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

Asp Asp Ala Ala Gly Asp Phe Arg Ser Gly Asp Glu Glu Phe Lys Gly
145                 150                 155                 160

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

Pro Gly
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<210> 671
<211> 646
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
<221> source

<223> /note="Gene Symbol: AKAP8L; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 8-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q9ULX6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000380557"

<400> 671
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1   5   10   15

Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Gly Tyr Gly
            20   25   30

Thr Trp Asn Ser Gly Thr Asn Arg Gly Tyr Glu Gly Tyr Gly Tyr Gly
        35   40   45

Tyr Gly Tyr Gly Gln Asp Asn Thr Thr Asn Tyr Gly Tyr Gly Met Ala
    50   55   60

Thr Ser His Ser Trp Glu Met Pro Ser Ser Asp Thr Asn Ala Asn Thr
65   70   75   80

Ser Ala Ser Gly Ser Ala Ser Ala Asp Ser Val Leu Ser Arg Ile Asn
                85   90   95

Gln Arg Leu Asp Met Val Pro His Leu Glu Thr Asp Met Met Gln Gly
            100   105   110

Gly Val Tyr Gly Ser Gly Gly Glu Arg Tyr Asp Ser Tyr Glu Ser Cys
        115   120   125

Asp Ser Arg Ala Val Leu Ser Glu Arg Asp Leu Tyr Arg Ser Gly Tyr
    130   135   140

Asp Tyr Ser Glu Leu Asp Pro Glu Met Glu Met Ala Tyr Glu Gly Gln
145   150   155   160

Tyr Asp Ala Tyr Arg Asp Gln Phe Arg Met Arg Gly Asn Asp Thr Phe

```
                165                 170                 175

Gly Pro Arg Ala Gln Gly Trp Ala Arg Asp Ala Arg Ser Gly Arg Pro
            180                 185                 190

Met Ala Ser Gly Tyr Gly Arg Met Trp Glu Asp Pro Met Gly Ala Arg
        195                 200                 205

Gly Gln Cys Met Ser Gly Ala Ser Arg Leu Pro Ser Leu Phe Ser Gln
    210                 215                 220

Asn Ile Ile Pro Glu Tyr Gly Met Phe Gln Gly Met Arg Gly Gly Gly
225                 230                 235                 240

Ala Phe Pro Gly Gly Ser Arg Phe Gly Phe Gly Phe Gly Asn Gly Met
                245                 250                 255

Lys Gln Met Arg Arg Thr Trp Lys Thr Trp Thr Thr Ala Asp Phe Arg
            260                 265                 270

Thr Lys Lys Lys Lys Arg Lys Gln Gly Gly Ser Pro Asp Glu Pro Asp
        275                 280                 285

Ser Lys Ala Thr Arg Thr Asp Cys Ser Asp Asn Ser Asp Ser Asp Asn
    290                 295                 300

Asp Glu Gly Thr Glu Gly Glu Ala Thr Glu Gly Leu Glu Gly Thr Glu
305                 310                 315                 320

Ala Val Glu Lys Gly Ser Arg Val Asp Gly Glu Asp Glu Glu Gly Lys
                325                 330                 335

Glu Asp Gly Arg Glu Glu Gly Lys Glu Asp Pro Glu Lys Gly Ala Leu
            340                 345                 350

Thr Thr Gln Asp Glu Asn Gly Gln Thr Lys Arg Lys Leu Gln Ala Gly
        355                 360                 365

Lys Lys Ser Gln Asp Lys Gln Lys Lys Arg Gln Arg Asp Arg Met Val
    370                 375                 380

Glu Arg Ile Gln Phe Val Cys Ser Leu Cys Lys Tyr Arg Thr Phe Tyr
385                 390                 395                 400
```

```
Glu Asp Glu Met Ala Ser His Leu Asp Ser Lys Phe His Lys Glu His
                405                 410                 415

Phe Lys Tyr Val Gly Thr Lys Leu Pro Lys Gln Thr Ala Asp Phe Leu
            420                 425                 430

Gln Glu Tyr Val Thr Asn Lys Thr Lys Lys Thr Glu Glu Leu Arg Lys
        435                 440                 445

Thr Val Glu Asp Leu Asp Gly Leu Ile Gln Gln Ile Tyr Arg Asp Gln
    450                 455                 460

Asp Leu Thr Gln Glu Ile Ala Met Glu His Phe Val Lys Lys Val Glu
465                 470                 475                 480

Ala Ala His Cys Ala Ala Cys Asp Leu Phe Ile Pro Met Gln Phe Gly
                485                 490                 495

Ile Ile Gln Lys His Leu Lys Thr Met Asp His Asn Arg Asn Arg Arg
            500                 505                 510

Leu Met Met Glu Gln Ser Lys Lys Ser Ser Leu Met Val Ala Arg Ser
        515                 520                 525

Ile Leu Asn Asn Lys Leu Ile Ser Lys Lys Leu Glu Arg Tyr Leu Lys
    530                 535                 540

Gly Glu Asn Pro Phe Thr Asp Ser Pro Glu Glu Glu Lys Glu Gln Glu
545                 550                 555                 560

Glu Ala Glu Gly Gly Ala Leu Asp Glu Gly Ala Gln Gly Glu Ala Ala
                565                 570                 575

Gly Ile Ser Glu Gly Ala Glu Gly Val Pro Ala Gln Pro Pro Val Pro
            580                 585                 590

Pro Glu Pro Ala Pro Gly Ala Val Ser Pro Pro Pro Pro Pro Pro Pro
        595                 600                 605

Glu Glu Glu Glu Glu Gly Ala Val Pro Leu Leu Gly Gly Ala Leu Gln
    610                 615                 620
```

```
Arg Gln Ile Arg Gly Ile Pro Gly Leu Asp Val Glu Asp Asp Glu Glu
625                 630                 635                 640


Gly Gly Gly Gly Ala Pro
                645


<210> 672
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8L; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 8-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470067"

<400> 672
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1               5                   10                  15


Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Gly Tyr Glu
            20                  25                  30


Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Gln Asp Asn Thr Thr Asn Tyr
        35                  40                  45


Gly Tyr Gly Met Ala Thr Ser His Ser Trp Glu Met Pro Ser Ser Asp
    50                  55                  60


Thr Asn Ala Asn Thr Ser Ala Ser Gly Ser Ala Ser Ala Asp Ser Val
65                  70                  75                  80


Leu Ser Arg Ile Asn Gln Arg Leu Asp Met Val Pro His Leu Glu Thr
                85                  90                  95


Asp Met Met Gln Gly Gly Val Tyr Gly Ser Gly Gly Glu Arg Tyr Asp
```

```
            100                 105                 110

Ser Tyr Glu Ser Cys Asp Ser Arg Ala Val Leu Ser Glu Arg Asp Leu
        115                 120                 125

Tyr Arg Ser Gly Tyr Asp Tyr Ser Glu Leu Asp Pro Glu Met Glu Met
    130                 135                 140

Ala Tyr Glu Gly Gln Tyr Asp Ala Tyr Arg Asp Gln Phe Arg Met Arg
145                 150                 155                 160

Gly Asn



<210> 673
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
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<223> /note="Gene Symbol: AKAP8L; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 8-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470906"

<400> 673
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1               5                   10                  15

Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Gly Tyr Gly
            20                  25                  30

Thr Trp Asn Ser Gly Thr Asn Arg Gly Tyr Glu Gly Tyr Gly Tyr Gly
        35                  40                  45

Tyr Gly Tyr Gly Gln Asp Asn Thr Thr Asn Tyr Gly Tyr Glu Leu Thr
    50                  55                  60
```

Ser Ala
65

<210> 674
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8L; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 8-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470912"

<400> 674
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1 5 10 15

Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Asp Thr Leu
20 25 30

Val Ser Val Phe Val Ser Val Ser Val Cys Leu Pro Ser Ala Cys Pro
35 40 45

His His Leu Ser Val Ser Val Ser Leu Thr Ala Gly Tyr Glu Gly Tyr
50 55 60

Gly Tyr Gly Tyr Gly Tyr Gly Gln Asp Asn Thr Thr Asn Tyr Gly Tyr
65 70 75 80

Gly Met Ala Thr Ser His Ser Trp Glu Met Pro Ser Ser Asp Thr Asn
85 90 95

Ala Asn Thr Ser Ala Ser Gly Ser Ala Ser Ala Asp Ser Val Leu Ser
100 105 110

Arg Ile Asn Gln Arg Leu Asp Met Val Pro His Leu Glu Thr Asp Met

```
        115                 120                 125

Met Gln Gly Gly Val Tyr Gly Ser Gly Gly Glu Arg Tyr Asp Ser Tyr
    130                 135                 140

Glu Ser Cys Asp Ser Arg Ala Val Leu Ser Glu Arg Asp Leu Tyr Arg
145                 150                 155                 160

Ser
```

<210> 675
<211> 585
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
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<223> /note="Gene Symbol: AKAP8L; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID: Q9ULX6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470952"

<400> 675

```
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1               5                   10                  15

Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Gly Tyr Gly
            20                  25                  30

Thr Trp Asn Ser Gly Thr Asn Arg Gly Tyr Glu Gly Tyr Gly Tyr Gly
        35                  40                  45

Tyr Gly Tyr Gly Gln Asp Asn Thr Thr Asn Tyr Gly Tyr Asp Ser Tyr
    50                  55                  60
```

```
Glu Ser Cys Asp Ser Arg Ala Val Leu Ser Glu Arg Asp Leu Tyr Arg
65                  70                  75                  80

Ser Gly Tyr Asp Tyr Ser Glu Leu Asp Pro Glu Met Glu Met Ala Tyr
                85                  90                  95

Glu Gly Gln Tyr Asp Ala Tyr Arg Asp Gln Phe Arg Met Arg Gly Asn
            100                 105                 110

Asp Thr Phe Gly Pro Arg Ala Gln Gly Trp Ala Arg Asp Ala Arg Ser
        115                 120                 125

Gly Arg Pro Met Ala Ser Gly Tyr Gly Arg Met Trp Glu Asp Pro Met
    130                 135                 140

Gly Ala Arg Gly Gln Cys Met Ser Gly Ala Ser Arg Leu Pro Ser Leu
145                 150                 155                 160

Phe Ser Gln Asn Ile Ile Pro Glu Tyr Gly Met Phe Gln Gly Met Arg
                165                 170                 175

Gly Gly Gly Ala Phe Pro Gly Gly Ser Arg Phe Gly Phe Gly Phe Gly
            180                 185                 190

Asn Gly Met Lys Gln Met Arg Arg Thr Trp Lys Thr Trp Thr Thr Ala
        195                 200                 205

Asp Phe Arg Thr Lys Lys Lys Lys Arg Lys Gln Gly Gly Ser Pro Asp
    210                 215                 220

Glu Pro Asp Ser Lys Ala Thr Arg Thr Asp Cys Ser Asp Asn Ser Asp
225                 230                 235                 240

Ser Asp Asn Asp Glu Gly Thr Glu Gly Glu Ala Thr Glu Gly Leu Glu
                245                 250                 255

Gly Thr Glu Ala Val Glu Lys Gly Ser Arg Val Asp Gly Glu Asp Glu
            260                 265                 270

Glu Gly Lys Glu Asp Gly Arg Glu Glu Gly Lys Glu Asp Pro Glu Lys
        275                 280                 285
```

```
Gly Ala Leu Thr Thr Gln Asp Glu Asn Gly Gln Thr Lys Arg Lys Leu
    290                 295                 300

Gln Ala Gly Lys Lys Ser Gln Asp Lys Gln Lys Lys Arg Gln Arg Asp
305                 310                 315                 320

Arg Met Val Glu Arg Ile Gln Phe Val Cys Ser Leu Cys Lys Tyr Arg
                325                 330                 335

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

Lys Glu His Phe Lys Tyr Val Gly Thr Lys Leu Pro Lys Gln Thr Ala
        355                 360                 365

Asp Phe Leu Gln Glu Tyr Val Thr Asn Lys Thr Lys Lys Thr Glu Glu
    370                 375                 380

Leu Arg Lys Thr Val Glu Asp Leu Asp Gly Leu Ile Gln Gln Ile Tyr
385                 390                 395                 400

Arg Asp Gln Asp Leu Thr Gln Glu Ile Ala Met Glu His Phe Val Lys
                405                 410                 415

Lys Val Glu Ala Ala His Cys Ala Ala Cys Asp Leu Phe Ile Pro Met
            420                 425                 430

Gln Phe Gly Ile Ile Gln Lys His Leu Lys Thr Met Asp His Asn Arg
        435                 440                 445

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

Ala Arg Ser Ile Leu Asn Asn Lys Leu Ile Ser Lys Lys Leu Glu Arg
465                 470                 475                 480

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

Glu Gln Glu Glu Ala Glu Gly Gly Ala Leu Asp Glu Gly Ala Gln Gly
            500                 505                 510

Glu Ala Ala Gly Ile Ser Glu Gly Ala Glu Gly Val Pro Ala Gln Pro
```

515 520 525

Pro Val Pro Pro Glu Pro Ala Pro Gly Ala Val Ser Pro Pro Pro Pro
530 535 540

Pro Pro Pro Glu Glu Glu Glu Glu Gly Ala Val Pro Leu Leu Gly Gly
545 550 555 560

Ala Leu Gln Arg Gln Ile Arg Gly Ile Pro Gly Leu Asp Val Glu Asp
565 570 575

Asp Glu Glu Gly Gly Gly Gly Ala Pro
580 585

<210> 676
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8L; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 8-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471958"

<400> 676
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1 5 10 15

Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Gly Tyr Gly
20 25 30

Thr Trp Asn Ser Gly Thr Asn Arg Glu Leu Thr Ser Ala
35 40 45

<210> 677
<211> 109
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8L; "

<220>
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<223> /note="Gene Name:
A kinase (PRKA) anchor prt 8-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472188"

<400> 677
Met Ala Thr Ser His Ser Trp Glu Met Pro Ser Ser Asp Thr Asn Ala
1 5 10 15

Asn Thr Ser Ala Ser Gly Ser Ala Ser Ala Asp Ser Val Leu Ser Arg
20 25 30

Ile Asn Gln Arg Leu Asp Met Val Pro His Leu Glu Thr Asp Met Met
35 40 45

Gln Gly Gly Val Tyr Gly Ser Gly Gly Glu Arg Tyr Asp Ser Tyr Glu
50 55 60

Ser Cys Asp Ser Arg Ala Val Leu Ser Glu Arg Asp Leu Tyr Arg Ser
65 70 75 80

Gly Tyr Asp Tyr Ser Glu Leu Asp Pro Glu Met Glu Met Ala Tyr Glu
85 90 95

Gly Gln Tyr Asp Ala Tyr Arg Asp Gln Phe Arg Met Arg
100 105

<210> 678
<211> 431
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 115; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP8L; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA) anchor prt 8-like; "

<220>
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<223> /note="ENSP ID: ENSP00000477434"

<400> 678
Met Ser Tyr Thr Gly Phe Val Gln Gly Ser Glu Thr Thr Leu Gln Ser
1 5 10 15

Thr Tyr Ser Asp Thr Ser Ala Gln Pro Thr Cys Asp Tyr Gly Tyr Gly
20 25 30

Thr Trp Asn Ser Gly Thr Asn Arg Gly Tyr Glu Gly Tyr Gly Tyr Gly
35 40 45

Tyr Gly Tyr Gly Gln Asp Asn Thr Thr Asn Tyr Gly Ile Asn Gln Arg
50 55 60

Leu Asp Met Val Pro His Leu Glu Thr Asp Met Met Gln Gly Gly Val
65 70 75 80

Tyr Gly Ser Gly Gly Glu Arg Tyr Asp Ser Tyr Glu Ser Cys Asp Ser
85 90 95

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

Ser Glu Leu Asp Pro Glu Met Glu Met Ala Tyr Glu Gly Gln Tyr Asp
115 120 125

Ala Tyr Arg Asp Gln Phe Arg Met Arg Gly Asn Asp Thr Phe Gly Pro
130 135 140

Arg Ala Gln Gly Trp Ala Arg Asp Ala Arg Ser Gly Arg Pro Met Ala
145 150 155 160

Ser Gly Tyr Gly Arg Met Trp Glu Asp Pro Met Gly Ala Arg Gly Gln
165 170 175

```
Cys Met Ser Gly Ala Ser Arg Leu Pro Ser Leu Phe Ser Gln Asn Ile
            180                 185                 190

Ile Pro Glu Tyr Gly Met Phe Gln Gly Met Arg Gly Gly Gly Ala Phe
        195                 200                 205

Pro Gly Gly Ser Arg Phe Gly Phe Gly Phe Gly Asn Gly Met Lys Gln
    210                 215                 220

Met Arg Arg Thr Trp Lys Thr Trp Thr Thr Ala Asp Phe Arg Thr Lys
225                 230                 235                 240

Lys Lys Lys Arg Lys Gln Gly Gly Ser Pro Asp Glu Pro Asp Ser Lys
                245                 250                 255

Ala Thr Arg Thr Asp Cys Ser Asp Asn Ser Asp Ser Asp Asn Asp Glu
            260                 265                 270

Gly Thr Glu Gly Glu Ala Thr Glu Gly Leu Glu Gly Thr Glu Ala Val
        275                 280                 285

Glu Lys Gly Ser Arg Val Asp Gly Glu Asp Glu Glu Gly Lys Glu Asp
    290                 295                 300

Gly Arg Glu Glu Gly Lys Glu Asp Pro Glu Lys Gly Ala Leu Thr Thr
305                 310                 315                 320

Gln Asp Glu Asn Gly Gln Thr Lys Arg Lys Leu Gln Ala Gly Lys Lys
                325                 330                 335

Ser Gln Asp Lys Gln Lys Lys Arg Gln Arg Asp Arg Met Val Glu Arg
            340                 345                 350

Ala Pro Ala Leu Ala Leu Ala Ser Ser Ala Ser Asp Ser Cys Ser Cys
        355                 360                 365

Trp Thr Phe Leu Ser Leu Ala Gly Ala Arg Pro Leu Gly Ser Pro Asp
    370                 375                 380

Lys Ala Asp Pro Val Ala Gln Ile Arg Thr Ser Gly Arg Gly Ser Ser
385                 390                 395                 400
```

```
Leu Cys Val Leu Cys Ala Asn Thr Gly Pro Ser Met Arg Thr Arg Trp
                405                 410                 415


Pro Ala Ile Leu Thr Ala Ser Ser Thr Arg Asn Thr Leu Ser Thr
            420                 425                 430


<210> 679
<211> 3907
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 116; "

<220>
<221> source
<223> /note="Gene Symbol: AKAP9; "

<220>
<221> source
<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 9; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99996; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000348573"

<400> 679
Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
1               5                   10                  15


Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
            20                  25                  30


Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
        35                  40                  45


Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
    50                  55                  60


Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
65                  70                  75                  80


Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
                85                  90                  95
```

```
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
            100                 105                 110

Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
        115                 120                 125

Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
    130                 135                 140

Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145                 150                 155                 160

Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
                165                 170                 175

Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
            180                 185                 190

Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
        195                 200                 205

Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
    210                 215                 220

Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225                 230                 235                 240

Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
                245                 250                 255

Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
            260                 265                 270

His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
        275                 280                 285

Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
    290                 295                 300

Ile Lys Val Tyr Glu Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn
305                 310                 315                 320
```

```
Lys Glu Glu Ile Gln Glu Lys Glu Thr Ile Ile Glu Glu Leu Asn Thr
                325                 330                 335

Lys Ile Ile Glu Glu Glu Lys Lys Thr Leu Glu Leu Lys Asp Lys Leu
            340                 345                 350

Thr Thr Ala Asp Lys Leu Leu Gly Glu Leu Gln Glu Gln Ile Val Gln
        355                 360                 365

Lys Asn Gln Glu Ile Lys Asn Met Lys Leu Glu Leu Thr Asn Ser Lys
    370                 375                 380

Gln Lys Glu Arg Gln Ser Ser Glu Glu Ile Lys Gln Leu Met Gly Thr
385                 390                 395                 400

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

Asp Ile Val Gln Arg Met Glu Gln Glu Thr Gln Arg Lys Leu Glu Gln
            420                 425                 430

Leu Arg Ala Glu Leu Asp Glu Met Tyr Gly Gln Gln Ile Val Gln Met
        435                 440                 445

Lys Gln Glu Leu Ile Arg Gln His Met Ala Gln Met Glu Glu Met Lys
    450                 455                 460

Thr Arg His Lys Gly Glu Met Glu Asn Ala Leu Arg Ser Tyr Ser Asn
465                 470                 475                 480

Ile Thr Val Asn Glu Asp Gln Ile Lys Leu Met Asn Val Ala Ile Asn
                485                 490                 495

Glu Leu Asn Ile Lys Leu Gln Asp Thr Asn Ser Gln Lys Glu Lys Leu
            500                 505                 510

Lys Glu Glu Leu Gly Leu Ile Leu Glu Glu Lys Cys Ala Leu Gln Arg
        515                 520                 525

Gln Leu Glu Asp Leu Val Glu Glu Leu Ser Phe Ser Arg Glu Gln Ile
    530                 535                 540
```

```
Gln Arg Ala Arg Gln Thr Ile Ala Glu Gln Glu Ser Lys Leu Asn Glu
545                 550                 555                 560

Ala His Lys Ser Leu Ser Thr Val Glu Asp Leu Lys Ala Glu Ile Val
                565                 570                 575

Ser Ala Ser Glu Ser Arg Lys Glu Leu Glu Leu Lys His Glu Ala Glu
            580                 585                 590

Val Thr Asn Tyr Lys Ile Lys Leu Glu Met Leu Glu Lys Glu Lys Asn
        595                 600                 605

Ala Val Leu Asp Arg Met Ala Glu Ser Gln Glu Ala Glu Leu Glu Arg
    610                 615                 620

Leu Arg Thr Gln Leu Leu Phe Ser His Glu Glu Glu Leu Ser Lys Leu
625                 630                 635                 640

Lys Glu Asp Leu Glu Ile Glu His Arg Ile Asn Ile Glu Lys Leu Lys
                645                 650                 655

Asp Asn Leu Gly Ile His Tyr Lys Gln Gln Ile Asp Gly Leu Gln Asn
            660                 665                 670

Glu Met Ser Gln Lys Ile Glu Thr Met Gln Phe Glu Lys Asp Asn Leu
        675                 680                 685

Ile Thr Lys Gln Asn Gln Leu Ile Leu Glu Ile Ser Lys Leu Lys Asp
    690                 695                 700

Leu Gln Gln Ser Leu Val Asn Ser Lys Ser Glu Glu Met Thr Leu Gln
705                 710                 715                 720

Ile Asn Glu Leu Gln Lys Glu Ile Glu Ile Leu Arg Gln Glu Glu Lys
                725                 730                 735

Glu Lys Gly Thr Leu Glu Gln Glu Val Gln Glu Leu Gln Leu Lys Thr
            740                 745                 750

Glu Leu Leu Glu Lys Gln Met Lys Glu Lys Glu Asn Asp Leu Gln Glu
        755                 760                 765

Lys Phe Ala Gln Leu Glu Ala Glu Asn Ser Ile Leu Lys Asp Glu Lys
```

770 775 780

Lys Thr Leu Glu Asp Met Leu Lys Ile His Thr Pro Val Ser Gln Glu
785 790 795 800

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

Val Trp Glu Lys Glu Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu
820 825 830

Lys Gln Gln Cys Ile Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn
835 840 845

Thr Phe Ser Phe Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu
850 855 860

Gln Glu Glu Tyr Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp
865 870 875 880

Ser Lys Asn Lys Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu
885 890 895

Asn Glu Glu Leu His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met
900 905 910

Lys Ser Ser Val Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu
915 920 925

Glu Met Gly Glu Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys
930 935 940

Leu Glu Val Thr Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser
945 950 955 960

Asp Leu Ser Glu Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu
965 970 975

Asn Glu Glu Val Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu
980 985 990

Arg Cys Arg Glu Leu Glu Ile Ile Ile Asn His Asn Arg Ala Glu
Asn

995 1000 1005

Val Gln Ser Cys Asp Thr Gln Val Ser Ser Leu Leu Asp Gly Val
1010 1015 1020

Val Thr Met Thr Ser Arg Gly Ala Glu Gly Ser Val Ser Lys Val
1025 1030 1035

Asn Lys Ser Phe Gly Glu Glu Ser Lys Ile Met Val Glu Asp Lys
1040 1045 1050

Val Ser Phe Glu Asn Met Thr Val Gly Glu Glu Ser Lys Gln Glu
1055 1060 1065

Gln Leu Ile Leu Asp His Leu Pro Ser Val Thr Lys Glu Ser Ser
1070 1075 1080

Leu Arg Ala Thr Gln Pro Ser Glu Asn Asp Lys Leu Gln Lys Glu
1085 1090 1095

Leu Asn Val Leu Lys Ser Glu Gln Asn Asp Leu Arg Leu Gln Met
1100 1105 1110

Glu Ala Gln Arg Ile Cys Leu Ser Leu Val Tyr Ser Thr His Val
1115 1120 1125

Asp Gln Val Arg Glu Tyr Met Glu Asn Glu Lys Asp Lys Ala Leu
1130 1135 1140

Cys Ser Leu Lys Glu Glu Leu Ile Phe Ala Gln Glu Glu Lys Ile
1145 1150 1155

Lys Glu Leu Gln Lys Ile His Gln Leu Glu Leu Gln Thr Met Lys
1160 1165 1170

Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu His Leu Leu Ile
1175 1180 1185

Gly Lys Leu Gln Lys Ala Val Ser Glu Glu Cys Ser Tyr Phe Leu
1190 1195 1200

Gln Thr Leu Cys Ser Val Leu Gly Glu Tyr Tyr Thr Pro Ala Leu
1205 1210 1215

```
Lys Cys  Glu Val Asn Ala Glu  Asp Lys Glu Asn Ser  Gly Asp Tyr
    1220                 1225                 1230

Ile Ser  Glu Asn Glu Asp Pro  Glu Leu Gln Asp Tyr  Arg Tyr Glu
    1235                 1240                 1245

Val Gln  Asp Phe Gln Glu Asn  Met His Thr Leu Leu  Asn Lys Val
    1250                 1255                 1260

Thr Glu  Glu Tyr Asn Lys Leu  Leu Val Leu Gln Thr  Arg Leu Ser
    1265                 1270                 1275

Lys Ile  Trp Gly Gln Gln Thr  Asp Gly Met Lys Leu  Glu Phe Gly
    1280                 1285                 1290

Glu Glu  Asn Leu Pro Lys Glu  Glu Thr Glu Phe Leu  Ser Ile His
    1295                 1300                 1305

Ser Gln  Met Thr Asn Leu Glu  Asp Ile Asp Val Asn  His Lys Ser
    1310                 1315                 1320

Lys Leu  Ser Ser Leu Gln Asp  Leu Glu Lys Thr Lys  Leu Glu Glu
    1325                 1330                 1335

Gln Val  Gln Glu Leu Glu Ser  Leu Ile Ser Ser Leu  Gln Gln Gln
    1340                 1345                 1350

Leu Lys  Glu Thr Glu Gln Asn  Tyr Glu Ala Glu Ile  His Cys Leu
    1355                 1360                 1365

Gln Lys  Arg Leu Gln Ala Val  Ser Glu Ser Thr Val  Pro Pro Ser
    1370                 1375                 1380

Leu Pro  Val Asp Ser Val Val  Ile Thr Glu Ser Asp  Ala Gln Arg
    1385                 1390                 1395

Thr Met  Tyr Pro Gly Ser Cys  Val Lys Lys Asn Ile  Asp Gly Thr
    1400                 1405                 1410

Ile Glu  Phe Ser Gly Glu Phe  Gly Val Lys Glu Glu  Thr Asn Ile
    1415                 1420                 1425
```

```
Val Lys  Leu Leu Glu Lys Gln  Tyr Gln Glu Gln Leu  Glu Glu Glu
    1430                1435                1440

Val Ala  Lys Val Ile Val Ser  Met Ser Ile Ala Phe  Ala Gln Gln
    1445                1450                1455

Thr Glu  Leu Ser Arg Ile Ser  Gly Gly Lys Glu Asn  Thr Ala Ser
    1460                1465                1470

Ser Lys  Gln Ala His Ala Val  Cys Gln Gln Glu Gln  His Tyr Phe
    1475                1480                1485

Asn Glu  Met Lys Leu Ser Gln  Asp Gln Ile Gly Phe  Gln Thr Phe
    1490                1495                1500

Glu Thr  Val Asp Val Lys Phe  Lys Glu Glu Phe Lys  Pro Leu Ser
    1505                1510                1515

Lys Glu  Leu Gly Glu His Gly  Lys Glu Ile Leu Leu  Ser Asn Ser
    1520                1525                1530

Asp Pro  His Asp Ile Pro Glu  Ser Lys Asp Cys Val  Leu Thr Ile
    1535                1540                1545

Ser Glu  Glu Met Phe Ser Lys  Asp Lys Thr Phe Ile  Val Arg Gln
    1550                1555                1560

Ser Ile  His Asp Glu Ile Ser  Val Ser Ser Met Asp  Ala Ser Arg
    1565                1570                1575

Gln Leu  Met Leu Asn Glu Glu  Gln Leu Glu Asp Met  Arg Gln Glu
    1580                1585                1590

Leu Val  Arg Gln Tyr Gln Glu  His Gln Gln Ala Thr  Glu Leu Leu
    1595                1600                1605

Arg Gln  Ala His Met Arg Gln  Met Glu Arg Gln Arg  Glu Asp Gln
    1610                1615                1620

Glu Gln  Leu Gln Glu Glu Ile  Lys Arg Leu Asn Arg  Gln Leu Ala
    1625                1630                1635
```

```
Gln Arg  Ser Ser Ile Asp Asn  Glu Asn Leu Val Ser  Glu Arg Glu
    1640                1645                1650

Arg Val  Leu Leu Glu Glu Leu  Glu Ala Leu Lys Gln  Leu Ser Leu
    1655                1660                1665

Ala Gly  Arg Glu Lys Leu Cys  Cys Glu Leu Arg Asn  Ser Ser Thr
    1670                1675                1680

Gln Thr  Gln Asn Gly Asn Glu  Asn Gln Gly Glu Val  Glu Glu Gln
    1685                1690                1695

Thr Phe  Lys Glu Lys Glu Leu  Asp Arg Lys Pro Glu  Asp Val Pro
    1700                1705                1710

Pro Glu  Ile Leu Ser Asn Glu  Arg Tyr Ala Leu Gln  Lys Ala Asn
    1715                1720                1725

Asn Arg  Leu Leu Lys Ile Leu  Leu Glu Val Val Lys  Thr Thr Ala
    1730                1735                1740

Ala Val  Glu Glu Thr Ile Gly  Arg His Val Leu Gly  Ile Leu Asp
    1745                1750                1755

Arg Ser  Ser Lys Ser Gln Ser  Ser Ala Ser Leu Ile  Trp Arg Ser
    1760                1765                1770

Glu Ala  Glu Ala Ser Val Lys  Ser Cys Val His Glu  Glu His Thr
    1775                1780                1785

Arg Val  Thr Asp Glu Ser Ile  Pro Ser Tyr Ser Gly  Ser Asp Met
    1790                1795                1800

Pro Arg  Asn Asp Ile Asn Met  Trp Ser Lys Val Thr  Glu Glu Gly
    1805                1810                1815

Thr Glu  Leu Ser Gln Arg Leu  Val Arg Ser Gly Phe  Ala Gly Thr
    1820                1825                1830

Glu Ile  Asp Pro Glu Asn Glu  Glu Leu Met Leu Asn  Ile Ser Ser
    1835                1840                1845

Arg Leu  Gln Ala Ala Val Glu  Lys Leu Leu Glu Ala  Ile Ser Glu
```

1850 1855 1860

Thr Ser Ser Gln Leu Glu His Ala Lys Val Thr Gln Thr Glu Leu
1865 1870 1875

Met Arg Glu Ser Phe Arg Gln Lys Gln Glu Ala Thr Glu Ser Leu
1880 1885 1890

Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His Glu Glu Ser Arg
1895 1900 1905

Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala Glu Gly Val
1910 1915 1920

Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg Gln Ile
1925 1930 1935

Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu Leu
1940 1945 1950

Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln
1955 1960 1965

Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met
1970 1975 1980

Lys Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr
1985 1990 1995

Glu Lys Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu
2000 2005 2010

Lys Val Arg Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile
2015 2020 2025

Asp Val Glu Glu Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu
2030 2035 2040

Lys Asn Thr Glu Leu Met Asp Leu Arg Gln Gln Asn Gln Ala Leu
2045 2050 2055

Glu Lys Gln Leu Glu Lys Met Arg Lys Phe Leu Asp Glu Gln Ala
2060 2065 2070

```
Ile Asp  Arg Glu His Glu Arg  Asp Val Phe Gln Gln  Glu Ile Gln
    2075                 2080                 2085

Lys Leu  Glu Gln Gln Leu Lys  Val Val Pro Arg Phe  Gln Pro Ile
    2090                 2095                 2100

Ser Glu  His Gln Thr Arg Glu  Val Glu Gln Leu Ala  Asn His Leu
    2105                 2110                 2115

Lys Glu  Lys Thr Asp Lys Cys  Ser Glu Leu Leu Leu  Ser Lys Glu
    2120                 2125                 2130

Gln Leu  Gln Arg Asp Ile Gln  Glu Arg Asn Glu Glu  Ile Glu Lys
    2135                 2140                 2145

Leu Glu  Phe Arg Val Arg Glu  Leu Glu Gln Ala Leu  Leu Val Ser
    2150                 2155                 2160

Ala Asp  Thr Phe Gln Lys Val  Glu Asp Arg Lys His  Phe Gly Ala
    2165                 2170                 2175

Val Glu  Ala Lys Pro Glu Leu  Ser Leu Glu Val Gln  Leu Gln Ala
    2180                 2185                 2190

Glu Arg  Asp Ala Ile Asp Arg  Lys Glu Lys Glu Ile  Thr Asn Leu
    2195                 2200                 2205

Glu Glu  Gln Leu Glu Gln Phe  Arg Glu Glu Leu Glu  Asn Lys Asn
    2210                 2215                 2220

Glu Glu  Val Gln Gln Leu His  Met Gln Leu Glu Ile  Gln Lys Lys
    2225                 2230                 2235

Glu Ser  Thr Thr Arg Leu Gln  Glu Leu Glu Gln Glu  Asn Lys Leu
    2240                 2245                 2250

Phe Lys  Asp Asp Met Glu Lys  Leu Gly Leu Ala Ile  Lys Glu Ser
    2255                 2260                 2265

Asp Ala  Met Ser Thr Gln Asp  Gln His Val Leu Phe  Gly Lys Phe
    2270                 2275                 2280
```

```
Ala Gln  Ile Ile Gln Glu Lys  Glu Val Glu Ile Asp  Gln Leu Asn
    2285                 2290                 2295

Glu Gln  Val Thr Lys Leu Gln  Gln Gln Leu Lys Ile  Thr Thr Asp
    2300                 2305                 2310

Asn Lys  Val Ile Glu Glu Lys  Asn Glu Leu Ile Arg  Asp Leu Glu
    2315                 2320                 2325

Thr Gln  Ile Glu Cys Leu Met  Ser Asp Gln Glu Cys  Val Lys Arg
    2330                 2335                 2340

Asn Arg  Glu Glu Glu Ile Glu  Gln Leu Asn Glu Val  Ile Glu Lys
    2345                 2350                 2355

Leu Gln  Gln Glu Leu Ala Asn  Ile Gly Gln Lys Thr  Ser Met Asn
    2360                 2365                 2370

Ala His  Ser Leu Ser Glu Glu  Ala Asp Ser Leu Lys  His Gln Leu
    2375                 2380                 2385

Asp Val  Val Ile Ala Glu Lys  Leu Ala Leu Glu Gln  Gln Val Glu
    2390                 2395                 2400

Thr Ala  Asn Glu Glu Met Thr  Phe Met Lys Asn Val  Leu Lys Glu
    2405                 2410                 2415

Thr Asn  Phe Lys Met Asn Gln  Leu Thr Gln Glu Leu  Phe Ser Leu
    2420                 2425                 2430

Lys Arg  Glu Arg Glu Ser Val  Glu Lys Ile Gln Ser  Ile Pro Glu
    2435                 2440                 2445

Asn Ser  Val Asn Val Ala Ile  Asp His Leu Ser Lys  Asp Lys Pro
    2450                 2455                 2460

Glu Leu  Glu Val Val Leu Thr  Glu Asp Ala Leu Lys  Ser Leu Glu
    2465                 2470                 2475

Asn Gln  Thr Tyr Phe Lys Ser  Phe Glu Glu Asn Gly  Lys Gly Ser
    2480                 2485                 2490
```

```
Ile Ile  Asn Leu Glu Thr Arg  Leu Leu Gln Leu Glu  Ser Thr Val
    2495                 2500                 2505

Ser Ala  Lys Asp Leu Glu Leu  Thr Gln Cys Tyr Lys  Gln Ile Lys
    2510                 2515                 2520

Asp Met  Gln Glu Gln Gly Gln  Phe Glu Thr Glu Met  Leu Gln Lys
    2525                 2530                 2535

Lys Ile  Val Asn Leu Gln Lys  Ile Val Glu Glu Lys  Val Ala Ala
    2540                 2545                 2550

Ala Leu  Val Ser Gln Ile Gln  Leu Glu Ala Val Gln  Glu Tyr Ala
    2555                 2560                 2565

Lys Phe  Cys Gln Asp Asn Gln  Thr Ile Ser Ser Glu  Pro Glu Arg
    2570                 2575                 2580

Thr Asn  Ile Gln Asn Leu Asn  Gln Leu Arg Glu Asp  Glu Leu Gly
    2585                 2590                 2595

Ser Asp  Ile Ser Ala Leu Thr  Leu Arg Ile Ser Glu  Leu Glu Ser
    2600                 2605                 2610

Gln Val  Val Glu Met His Thr  Ser Leu Ile Leu Glu  Lys Glu Gln
    2615                 2620                 2625

Val Glu  Ile Ala Glu Lys Asn  Val Leu Glu Lys Glu  Lys Lys Leu
    2630                 2635                 2640

Leu Glu  Leu Gln Lys Leu Leu  Glu Gly Asn Glu Lys  Lys Gln Arg
    2645                 2650                 2655

Glu Lys  Glu Lys Lys Arg Ser  Pro Gln Asp Val Glu  Val Leu Lys
    2660                 2665                 2670

Thr Thr  Thr Glu Leu Phe His  Ser Asn Glu Glu Ser  Gly Phe Phe
    2675                 2680                 2685

Asn Glu  Leu Glu Ala Leu Arg  Ala Glu Ser Val Ala  Thr Lys Ala
    2690                 2695                 2700

Glu Leu  Ala Ser Tyr Lys Glu  Lys Ala Glu Lys Leu  Gln Glu Glu
```

2705 2710 2715

Leu Leu Val Lys Glu Thr Asn Met Thr Ser Leu Gln Lys Asp Leu
2720 2725 2730

Ser Gln Val Arg Asp His Leu Ala Glu Ala Lys Glu Lys Leu Ser
2735 2740 2745

Ile Leu Glu Lys Glu Asp Glu Thr Glu Val Gln Glu Ser Lys Lys
2750 2755 2760

Ala Cys Met Phe Glu Pro Leu Pro Ile Lys Leu Ser Lys Ser Ile
2765 2770 2775

Ala Ser Gln Thr Asp Gly Thr Leu Lys Ile Ser Ser Ser Asn Gln
2780 2785 2790

Thr Pro Gln Ile Leu Val Lys Asn Ala Gly Ile Gln Ile Asn Leu
2795 2800 2805

Gln Ser Glu Cys Ser Ser Glu Glu Val Thr Glu Ile Ile Ser Gln
2810 2815 2820

Phe Thr Glu Lys Ile Glu Lys Met Gln Glu Leu His Ala Ala Glu
2825 2830 2835

Ile Leu Asp Met Glu Ser Arg His Ile Ser Glu Thr Glu Thr Leu
2840 2845 2850

Lys Arg Glu His Tyr Val Ala Val Gln Leu Leu Lys Glu Glu Cys
2855 2860 2865

Gly Thr Leu Lys Ala Val Ile Gln Cys Leu Arg Ser Lys Glu Gly
2870 2875 2880

Ser Ser Ile Pro Glu Leu Ala His Ser Asp Ala Tyr Gln Thr Arg
2885 2890 2895

Glu Ile Cys Ser Ser Asp Ser Gly Ser Asp Trp Gly Gln Gly Ile
2900 2905 2910

Tyr Leu Thr His Ser Gln Gly Phe Asp Ile Ala Ser Glu Gly Arg
2915 2920 2925

```
Gly Glu  Glu Ser Glu Ser Ala  Thr Asp Ser Phe Pro  Lys Lys Ile
    2930                 2935                 2940

Lys Gly  Leu Leu Arg Ala Val  His Asn Glu Gly Met  Gln Val Leu
    2945                 2950                 2955

Ser Leu  Thr Glu Ser Pro Tyr  Ser Asp Gly Glu Asp  His Ser Ile
    2960                 2965                 2970

Gln Gln  Val Ser Glu Pro Trp  Leu Glu Glu Arg Lys  Ala Tyr Ile
    2975                 2980                 2985

Asn Thr  Ile Ser Ser Leu Lys  Asp Leu Ile Thr Lys  Met Gln Leu
    2990                 2995                 3000

Gln Arg  Glu Ala Glu Val Tyr  Asp Ser Ser Gln Ser  His Glu Ser
    3005                 3010                 3015

Phe Ser  Asp Trp Arg Gly Glu  Leu Leu Leu Ala Leu  Gln Gln Val
    3020                 3025                 3030

Phe Leu  Glu Glu Arg Ser Val  Leu Leu Ala Ala Phe  Arg Thr Glu
    3035                 3040                 3045

Leu Thr  Ala Leu Gly Thr Thr  Asp Ala Val Gly Leu  Leu Asn Cys
    3050                 3055                 3060

Leu Glu  Gln Arg Ile Gln Glu  Gln Gly Val Glu Tyr  Gln Ala Ala
    3065                 3070                 3075

Met Glu  Cys Leu Gln Lys Ala  Asp Arg Arg Ser Leu  Leu Ser Glu
    3080                 3085                 3090

Ile Gln  Ala Leu His Ala Gln  Met Asn Gly Arg Lys  Ile Thr Leu
    3095                 3100                 3105

Lys Arg  Glu Gln Glu Ser Glu  Lys Pro Ser Gln Glu  Leu Leu Glu
    3110                 3115                 3120

Tyr Asn  Ile Gln Gln Lys Gln  Ser Gln Met Leu Glu  Met Gln Val
    3125                 3130                 3135
```

```
Glu Leu  Ser Ser Met Lys Asp  Arg Ala Thr Glu Leu  Gln Glu Gln
    3140                3145                3150

Leu Ser  Ser Glu Lys Met Val  Val Ala Glu Leu Lys  Ser Glu Leu
    3155                3160                3165

Ala Gln  Thr Lys Leu Glu Leu  Glu Thr Thr Leu Lys  Ala Gln His
    3170                3175                3180

Lys His  Leu Lys Glu Leu Glu  Ala Phe Arg Leu Glu  Val Lys Asp
    3185                3190                3195

Lys Thr  Asp Glu Val His Leu  Leu Asn Asp Thr Leu  Ala Ser Glu
    3200                3205                3210

Gln Lys  Lys Ser Arg Glu Leu  Gln Trp Ala Leu Glu  Lys Glu Lys
    3215                3220                3225

Ala Lys  Leu Gly Arg Ser Glu  Glu Arg Asp Lys Glu  Glu Leu Glu
    3230                3235                3240

Asp Leu  Lys Phe Ser Leu Glu  Ser Gln Lys Gln Arg  Asn Leu Gln
    3245                3250                3255

Leu Asn  Leu Leu Leu Glu Gln  Gln Lys Gln Leu Leu  Asn Glu Ser
    3260                3265                3270

Gln Gln  Lys Ile Glu Ser Gln  Arg Met Leu Tyr Asp  Ala Gln Leu
    3275                3280                3285

Ser Glu  Glu Gln Gly Arg Asn  Leu Glu Leu Gln Val  Leu Leu Glu
    3290                3295                3300

Ser Glu  Lys Val Arg Ile Arg  Glu Met Ser Ser Thr  Leu Asp Arg
    3305                3310                3315

Glu Arg  Glu Leu His Ala Gln  Leu Gln Ser Ser Asp  Gly Thr Gly
    3320                3325                3330

Gln Ser  Arg Pro Pro Leu Pro  Ser Glu Asp Leu Leu  Lys Glu Leu
    3335                3340                3345
```

```
Gln Lys  Gln Leu Glu Glu Lys  His Ser Arg Ile Val  Glu Leu Leu
    3350                 3355                 3360

Asn Glu  Thr Glu Lys Tyr Lys  Leu Asp Ser Leu Gln  Thr Arg Gln
    3365                 3370                 3375

Gln Met  Glu Lys Asp Arg Gln  Val His Arg Lys Thr  Leu Gln Thr
    3380                 3385                 3390

Glu Gln  Glu Ala Asn Thr Glu  Gly Gln Lys Lys Met  His Glu Leu
    3395                 3400                 3405

Gln Ser  Lys Val Glu Asp Leu  Gln Arg Gln Leu Glu  Glu Lys Arg
    3410                 3415                 3420

Gln Gln  Val Tyr Lys Leu Asp  Leu Glu Gly Gln Arg  Leu Gln Gly
    3425                 3430                 3435

Ile Met  Gln Glu Phe Gln Lys  Gln Glu Leu Glu Arg  Glu Glu Lys
    3440                 3445                 3450

Arg Glu  Ser Arg Arg Ile Leu  Tyr Gln Asn Leu Asn  Glu Pro Thr
    3455                 3460                 3465

Thr Trp  Ser Leu Thr Ser Asp  Arg Thr Arg Asn Trp  Val Leu Gln
    3470                 3475                 3480

Gln Lys  Ile Glu Gly Glu Thr  Lys Glu Ser Asn Tyr  Ala Lys Leu
    3485                 3490                 3495

Ile Glu  Met Asn Gly Gly Gly  Thr Gly Cys Asn His  Glu Leu Glu
    3500                 3505                 3510

Met Ile  Arg Gln Lys Leu Gln  Cys Val Ala Ser Lys  Leu Gln Val
    3515                 3520                 3525

Leu Pro  Gln Lys Ala Ser Glu  Arg Leu Gln Phe Glu  Thr Ala Asp
    3530                 3535                 3540

Asp Glu  Asp Phe Ile Trp Val  Gln Glu Asn Ile Asp  Glu Ile Ile
    3545                 3550                 3555

Leu Gln  Leu Gln Lys Leu Thr  Gly Gln Gln Gly Glu  Glu Pro Ser
```

```
    3560                3565                3570

Leu Val  Ser Pro Ser Thr Ser  Cys Gly Ser Leu Thr  Glu Arg Leu
    3575                3580                3585

Leu Arg  Gln Asn Ala Glu Leu  Thr Gly His Ile Ser  Gln Leu Thr
    3590                3595                3600

Glu Glu  Lys Asn Asp Leu Arg  Asn Met Val Met Lys  Leu Glu Glu
    3605                3610                3615

Gln Ile  Arg Trp Tyr Arg Gln  Thr Gly Ala Gly Arg  Asp Asn Ser
    3620                3625                3630

Ser Arg  Phe Ser Leu Asn Gly  Gly Ala Asn Ile Glu  Ala Ile Ile
    3635                3640                3645

Ala Ser  Glu Lys Glu Val Trp  Asn Arg Glu Lys Leu  Thr Leu Gln
    3650                3655                3660

Lys Ser  Leu Lys Arg Ala Glu  Ala Glu Val Tyr Lys  Leu Lys Ala
    3665                3670                3675

Glu Leu  Arg Asn Asp Ser Leu  Leu Gln Thr Leu Ser  Pro Asp Ser
    3680                3685                3690

Glu His  Val Thr Leu Lys Arg  Ile Tyr Gly Lys Tyr  Leu Arg Ala
    3695                3700                3705

Glu Ser  Phe Arg Lys Ala Leu  Ile Tyr Gln Lys Lys  Tyr Leu Leu
    3710                3715                3720

Leu Leu  Leu Gly Gly Phe Gln  Glu Cys Glu Asp Ala  Thr Leu Ala
    3725                3730                3735

Leu Leu  Ala Arg Met Gly Gly  Gln Pro Ala Phe Thr  Asp Leu Glu
    3740                3745                3750

Val Ile  Thr Asn Arg Pro Lys  Gly Phe Thr Arg Phe  Arg Ser Ala
    3755                3760                3765

Val Arg  Val Ser Ile Ala Ile  Ser Arg Met Lys Phe  Leu Val Arg
    3770                3775                3780
```

```
Arg Trp  His Arg Val Thr Gly  Ser Val Ser Ile Asn  Ile Asn Arg
    3785                 3790                 3795

Asp Gly  Phe Gly Leu Asn Gln  Gly Ala Glu Lys Thr  Asp Ser Phe
    3800                 3805                 3810

Tyr His  Ser Ser Gly Gly Leu  Glu Leu Tyr Gly Glu  Pro Arg His
    3815                 3820                 3825

Thr Thr  Tyr Arg Ser Arg Ser  Asp Leu Asp Tyr Ile  Arg Ser Pro
    3830                 3835                 3840

Leu Pro  Phe Gln Asn Arg Tyr  Pro Gly Thr Pro Ala  Asp Phe Asn
    3845                 3850                 3855

Pro Gly  Ser Leu Ala Cys Ser  Gln Leu Gln Asn Tyr  Asp Pro Asp
    3860                 3865                 3870

Arg Ala  Leu Thr Asp Tyr Ile  Thr Arg Leu Glu Ala  Leu Gln Arg
    3875                 3880                 3885

Arg Leu  Gly Thr Ile Gln Ser  Gly Ser Thr Thr Gln  Phe His Ala
    3890                 3895                 3900

Gly Met  Arg Arg
    3905


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20 25 30

Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
35 40 45

Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
50 55 60

Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
65 70 75 80

Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
85 90 95

Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100 105 110

Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115 120 125

Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130 135 140

Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145 150 155 160

Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165 170 175

Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180 185 190

Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195 200 205

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

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    210                 215                 220

Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225                 230                 235                 240

Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
                245                 250                 255

Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
            260                 265                 270

His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
        275                 280                 285

Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
    290                 295                 300

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

Lys Glu Glu Ile Gln Glu Lys Glu Thr Ile Ile Glu Glu Leu Asn Thr
                325                 330                 335

Lys Ile Ile Glu Glu Glu Lys Lys Thr Leu Glu Leu Lys Asp Lys Leu
            340                 345                 350

Thr Thr Ala Asp Lys Leu Leu Gly Glu Leu Gln Glu Gln Ile Val Gln
        355                 360                 365

Lys Asn Gln Glu Ile Lys Asn Met Lys Leu Glu Leu Thr Asn Ser Lys
    370                 375                 380

Gln Lys Glu Arg Gln Ser Ser Glu Glu Ile Lys Gln Leu Met Gly Thr
385                 390                 395                 400

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

Asp Ile Val Gln Arg Met Glu Gln Glu Thr Gln Arg Lys Leu Glu Gln
            420                 425                 430

Leu Arg Ala Glu Leu Asp Glu Met Tyr Gly Gln Gln Ile Val Gln Met
        435                 440                 445
```

```
Lys Gln Glu Leu Ile Arg Gln His Met Ala Gln Met Glu Glu Met Lys
    450                 455                 460

Thr Arg His Lys Gly Glu Met Glu Asn Ala Leu Arg Ser Tyr Ser Asn
465                 470                 475                 480

Ile Thr Val Asn Glu Asp Gln Ile Lys Leu Met Asn Val Ala Ile Asn
                485                 490                 495

Glu Leu Asn Ile Lys Leu Gln Asp Thr Asn Ser Gln Lys Glu Lys Leu
            500                 505                 510

Lys Glu Glu Leu Gly Leu Ile Leu Glu Glu Lys Cys Ala Leu Gln Arg
        515                 520                 525

Gln Leu Glu Asp Leu Val Glu Glu Leu Ser Phe Ser Arg Glu Gln Ile
    530                 535                 540

Gln Arg Ala Arg Gln Thr Ile Ala Glu Gln Glu Ser Lys Leu Asn Glu
545                 550                 555                 560

Ala His Lys Ser Leu Ser Thr Val Glu Asp Leu Lys Ala Glu Ile Val
                565                 570                 575

Ser Ala Ser Glu Ser Arg Lys Glu Leu Glu Leu Lys His Glu Ala Glu
            580                 585                 590

Val Thr Asn Tyr Lys Ile Lys Leu Glu Met Leu Glu Lys Glu Lys Asn
        595                 600                 605

Ala Val Leu Asp Arg Met Ala Glu Ser Gln Glu Ala Glu Leu Glu Arg
    610                 615                 620

Leu Arg Thr Gln Leu Leu Phe Ser His Glu Glu Glu Leu Ser Lys Leu
625                 630                 635                 640

Lys Glu Asp Leu Glu Ile Glu His Arg Ile Asn Ile Glu Lys Leu Lys
                645                 650                 655

Asp Asn Leu Gly Ile His Tyr Lys Gln Gln Ile Asp Gly Leu Gln Asn
            660                 665                 670
```

```
Glu Met Ser Gln Lys Ile Glu Thr Met Gln Phe Glu Lys Asp Asn Leu
        675                 680                 685

Ile Thr Lys Gln Asn Gln Leu Ile Leu Glu Ile Ser Lys Leu Lys Asp
    690                 695                 700

Leu Gln Gln Ser Leu Val Asn Ser Lys Ser Glu Glu Met Thr Leu Gln
705                 710                 715                 720

Ile Asn Glu Leu Gln Lys Glu Ile Glu Ile Leu Arg Gln Glu Glu Lys
                725                 730                 735

Glu Lys Gly Thr Leu Glu Gln Glu Val Gln Glu Leu Gln Leu Lys Thr
            740                 745                 750

Glu Leu Leu Glu Lys Gln Met Lys Glu Lys Glu Asn Asp Leu Gln Glu
        755                 760                 765

Lys Phe Ala Gln Leu Glu Ala Glu Asn Ser Ile Leu Lys Asp Glu Lys
    770                 775                 780

Lys Thr Leu Glu Asp Met Leu Lys Ile His Thr Pro Val Ser Gln Glu
785                 790                 795                 800

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

Val Trp Glu Lys Glu Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu
            820                 825                 830

Lys Gln Gln Cys Ile Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn
        835                 840                 845

Thr Phe Ser Phe Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu
    850                 855                 860

Gln Glu Glu Tyr Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp
865                 870                 875                 880

Ser Lys Asn Lys Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu
                885                 890                 895
```

```
Asn Glu Glu Leu His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met
            900                 905                 910

Lys Ser Ser Val Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu
        915                 920                 925

Glu Met Gly Glu Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys
    930                 935                 940

Leu Glu Val Thr Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser
945                 950                 955                 960

Asp Leu Ser Glu Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu
                965                 970                 975

Asn Glu Glu Val Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu
            980                 985                 990

Arg Cys Arg Glu Leu Glu Ile Ile  Ile Asn His Asn Arg  Ala Glu
Asn
        995                 1000                1005

Val Gln  Ser Cys Asp Thr Gln  Val Ser Ser Leu Leu  Asp Gly Val
    1010                1015                1020

Val Thr  Met Thr Ser Arg Gly  Ala Glu Gly Ser Val  Ser Lys Val
    1025                1030                1035

Asn Lys  Ser Phe Gly Glu Glu  Ser Lys Ile Met Val  Glu Asp Lys
    1040                1045                1050

Val Ser  Phe Glu Asn Met Thr  Val Gly Glu Glu Ser  Lys Gln Glu
    1055                1060                1065

Gln Leu  Ile Leu Asp His Leu  Pro Ser Val Thr Lys  Glu Ser Ser
    1070                1075                1080

Leu Arg  Ala Thr Gln Pro Ser  Glu Asn Asp Lys Leu  Gln Lys Glu
    1085                1090                1095

Leu Asn  Val Leu Lys Ser Glu  Gln Asn Asp Leu Arg  Leu Gln Met
    1100                1105                1110
```

Glu Ala Gln Arg Ile Cys Leu Ser Leu Val Tyr Ser Thr His Val
1115 1120 1125

Asp Gln Val Arg Glu Tyr Met Glu Asn Glu Lys Asp Lys Ala Leu
1130 1135 1140

Cys Ser Leu Lys Glu Glu Leu Ile Phe Ala Gln Glu Glu Lys Ile
1145 1150 1155

Lys Glu Leu Gln Lys Ile His Gln Leu Glu Leu Gln Thr Met Lys
1160 1165 1170

Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu His Leu Leu Ile
1175 1180 1185

Gly Lys Leu Gln Lys Ala Val Ser Glu Glu Cys Ser Tyr Phe Leu
1190 1195 1200

Gln Thr Leu Cys Ser Val Leu Gly Glu Tyr Tyr Thr Pro Ala Leu
1205 1210 1215

Lys Cys Glu Val Asn Ala Glu Asp Lys Glu Asn Ser Gly Asp Tyr
1220 1225 1230

Ile Ser Glu Asn Glu Asp Pro Glu Leu Gln Asp Tyr Arg Tyr Glu
1235 1240 1245

Val Gln Asp Phe Gln Glu Asn Met His Thr Leu Leu Asn Lys Val
1250 1255 1260

Thr Glu Glu Tyr Asn Lys Leu Leu Val Leu Gln Thr Arg Leu Ser
1265 1270 1275

Lys Ile Trp Gly Gln Gln Thr Asp Gly Met Lys Leu Glu Phe Gly
1280 1285 1290

Glu Glu Asn Leu Pro Lys Glu Glu Thr Glu Phe Leu Ser Ile His
1295 1300 1305

Ser Gln Met Thr Asn Leu Glu Asp Ile Asp Val Asn His Lys Ser
1310 1315 1320

Lys Leu Ser Ser Leu Gln Asp Leu Glu Lys Thr Lys Leu Glu Glu

1325 1330 1335

Gln Val Gln Glu Leu Glu Ser Leu Ile Ser Ser Leu Gln Gln Gln
1340 1345 1350

Leu Lys Glu Thr Glu Gln Asn Tyr Glu Ala Glu Ile His Cys Leu
1355 1360 1365

Gln Lys Arg Leu Gln Ala Val Ser Glu Ser Thr Val Pro Pro Ser
1370 1375 1380

Leu Pro Val Asp Ser Val Val Ile Thr Glu Ser Asp Ala Gln Arg
1385 1390 1395

Thr Met Tyr Pro Gly Ser Cys Val Lys Lys Asn Ile Asp Gly Thr
1400 1405 1410

Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu Glu Thr Asn Ile
1415 1420 1425

Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu Glu Glu Glu
1430 1435 1440

Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala Gln Gln
1445 1450 1455

Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala Ser
1460 1465 1470

Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe
1475 1480 1485

Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe
1490 1495 1500

Glu Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser
1505 1510 1515

Lys Glu Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser
1520 1525 1530

Asp Pro His Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile
1535 1540 1545

```
Ser Glu  Glu Met Phe Ser Lys  Asp Lys Thr Phe Ile  Val Arg Gln
    1550                1555                1560

Ser Ile  His Asp Glu Ile Ser  Val Ser Ser Met Asp  Ala Ser Arg
    1565                1570                1575

Gln Leu  Met Leu Asn Glu Glu  Gln Leu Glu Asp Met  Arg Gln Glu
    1580                1585                1590

Leu Val  Arg Gln Tyr Gln Glu  His Gln Gln Ala Thr  Glu Leu Leu
    1595                1600                1605

Arg Gln  Ala His Met Arg Gln  Met Glu Arg Gln Arg  Glu Asp Gln
    1610                1615                1620

Glu Gln  Leu Gln Glu Glu Ile  Lys Arg Leu Asn Arg  Gln Leu Ala
    1625                1630                1635

Gln Asn  Gly Asn Glu Asn Gln  Gly Glu Val Glu Glu  Gln Thr Phe
    1640                1645                1650

Lys Glu  Lys Glu Leu Asp Arg  Lys Pro Glu Asp Val  Pro Pro Glu
    1655                1660                1665

Ile Leu  Ser Asn Glu Arg Tyr  Ala Leu Gln Lys Ala  Asn Asn Arg
    1670                1675                1680

Leu Leu  Lys Ile Leu Leu Glu  Val Val Lys Thr Thr  Ala Ala Val
    1685                1690                1695

Glu Glu  Thr Ile Gly Arg His  Val Leu Gly Ile Leu  Asp Arg Ser
    1700                1705                1710

Ser Lys  Ser Gln Ser Ser Ala  Ser Leu Ile Trp Arg  Ser Glu Ala
    1715                1720                1725

Glu Ala  Ser Val Lys Ser Cys  Val His Glu Glu His  Thr Arg Val
    1730                1735                1740

Thr Asp  Glu Ser Ile Pro Ser  Tyr Ser Gly Ser Asp  Met Pro Arg
    1745                1750                1755
```

```
Asn Asp  Ile Asn Met Trp Ser  Lys Val Thr Glu Glu  Gly Thr Glu
    1760                1765                1770

Leu Ser  Gln Arg Leu Val Arg  Ser Gly Phe Ala Gly  Thr Glu Ile
    1775                1780                1785

Asp Pro  Glu Asn Glu Glu Leu  Met Leu Asn Ile Ser  Ser Arg Leu
    1790                1795                1800

Gln Ala  Ala Val Glu Lys Leu  Leu Glu Ala Ile Ser  Glu Thr Ser
    1805                1810                1815

Ser Gln  Leu Glu His Ala Lys  Val Thr Gln Thr Glu  Leu Met Arg
    1820                1825                1830

Glu Ser  Phe Arg Gln Lys Gln  Glu Ala Thr Glu Ser  Leu Lys Cys
    1835                1840                1845

Gln Glu  Glu Leu Arg Glu Arg  Leu His Glu Glu Ser  Arg Ala Arg
    1850                1855                1860

Glu Gln  Leu Ala Val Glu Leu  Ser Lys Ala Glu Gly  Val Ile Asp
    1865                1870                1875

Gly Tyr  Ala Asp Glu Lys Thr  Leu Phe Glu Arg Gln  Ile Gln Glu
    1880                1885                1890

Lys Thr  Asp Ile Ile Asp Arg  Leu Glu Gln Glu Leu  Leu Cys Ala
    1895                1900                1905

Ser Asn  Arg Leu Gln Glu Leu  Glu Ala Glu Gln Gln  Gln Ile Gln
    1910                1915                1920

Glu Glu  Arg Glu Leu Leu Ser  Arg Gln Lys Glu Ala  Met Lys Ala
    1925                1930                1935

Glu Ala  Gly Pro Val Glu Gln  Gln Leu Leu Gln Glu  Thr Glu Lys
    1940                1945                1950

Leu Met  Lys Glu Lys Leu Glu  Val Gln Cys Gln Ala  Glu Lys Val
    1955                1960                1965
```

Arg Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val
1970 1975 1980

Glu Glu Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn
1985 1990 1995

Thr Glu Leu Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys
2000 2005 2010

Gln Leu Glu Lys Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp
2015 2020 2025

Arg Glu His Glu Arg Asp Val Phe Gln Gln Glu Ile Gln Lys Leu
2030 2035 2040

Glu Gln Gln Leu Lys Val Val Pro Arg Phe Gln Pro Ile Ser Glu
2045 2050 2055

His Gln Thr Arg Glu Val Glu Gln Leu Ala Asn His Leu Lys Glu
2060 2065 2070

Lys Thr Asp Lys Cys Ser Glu Leu Leu Leu Ser Lys Glu Gln Leu
2075 2080 2085

Gln Arg Asp Ile Gln Glu Arg Asn Glu Glu Ile Glu Lys Leu Glu
2090 2095 2100

Phe Arg Val Arg Glu Leu Glu Gln Ala Leu Leu Val Ser Ala Asp
2105 2110 2115

Thr Phe Gln Lys Val Glu Asp Arg Lys His Phe Gly Ala Val Glu
2120 2125 2130

Ala Lys Pro Glu Leu Ser Leu Glu Val Gln Leu Gln Ala Glu Arg
2135 2140 2145

Asp Ala Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu Glu Glu
2150 2155 2160

Gln Leu Glu Gln Phe Arg Glu Glu Leu Glu Asn Lys Asn Glu Glu
2165 2170 2175

Val Gln Gln Leu His Met Gln Leu Glu Ile Gln Lys Lys Glu Ser

2180 2185 2190

Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu Asn Lys Leu Phe Lys
2195 2200 2205

Asp Asp Met Glu Lys Leu Gly Leu Ala Ile Lys Glu Ser Asp Ala
2210 2215 2220

Met Ser Thr Gln Asp Gln His Val Leu Phe Gly Lys Phe Ala Gln
2225 2230 2235

Ile Ile Gln Glu Lys Glu Val Glu Ile Asp Gln Leu Asn Glu Gln
2240 2245 2250

Val Thr Lys Leu Gln Gln Gln Leu Lys Ile Thr Thr Asp Asn Lys
2255 2260 2265

Val Ile Glu Glu Lys Asn Glu Leu Ile Arg Asp Leu Glu Thr Gln
2270 2275 2280

Ile Glu Cys Leu Met Ser Asp Gln Glu Cys Val Lys Arg Asn Arg
2285 2290 2295

Glu Glu Glu Ile Glu Gln Leu Asn Glu Val Ile Glu Lys Leu Gln
2300 2305 2310

Gln Glu Leu Ala Asn Ile Gly Gln Lys Thr Ser Met Asn Ala His
2315 2320 2325

Ser Leu Ser Glu Glu Ala Asp Ser Leu Lys His Gln Leu Asp Val
2330 2335 2340

Val Ile Ala Glu Lys Leu Ala Leu Glu Gln Gln Val Glu Thr Ala
2345 2350 2355

Asn Glu Glu Met Thr Phe Met Lys Asn Val Leu Lys Glu Thr Asn
2360 2365 2370

Phe Lys Met Asn Gln Leu Thr Gln Glu Leu Phe Ser Leu Lys Arg
2375 2380 2385

Glu Arg Glu Ser Val Glu Lys Ile Gln Ser Ile Pro Glu Asn Ser
2390 2395 2400

```
Val Asn  Val Ala Ile Asp His  Leu Ser Lys Asp Lys  Pro Glu Leu
    2405                2410                2415

Glu Val  Val Leu Thr Glu Asp  Ala Leu Lys Ser Leu  Glu Asn Gln
    2420                2425                2430

Thr Tyr  Phe Lys Ser Phe Glu  Glu Asn Gly Lys Gly  Ser Ile Ile
    2435                2440                2445

Asn Leu  Glu Thr Arg Leu Leu  Gln Leu Glu Ser Thr  Val Ser Ala
    2450                2455                2460

Lys Asp  Leu Glu Leu Thr Gln  Cys Tyr Lys Gln Ile  Lys Asp Met
    2465                2470                2475

Gln Glu  Gln Gly Gln Phe Glu  Thr Glu Met Leu Gln  Lys Lys Ile
    2480                2485                2490

Val Asn  Leu Gln Lys Ile Val  Glu Glu Lys Val Ala  Ala Ala Leu
    2495                2500                2505

Val Ser  Gln Ile Gln Leu Glu  Ala Val Gln Glu Tyr  Ala Lys Phe
    2510                2515                2520

Cys Gln  Asp Asn Gln Thr Ile  Ser Ser Glu Pro Glu  Arg Thr Asn
    2525                2530                2535

Ile Gln  Asn Leu Asn Gln Leu  Arg Glu Asp Glu Leu  Gly Ser Asp
    2540                2545                2550

Ile Ser  Ala Leu Thr Leu Arg  Ile Ser Glu Leu Glu  Ser Gln Val
    2555                2560                2565

Val Glu  Met His Thr Ser Leu  Ile Leu Glu Lys Glu  Gln Val Glu
    2570                2575                2580

Ile Ala  Glu Lys Asn Val Leu  Glu Lys Glu Lys Lys  Leu Leu Glu
    2585                2590                2595

Leu Gln  Lys Leu Leu Glu Gly  Asn Glu Lys Lys Gln  Arg Glu Lys
    2600                2605                2610
```

```
Glu Lys  Lys Arg Ser Pro Gln  Asp Val Glu Val Leu  Lys Thr Thr
    2615                2620                2625

Thr Glu  Leu Phe His Ser Asn  Glu Glu Ser Gly Phe  Phe Asn Glu
    2630                2635                2640

Leu Glu  Ala Leu Arg Ala Glu  Ser Val Ala Thr Lys  Ala Glu Leu
    2645                2650                2655

Ala Ser  Tyr Lys Glu Lys Ala  Glu Lys Leu Gln Glu  Glu Leu Leu
    2660                2665                2670

Val Lys  Glu Thr Asn Met Thr  Ser Leu Gln Lys Asp  Leu Ser Gln
    2675                2680                2685

Val Arg  Asp His Leu Ala Glu  Ala Lys Glu Lys Leu  Ser Ile Leu
    2690                2695                2700

Glu Lys  Glu Asp Glu Thr Glu  Val Gln Glu Ser Lys  Lys Ala Cys
    2705                2710                2715

Met Phe  Glu Pro Leu Pro Ile  Lys Leu Ser Lys Ser  Ile Ala Ser
    2720                2725                2730

Gln Thr  Asp Gly Thr Leu Lys  Ile Ser Ser Ser Asn  Gln Thr Pro
    2735                2740                2745

Gln Ile  Leu Val Lys Asn Ala  Gly Ile Gln Ile Asn  Leu Gln Ser
    2750                2755                2760

Glu Cys  Ser Ser Glu Glu Val  Thr Glu Ile Ile Ser  Gln Phe Thr
    2765                2770                2775

Glu Lys  Ile Glu Lys Met Gln  Glu Leu His Ala Ala  Glu Ile Leu
    2780                2785                2790

Asp Met  Glu Ser Arg His Ile  Ser Glu Thr Glu Thr  Leu Lys Arg
    2795                2800                2805

Glu His  Tyr Val Ala Val Gln  Leu Leu Lys Glu Glu  Cys Gly Thr
    2810                2815                2820
```

```
Leu Lys  Ala Val Ile Gln Cys  Leu Arg Ser Lys Glu  Gly Ser Ser
    2825                 2830                 2835

Ile Pro  Glu Leu Ala His Ser  Asp Ala Tyr Gln Thr  Arg Glu Ile
    2840                 2845                 2850

Cys Ser  Ser Asp Ser Gly Ser  Asp Trp Gly Gln Gly  Ile Tyr Leu
    2855                 2860                 2865

Thr His  Ser Gln Gly Phe Asp  Ile Ala Ser Glu Gly  Arg Gly Glu
    2870                 2875                 2880

Glu Ser  Glu Ser Ala Thr Asp  Ser Phe Pro Lys Lys  Ile Lys Gly
    2885                 2890                 2895

Leu Leu  Arg Ala Val His Asn  Glu Gly Met Gln Val  Leu Ser Leu
    2900                 2905                 2910

Thr Glu  Ser Pro Tyr Ser Asp  Gly Glu Asp His Ser  Ile Gln Gln
    2915                 2920                 2925

Val Ser  Glu Pro Trp Leu Glu  Glu Arg Lys Ala Tyr  Ile Asn Thr
    2930                 2935                 2940

Ile Ser  Ser Leu Lys Asp Leu  Ile Thr Lys Met Gln  Leu Gln Arg
    2945                 2950                 2955

Glu Ala  Glu Val Tyr Asp Ser  Ser Gln Ser His Glu  Ser Phe Ser
    2960                 2965                 2970

Asp Trp  Arg Gly Glu Leu Leu  Leu Ala Leu Gln Gln  Val Phe Leu
    2975                 2980                 2985

Glu Glu  Arg Ser Val Leu Leu  Ala Ala Phe Arg Thr  Glu Leu Thr
    2990                 2995                 3000

Ala Leu  Gly Thr Thr Asp Ala  Val Gly Leu Leu Asn  Cys Leu Glu
    3005                 3010                 3015

Gln Arg  Ile Gln Glu Gln Gly  Val Glu Tyr Gln Ala  Ala Met Glu
    3020                 3025                 3030

Cys Leu  Gln Lys Ala Asp Arg  Arg Ser Leu Leu Ser  Glu Ile Gln
```

```
    3035                3040                3045

Ala Leu  His Ala Gln Met Asn  Gly Arg Lys Ile Thr  Leu Lys Arg
    3050                3055                3060

Glu Gln  Glu Ser Glu Lys Pro  Ser Gln Gly Met Leu  Tyr Asp Lys
    3065                3070                3075

Leu Ile  Trp Leu His Lys Gln  Val Lys Arg Phe His  Phe Val Phe
    3080                3085                3090

Phe Leu  Ile Ile Ile Lys Leu  Lys His Ile Phe Leu  Val Thr Phe
    3095                3100                3105

Ser Ser  His Ser His Asn Val  Lys Asp Thr Ile Tyr  Ile Asn Tyr
    3110                3115                3120

Ser Arg  Gly
    3125


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Val Gly Glu Pro Glu Gly Tyr Phe Leu Phe Ser Leu Ala Gln Phe Arg
            20                  25                  30
```

```
Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro Ser Lys Lys Gln Lys
        35                  40                  45

Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp Val Ser Ala His His
    50                  55                  60

Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu Met Tyr Ile Asn Ser
65                  70                  75                  80

Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu Ser Thr Ile Met Arg
                85                  90                  95

Thr Leu His Ser Gly Glu Ile Thr Ser His Glu Gln Gly Phe Ser Val
            100                 105                 110

Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp Asp Cys Ser Ser Glu
        115                 120                 125

Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly Lys Pro Thr Asn Leu
    130                 135                 140

Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser Tyr Ser Glu Gln Gly
145                 150                 155                 160

Ala Gln Asp Ser Pro Thr His Leu Glu Met Met Glu Ser Glu Leu Ala
                165                 170                 175

Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg Glu Leu Glu Glu Met
            180                 185                 190

Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln Leu Gln Glu Phe Glu
        195                 200                 205

Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr Gln Leu Thr Ala Asn
    210                 215                 220

Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr Met Arg Glu Phe Leu
225                 230                 235                 240

Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile Gln Phe Gln Gln Leu
                245                 250                 255
```

```
Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His Ser Ser Thr Ala Ala
            260                 265                 270

Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr His Gln Gln Gln Leu
        275                 280                 285

Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln Lys Lys Lys Glu Asp
    290                 295                 300

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

Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn Lys Glu Glu Ile Gln
                325                 330                 335

Glu Lys Glu Thr Ile Ile Glu Glu Leu Asn Thr Lys Ile Ile Glu Glu
            340                 345                 350

Glu Lys Lys Thr Leu Glu Leu Lys Asp Lys Leu Thr Thr Ala Asp Lys
        355                 360                 365

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

Lys Asn Met Lys Leu Glu Leu Thr Asn Ser Lys Gln Lys Glu Arg Gln
385                 390                 395                 400

Ser Ser Glu Glu Ile Lys Gln Leu Met Gly Thr Val Glu Glu Leu Gln
                405                 410                 415

Lys Arg Asn His Lys Asp Ser Gln Phe Glu Thr Asp Ile Val Gln Arg
            420                 425                 430

Met Glu Gln Glu Thr Gln Arg Lys Leu Glu Gln Leu Arg Ala Glu Leu
        435                 440                 445

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

Arg Gln His Met Ala Gln Met Glu Glu Met Lys Thr Arg His Lys Gly
465                 470                 475                 480

Glu Met Glu Asn Ala Leu Arg Ser Tyr Ser Asn Ile Thr Val Asn Glu
```

485 490 495

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

Leu Gln Asp Thr Asn Ser Gln Lys Glu Lys Leu Lys Glu Glu Leu Gly
515 520 525

Leu Ile Leu Glu Glu Lys Cys Ala Leu Gln Arg Gln Leu Glu Asp Leu
530 535 540

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

Thr Ile Ala Glu Gln Glu Ser Lys Leu Asn Glu Ala His Lys Ser Leu
565 570 575

Ser Thr Val Glu Asp Leu Lys Ala Glu Ile Val Ser Ala Ser Glu Ser
580 585 590

Arg Lys Glu Leu Glu Leu Lys His Glu Ala Glu Val Thr Asn Tyr Lys
595 600 605

Ile Lys Leu Glu Met Leu Glu Lys Glu Lys Asn Ala Val Leu Asp Arg
610 615 620

Met Ala Glu Ser Gln Glu Ala Glu Leu Glu Arg Leu Arg Thr Gln Leu
625 630 635 640

Leu Phe Ser His Glu Glu Glu Leu Ser Lys Leu Lys Glu Asp Leu Glu
645 650 655

Ile Glu His Arg Ile Asn Ile Glu Lys Leu Lys Asp Asn Leu Gly Ile
660 665 670

His Tyr Lys Gln Gln Ile Asp Gly Leu Gln Asn Glu Met Ser Gln Lys
675 680 685

Ile Glu Thr Met Gln Phe Glu Lys Asp Asn Leu Ile Thr Lys Gln Asn
690 695 700

Gln Leu Ile Leu Glu Ile Ser Lys Leu Lys Asp Leu Gln Gln Ser Leu
705 710 715 720

```
Val Asn Ser Lys Ser Glu Glu Met Thr Leu Gln Ile Asn Glu Leu Gln
                725                 730                 735

Lys Glu Ile Glu Ile Leu Arg Gln Glu Glu Lys Glu Lys Gly Thr Leu
            740                 745                 750

Glu Gln Glu Val Gln Glu Leu Gln Leu Lys Thr Glu Leu Leu Glu Lys
        755                 760                 765

Gln Met Lys Glu Lys Glu Asn Asp Leu Gln Glu Lys Phe Ala Gln Leu
    770                 775                 780

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

Met Leu Lys Ile His Thr Pro Val Ser Gln Glu Glu Arg Leu Ile Phe
                805                 810                 815

Leu Asp Ser Ile Lys Ser Lys Ser Lys Asp Ser Val Trp Glu Lys Glu
            820                 825                 830

Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu Lys Gln Gln Cys Ile
        835                 840                 845

Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn Thr Phe Ser Phe Ala
    850                 855                 860

Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu Gln Glu Glu Tyr Ala
865                 870                 875                 880

Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp Ser Lys Asn Lys Gln
                885                 890                 895

Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu Asn Glu Glu Leu His
            900                 905                 910

Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met Lys Ser Ser Val Phe
        915                 920                 925

Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu Glu Met Gly Glu Val
    930                 935                 940
```

```
Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys Leu Glu Val Thr Lys
945                 950                 955                 960

Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser Asp Leu Ser Glu Gln
                965                 970                 975

Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu Asn Glu Glu Val Lys
            980                 985                 990

Ser Leu Lys Gln Glu Lys Glu Gln  Val Ser Leu Arg Cys  Arg Glu
Leu
        995                 1000                1005

Glu Ile  Ile Ile Asn His Asn  Arg Ala Glu Asn Val  Gln Ser Cys
    1010                1015                1020

Asp Thr  Gln Val Ser Ser Leu  Leu Asp Gly Val Val  Thr Met Thr
    1025                1030                1035

Ser Arg  Gly Ala Glu Gly Ser  Val Ser Lys Val Asn  Lys Ser Phe
    1040                1045                1050

Gly Glu  Glu Ser Lys Ile Met  Val Glu Asp Lys Val  Ser Phe Glu
    1055                1060                1065

Asn Met  Thr Val Gly Glu Glu  Ser Lys Gln Glu Gln  Leu Ile Leu
    1070                1075                1080

Asp His  Leu Pro Ser Val Thr  Lys Glu Ser Ser Leu  Arg Ala Thr
    1085                1090                1095

Gln Pro  Ser Glu Asn Asp Lys  Leu Gln Lys Glu Leu  Asn Val Leu
    1100                1105                1110

Lys Ser  Glu Gln Asn Asp Leu  Arg Leu Gln Met Glu  Ala Gln Arg
    1115                1120                1125

Ile Cys  Leu Ser Leu Val Tyr  Ser Thr His Val Asp  Gln Val Arg
    1130                1135                1140

Glu Tyr  Met Glu Asn Glu Lys  Asp Lys Ala Leu Cys  Ser Leu Lys
    1145                1150                1155
```

```
Glu Glu  Leu Ile Phe Ala Gln  Glu Glu Lys Ile Lys  Glu Leu Gln
    1160                 1165                 1170

Lys Ile  His Gln Leu Glu Leu  Gln Thr Met Lys Thr  Gln Glu Thr
    1175                 1180                 1185

Gly Asp  Glu Gly Lys Pro Leu  His Leu Leu Ile Gly  Lys Leu Gln
    1190                 1195                 1200

Lys Ala  Val Ser Glu Glu Cys  Ser Tyr Phe Leu Gln  Thr Leu Cys
    1205                 1210                 1215

Ser Val  Leu Gly Glu Tyr Tyr  Thr Pro Ala Leu Lys  Cys Glu Val
    1220                 1225                 1230

Asn Ala  Glu Asp Lys Glu Asn  Ser Gly Asp Tyr Ile  Ser Glu Asn
    1235                 1240                 1245

Glu Asp  Pro Glu Leu Gln Asp  Tyr Arg Tyr Glu Val  Gln Asp Phe
    1250                 1255                 1260

Gln Glu  Asn Met His Thr Leu  Leu Asn Lys Val Thr  Glu Glu Tyr
    1265                 1270                 1275

Asn Lys  Leu Leu Val Leu Gln  Thr Arg Leu Ser Lys  Ile Trp Gly
    1280                 1285                 1290

Gln Gln  Thr Asp Gly Met Lys  Leu Glu Phe Gly Glu  Glu Asn Leu
    1295                 1300                 1305

Pro Lys  Glu Glu Thr Glu Phe  Leu Ser Ile His Ser  Gln Met Thr
    1310                 1315                 1320

Asn Leu  Glu Asp Ile Asp Val  Asn His Lys Ser Lys  Leu Ser Ser
    1325                 1330                 1335

Leu Gln  Asp Leu Glu Lys Thr  Lys Leu Glu Glu Gln  Val Gln Glu
    1340                 1345                 1350

Leu Glu  Ser Leu Ile Ser Ser  Leu Gln Gln Gln Leu  Lys Glu Thr
    1355                 1360                 1365
```

```
Glu Gln  Asn Tyr Glu Ala Glu  Ile His Cys Leu Gln  Lys Arg Leu
    1370                1375                1380

Gln Ala  Val Ser Glu Ser Thr  Val Pro Pro Ser Leu  Pro Val Asp
    1385                1390                1395

Ser Val  Val Ile Thr Glu Ser  Asp Ala Gln Arg Thr  Met Tyr Pro
    1400                1405                1410

Gly Ser  Cys Val Lys Lys Asn  Ile Asp Gly Thr Ile  Glu Phe Ser
    1415                1420                1425

Gly Glu  Phe Gly Val Lys Glu  Glu Thr Asn Ile Val  Lys Leu Leu
    1430                1435                1440

Glu Lys  Gln Tyr Gln Glu Gln  Leu Glu Glu Glu Val  Ala Lys Val
    1445                1450                1455

Ile Val  Ser Met Ser Ile Ala  Phe Ala Gln Gln Thr  Glu Leu Ser
    1460                1465                1470

Arg Ile  Ser Gly Gly Lys Glu  Asn Thr Ala Ser Ser  Lys Gln Ala
    1475                1480                1485

His Ala  Val Cys Gln Gln Glu  Gln His Tyr Phe Asn  Glu Met Lys
    1490                1495                1500

Leu Ser  Gln Asp Gln Ile Gly  Phe Gln Thr Phe Glu  Thr Val Asp
    1505                1510                1515

Val Lys  Phe Lys Glu Glu Phe  Lys Pro Leu Ser Lys  Glu Leu Gly
    1520                1525                1530

Glu His  Gly Lys Glu Ile Leu  Leu Ser Asn Ser Asp  Pro His Asp
    1535                1540                1545

Ile Pro  Glu Ser Lys Asp Cys  Val Leu Thr Ile Ser  Glu Glu Met
    1550                1555                1560

Phe Ser  Lys Asp Lys Thr Phe  Ile Val Arg Gln Ser  Ile His Asp
    1565                1570                1575

Glu Ile  Ser Val Ser Ser Met  Asp Ala Ser Arg Gln  Leu Met Leu
```

```
    1580                1585                1590

Asn Glu  Glu Gln Leu Glu Asp  Met Arg Gln Glu Leu  Val Arg Gln
    1595                1600                1605

Tyr Gln  Glu His Gln Gln Ala  Thr Glu Leu Leu Arg  Gln Ala His
    1610                1615                1620

Met Arg  Gln Met Glu Arg Gln  Arg Glu Asp Gln Glu  Gln Leu Gln
    1625                1630                1635

Glu Glu  Ile Lys Arg Leu Asn  Arg Gln Leu Ala Gln  Arg Ser Ser
    1640                1645                1650

Ile Asp  Asn Glu Asn Leu Val  Ser Glu Arg Glu Arg  Val Leu Leu
    1655                1660                1665

Glu Glu  Leu Glu Ala Leu Lys  Gln Leu Ser Leu Ala  Gly Arg Glu
    1670                1675                1680

Lys Leu  Cys Cys Glu Leu Arg  Asn Ser Ser Thr Gln  Thr Gln Asn
    1685                1690                1695

Gly Asn  Glu Asn Gln Gly Glu  Val Glu Glu Gln Thr  Phe Lys Glu
    1700                1705                1710

Lys Glu  Leu Asp Arg Lys Pro  Glu Asp Val Pro Pro  Glu Ile Leu
    1715                1720                1725

Ser Asn  Glu Arg Tyr Ala Leu  Gln Lys Ala Asn Asn  Arg Leu Leu
    1730                1735                1740

Lys Ile  Leu Leu Glu Val Val  Lys Thr Thr Ala Ala  Val Glu Glu
    1745                1750                1755

Thr Ile  Gly Arg His Val Leu  Gly Ile Leu Asp Arg  Ser Ser Lys
    1760                1765                1770

Ser Gln  Ser Ser Ala Ser Leu  Ile Trp Arg Ser Glu  Ala Glu Ala
    1775                1780                1785

Ser Val  Lys Ser Cys Val His  Glu Glu His Thr Arg  Val Thr Asp
    1790                1795                1800
```

```
Glu Ser  Ile Pro Ser Tyr Ser  Gly Ser Asp Met Pro  Arg Asn Asp
    1805                 1810                 1815

Ile Asn  Met Trp Ser Lys Val  Thr Glu Glu Gly Thr  Glu Leu Ser
    1820                 1825                 1830

Gln Arg  Leu Val Arg Ser Gly  Phe Ala Gly Thr Glu  Ile Asp Pro
    1835                 1840                 1845

Glu Asn  Glu Glu Leu Met Leu  Asn Ile Ser Ser Arg  Leu Gln Ala
    1850                 1855                 1860

Ala Val  Glu Lys Leu Leu Glu  Ala Ile Ser Glu Thr  Ser Ser Gln
    1865                 1870                 1875

Leu Glu  His Ala Lys Val Thr  Gln Thr Glu Leu Met  Arg Glu Ser
    1880                 1885                 1890

Phe Arg  Gln Lys Gln Glu Ala  Thr Glu Ser Leu Lys  Cys Gln Glu
    1895                 1900                 1905

Glu Leu  Arg Glu Arg Leu His  Glu Glu Ser Arg Ala  Arg Glu Gln
    1910                 1915                 1920

Leu Ala  Val Glu Leu Ser Lys  Ala Glu Gly Val Ile  Asp Gly Tyr
    1925                 1930                 1935

Ala Asp  Glu Lys Thr Leu Phe  Glu Arg Gln Ile Gln  Glu Lys Thr
    1940                 1945                 1950

Asp Ile  Ile Asp Arg Leu Glu  Gln Glu Leu Leu Cys  Ala Ser Asn
    1955                 1960                 1965

Arg Leu  Gln Glu Leu Glu Ala  Glu Gln Gln Gln Ile  Gln Glu Glu
    1970                 1975                 1980

Arg Glu  Leu Leu Ser Arg Gln  Lys Glu Ala Met Lys  Ala Glu Ala
    1985                 1990                 1995

Gly Pro  Val Glu Gln Gln Leu  Leu Gln Glu Thr Glu  Lys Leu Met
    2000                 2005                 2010
```

Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg Asp
2015 2020 2025

Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu
2030 2035 2040

Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu
2045 2050 2055

Leu Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu
2060 2065 2070

Glu Lys Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu
2075 2080 2085

His Glu Arg Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln
2090 2095 2100

Gln Leu Lys Val Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln
2105 2110 2115

Thr Arg Glu Val Glu Gln Leu Ala Asn His Leu Lys Glu Lys Thr
2120 2125 2130

Asp Lys Cys Ser Glu Leu Leu Leu Ser Lys Glu Gln Leu Gln Arg
2135 2140 2145

Asp Ile Gln Glu Arg Asn Glu Glu Ile Glu Lys Leu Glu Phe Arg
2150 2155 2160

Val Arg Glu Leu Glu Gln Ala Leu Leu Val Ser Ala Asp Thr Phe
2165 2170 2175

Gln Lys Val Glu Asp Arg Lys His Phe Gly Ala Val Glu Ala Lys
2180 2185 2190

Pro Glu Leu Ser Leu Glu Val Gln Leu Gln Ala Glu Arg Asp Ala
2195 2200 2205

Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu Glu Glu Gln Leu
2210 2215 2220

```
Glu Gln  Phe Arg Glu Glu Leu  Glu Asn Lys Asn Glu  Glu Val Gln
     2225                 2230                 2235

Gln Leu  His Met Gln Leu Glu  Ile Gln Lys Lys Glu  Ser Thr Thr
     2240                 2245                 2250

Arg Leu  Gln Glu Leu Glu Gln  Glu Asn Lys Leu Phe  Lys Asp Asp
     2255                 2260                 2265

Met Glu  Lys Leu Gly Leu Ala  Ile Lys Glu Ser Asp  Ala Met Ser
     2270                 2275                 2280

Thr Gln  Asp Gln His Val Leu  Phe Gly Lys Phe Ala  Gln Ile Ile
     2285                 2290                 2295

Gln Glu  Lys Glu Val Glu Ile  Asp Gln Leu Asn Glu  Gln Val Thr
     2300                 2305                 2310

Lys Leu  Gln Gln Gln Leu Lys  Ile Thr Thr Asp Asn  Lys Val Ile
     2315                 2320                 2325

Glu Glu  Lys Asn Glu Leu Ile  Arg Asp Leu Glu Thr  Gln Ile Glu
     2330                 2335                 2340

Cys Leu  Met Ser Asp Gln Glu  Cys Val Lys Arg Asn  Arg Glu Glu
     2345                 2350                 2355

Glu Ile  Glu Gln Leu Asn Glu  Val Ile Glu Lys Leu  Gln Gln Glu
     2360                 2365                 2370

Leu Ala  Asn Ile Gly Gln Lys  Thr Ser Met Asn Ala  His Ser Leu
     2375                 2380                 2385

Ser Glu  Glu Ala Asp Ser Leu  Lys His Gln Leu Asp  Val Val Ile
     2390                 2395                 2400

Ala Glu  Lys Leu Ala Leu Glu  Gln Gln Val Glu Thr  Ala Asn Glu
     2405                 2410                 2415

Glu Met  Thr Phe Met Lys Asn  Val Leu Lys Glu Thr  Asn Phe Lys
     2420                 2425                 2430

Met Asn  Gln Leu Thr Gln Glu  Leu Phe Ser Leu Lys  Arg Glu Arg
```

2435 2440 2445

Glu Ser Val Glu Lys Ile Gln Ser Ile Pro Glu Asn Ser Val Asn
2450 2455 2460

Val Ala Ile Asp His Leu Ser Lys Asp Lys Pro Glu Leu Glu Val
2465 2470 2475

Val Leu Thr Glu Asp Ala Leu Lys Ser Leu Glu Asn Gln Thr Tyr
2480 2485 2490

Phe Lys Ser Phe Glu Glu Asn Gly Lys Gly Ser Ile Ile Asn Leu
2495 2500 2505

Glu Thr Arg Leu Leu Gln Leu Glu Ser Thr Val Ser Ala Lys Asp
2510 2515 2520

Leu Glu Leu Thr Gln Cys Tyr Lys Gln Ile Lys Asp Met Gln Glu
2525 2530 2535

Gln Gly Gln Phe Glu Thr Glu Met Leu Gln Lys Lys Ile Val Asn
2540 2545 2550

Leu Gln Lys Ile Val Glu Glu Lys Val Ala Ala Ala Leu Val Ser
2555 2560 2565

Gln Ile Gln Leu Glu Ala Val Gln Glu Tyr Ala Lys Phe Cys Gln
2570 2575 2580

Asp Asn Gln Thr Ile Ser Ser Glu Pro Glu Arg Thr Asn Ile Gln
2585 2590 2595

Asn Leu Asn Gln Leu Arg Glu Asp Glu Leu Gly Ser Asp Ile Ser
2600 2605 2610

Ala Leu Thr Leu Arg Ile Ser Glu Leu Glu Ser Gln Val Val Glu
2615 2620 2625

Met His Thr Ser Leu Ile Leu Glu Lys Glu Gln Val Glu Ile Ala
2630 2635 2640

Glu Lys Asn Val Leu Glu Lys Glu Lys Lys Leu Leu Glu Leu Gln
2645 2650 2655

```
Lys Leu  Leu Glu Gly Asn Glu  Lys Lys Gln Arg Glu  Lys Glu Lys
    2660                2665                2670

Lys Arg  Ser Pro Gln Asp Val  Glu Val Leu Lys Thr  Thr Thr Glu
    2675                2680                2685

Leu Phe  His Ser Asn Glu Glu  Ser Gly Phe Phe Asn  Glu Leu Glu
    2690                2695                2700

Ala Leu  Arg Ala Glu Ser Val  Ala Thr Lys Ala Glu  Leu Ala Ser
    2705                2710                2715

Tyr Lys  Glu Lys Ala Glu Lys  Leu Gln Glu Glu Leu  Leu Val Lys
    2720                2725                2730

Glu Thr  Asn Met Thr Ser Leu  Gln Lys Asp Leu Ser  Gln Val Arg
    2735                2740                2745

Asp His  Leu Ala Glu Ala Lys  Glu Lys Leu Ser Ile  Leu Glu Lys
    2750                2755                2760

Glu Asp  Glu Thr Glu Val Gln  Glu Ser Lys Lys Ala  Cys Met Phe
    2765                2770                2775

Glu Pro  Leu Pro Ile Lys Leu  Ser Lys Ser Ile Ala  Ser Gln Thr
    2780                2785                2790

Asp Gly  Thr Leu Lys Ile Ser  Ser Ser Asn Gln Thr  Pro Gln Ile
    2795                2800                2805

Leu Val  Lys Asn Ala Gly Ile  Gln Ile Asn Leu Gln  Ser Glu Cys
    2810                2815                2820

Ser Ser  Glu Glu Val Thr Glu  Ile Ile Ser Gln Phe  Thr Glu Lys
    2825                2830                2835

Ile Glu  Lys Met Gln Glu Leu  His Ala Ala Glu Ile  Leu Asp Met
    2840                2845                2850

Glu Ser  Arg His Ile Ser Glu  Thr Glu Thr Leu Lys  Arg Glu His
    2855                2860                2865
```

```
Tyr Val  Ala Val Gln Leu Leu  Lys Glu Glu Cys Gly  Thr Leu Lys
    2870                2875                2880

Ala Val  Ile Gln Cys Leu Arg  Ser Lys Glu Val Phe  Gly Phe Tyr
    2885                2890                2895

Asn Met  Cys Phe Ser Thr Leu  Cys Asp Ser Gly Ser  Asp Trp Gly
    2900                2905                2910

Gln Gly  Ile Tyr Leu Thr His  Ser Gln Gly Phe Asp  Ile Ala Ser
    2915                2920                2925

Glu Gly  Arg Gly Glu Glu Ser  Glu Ser Ala Thr Asp  Ser Phe Pro
    2930                2935                2940

Lys Lys  Ile Lys Gly Leu Leu  Arg Ala Val His Asn  Glu Gly Met
    2945                2950                2955

Gln Val  Leu Ser Leu Thr Glu  Ser Pro Tyr Ser Asp  Gly Glu Asp
    2960                2965                2970

His Ser  Ile Gln Gln Val Ser  Glu Pro Trp Leu Glu  Glu Arg Lys
    2975                2980                2985

Ala Tyr  Ile Asn Thr Ile Ser  Ser Leu Lys Asp Leu  Ile Thr Lys
    2990                2995                3000

Met Gln  Leu Gln Arg Glu Ala  Glu Val Tyr Asp Ser  Ser Gln Ser
    3005                3010                3015

His Glu  Ser Phe Ser Asp Trp  Arg Gly Glu Leu Leu  Leu Ala Leu
    3020                3025                3030

Gln Gln  Val Phe Leu Glu Glu  Arg Ser Val Leu Leu  Ala Ala Phe
    3035                3040                3045

Arg Thr  Glu Leu Thr Ala Leu  Gly Thr Thr Asp Ala  Val Gly Leu
    3050                3055                3060

Leu Asn  Cys Leu Glu Gln Arg  Ile Gln Glu Gln Gly  Val Glu Tyr
    3065                3070                3075
```

```
Gln Ala  Ala Met Glu Cys Leu  Gln Lys Ala Asp Arg  Arg Ser Leu
    3080                 3085                 3090

Leu Ser  Glu Ile Gln Ala Leu  His Ala Gln Met Asn  Gly Arg Lys
    3095                 3100                 3105

Ile Thr  Leu Lys Arg Glu Gln  Glu Ser Glu Lys Pro  Ser Gln Glu
    3110                 3115                 3120

Leu Leu  Glu Tyr Asn Ile Gln  Gln Lys Gln Ser Gln  Met Leu Glu
    3125                 3130                 3135

Met Gln  Val Glu Leu Ser Ser  Met Lys Asp Arg Ala  Thr Glu Leu
    3140                 3145                 3150

Gln Glu  Gln Leu Ser Ser Glu  Lys Met Val Val Ala  Glu Leu Lys
    3155                 3160                 3165

Ser Glu  Leu Ala Gln Thr Lys  Leu Glu Leu Glu Thr  Thr Leu Lys
    3170                 3175                 3180

Ala Gln  His Lys His Leu Lys  Glu Leu Glu Ala Phe  Arg Leu Glu
    3185                 3190                 3195

Val Lys  Asp Lys Thr Asp Glu  Val His Leu Leu Asn  Asp Thr Leu
    3200                 3205                 3210

Ala Ser  Glu Gln Lys Lys Ser  Arg Glu Leu Gln Trp  Ala Leu Glu
    3215                 3220                 3225

Lys Glu  Lys Ala Lys Leu Gly  Arg Ser Glu Glu Arg  Asp Lys Glu
    3230                 3235                 3240

Glu Leu  Glu Asp Leu Lys Phe  Ser Leu Glu Ser Gln  Lys Gln Arg
    3245                 3250                 3255

Asn Leu  Gln Leu Asn Leu Leu  Leu Glu Gln Gln Lys  Gln Leu Leu
    3260                 3265                 3270

Asn Glu  Ser Gln Gln Lys Ile  Glu Ser Gln Arg Met  Leu Tyr Asp
    3275                 3280                 3285

Ala Gln  Leu Ser Glu Glu Gln  Gly Arg Asn Leu Glu  Leu Gln Val
```

```
    3290                3295                3300

Leu Leu  Glu Ser Glu Lys Val  Arg Ile Arg Glu Met  Ser Ser Thr
    3305                3310                3315

Leu Asp  Arg Glu Arg Glu Leu  His Ala Gln Leu Gln  Ser Ser Asp
    3320                3325                3330

Gly Thr  Gly Gln Ser Arg Pro  Pro Leu Pro Ser Glu  Asp Leu Leu
    3335                3340                3345

Lys Glu  Leu Gln Lys Gln Leu  Glu Glu Lys His Ser  Arg Ile Val
    3350                3355                3360

Glu Leu  Leu Asn Glu Thr Glu  Lys Tyr Lys Leu Asp  Ser Leu Gln
    3365                3370                3375

Thr Arg  Gln Gln Met Glu Lys  Asp Arg Gln Val His  Arg Lys Thr
    3380                3385                3390

Leu Gln  Thr Glu Gln Glu Ala  Asn Thr Glu Gly Gln  Lys Lys Met
    3395                3400                3405

His Glu  Leu Gln Ser Lys Val  Glu Asp Leu Gln Arg  Gln Leu Glu
    3410                3415                3420

Glu Lys  Arg Gln Gln Val Tyr  Lys Leu Asp Leu Glu  Gly Gln Arg
    3425                3430                3435

Leu Gln  Gly Ile Met Gln Glu  Phe Gln Lys Gln Glu  Leu Glu Arg
    3440                3445                3450

Glu Glu  Lys Arg Glu Ser Arg  Arg Ile Leu Tyr Gln  Asn Leu Asn
    3455                3460                3465

Glu Pro  Thr Thr Trp Ser Leu  Thr Ser Asp Arg Thr  Arg Asn Trp
    3470                3475                3480

Val Leu  Gln Gln Lys Ile Glu  Gly Glu Thr Lys Glu  Ser Asn Tyr
    3485                3490                3495

Ala Lys  Leu Ile Glu Met Asn  Gly Gly Gly Thr Gly  Cys Asn His
    3500                3505                3510
```

```
Glu Leu  Glu Met Ile Arg Gln  Lys Leu Gln Cys Val  Ala Ser Lys
    3515                 3520                 3525

Leu Gln  Val Leu Pro Gln Lys  Ala Ser Glu Arg Leu  Gln Phe Glu
    3530                 3535                 3540

Thr Ala  Asp Asp Glu Asp Phe  Ile Trp Val Gln Glu  Asn Ile Asp
    3545                 3550                 3555

Glu Ile  Ile Leu Gln Leu Gln  Lys Leu Thr Gly Gln  Gln Gly Glu
    3560                 3565                 3570

Glu Pro  Ser Leu Val Ser Pro  Ser Thr Ser Cys Gly  Ser Leu Thr
    3575                 3580                 3585

Glu Arg  Leu Leu Arg Gln Asn  Ala Glu Leu Thr Gly  His Ile Ser
    3590                 3595                 3600

Gln Leu  Thr Glu Glu Lys Asn  Asp Leu Arg Asn Met  Val Met Lys
    3605                 3610                 3615

Leu Glu  Glu Gln Ile Arg Trp  Tyr Arg Gln Thr Gly  Ala Gly Arg
    3620                 3625                 3630

Asp Asn  Ser Ser Arg Phe Ser  Leu Asn Gly Gly Ala  Asn Ile Glu
    3635                 3640                 3645

Ala Ile  Ile Ala Ser Glu Lys  Glu Val Trp Asn Arg  Glu Lys Leu
    3650                 3655                 3660

Thr Leu  Gln Lys Ser Leu Lys  Arg Ala Glu Ala Glu  Val Tyr Lys
    3665                 3670                 3675

Leu Lys  Ala Glu Leu Arg Asn  Asp Ser Leu Leu Gln  Thr Leu Ser
    3680                 3685                 3690

Pro Asp  Ser Glu His Val Thr  Leu Lys Arg Ile Tyr  Gly Lys Tyr
    3695                 3700                 3705

Leu Arg  Ala Glu Ser Phe Arg  Lys Ala Leu Ile Tyr  Gln Lys Lys
    3710                 3715                 3720
```

```
Tyr Leu  Leu Leu Leu Leu Gly  Gly Phe Gln Glu Cys  Glu Asp Ala
    3725                3730                3735

Thr Leu  Ala Leu Leu Ala Arg  Met Gly Gly Gln Pro  Ala Phe Thr
    3740                3745                3750

Asp Leu  Glu Val Ile Thr Asn  Arg Pro Lys Gly Phe  Thr Arg Phe
    3755                3760                3765

Arg Ser  Ala Val Arg Val Ser  Ile Ala Ile Ser Arg  Met Lys Phe
    3770                3775                3780

Leu Val  Arg Arg Trp His Arg  Val Thr Gly Ser Val  Ser Ile Asn
    3785                3790                3795

Ile Asn  Arg Asp Gly Phe Gly  Leu Asn Gln Gly Ala  Glu Lys Thr
    3800                3805                3810

Asp Ser  Phe Tyr His Ser Ser  Gly Gly Leu Glu Leu  Tyr Gly Glu
    3815                3820                3825

Pro Arg  His Thr Thr Tyr Arg  Ser Arg Ser Asp Leu  Asp Tyr Ile
    3830                3835                3840

Arg Ser  Pro Leu Pro Phe Gln  Asn Arg Tyr Pro Gly  Thr Pro Ala
    3845                3850                3855

Asp Phe  Asn Pro Gly Ser Leu  Ala Cys Ser Gln Leu  Gln Asn Tyr
    3860                3865                3870

Asp Pro  Asp Arg Ala Leu Thr  Asp Tyr Ile Thr Arg  Leu Glu Ala
    3875                3880                3885

Leu Gln  Arg Arg Leu Gly Thr  Ile Gln Ser Gly Ser  Thr Thr Gln
    3890                3895                3900

Phe His  Ala Gly Met Arg Arg
    3905                3910
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Glu Asp Arg Lys His Phe Gly Ala Val Glu Ala Lys Pro Glu Leu Ser
20 25 30

Leu Glu Val Gln Leu Gln Ala Glu Arg Asp Ala Ile Asp Arg Lys Glu
35 40 45

Lys Glu Ile Thr Asn Leu Glu Glu Gln Leu Glu Gln Phe Arg Glu Glu
50 55 60

Leu Glu Asn Lys Asn Glu Glu Val Gln Gln Leu His Met Gln Leu Glu
65 70 75 80

Ile Gln Lys Lys Glu Ser Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu
85 90 95

Asn Lys Leu Phe Lys Asp Asp Met Glu Lys Leu Gly Leu Ala Ile Lys
100 105 110

Glu Ser Asp Ala Met Ser Thr Gln Asp Gln His Val Leu Phe Gly Lys
115 120 125

Phe Ala Gln Ile Ile Gln Glu Lys Glu Val Glu Ile Asp Gln Leu Asn
130 135 140

Glu Gln Val Thr Lys Leu Gln Gln Gln Leu Lys Ile Thr Thr Asp Asn
145 150 155 160

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

Ile Glu Cys Leu Met Ser Asp Gln Glu Cys Val Lys Arg Asn Arg Glu
            180                 185                 190

Glu Glu Ile Glu Gln Leu Asn Glu Val Ile Glu Lys Leu Gln Gln Glu
        195                 200                 205

Leu Ala Asn Ile Gly Gln Lys Thr Ser Met Asn Ala His Ser Leu Ser
    210                 215                 220

Glu Glu Ala Asp Ser Leu Lys His Gln Leu Asp Val Val Ile Ala Glu
225                 230                 235                 240

Lys Leu Ala Leu Glu Gln Gln Val Glu Thr Ala Asn Glu Glu Met Thr
                245                 250                 255

Phe Met Lys Asn Val Leu Lys Glu Thr Asn Phe Lys Met Asn Gln Leu
            260                 265                 270

Thr Gln Glu Leu Phe Ser Leu Lys Arg Glu Arg Glu Ser Val Glu Lys
        275                 280                 285

Ile Gln Ser Ile Pro Glu Asn Ser Val Asn Val Ala Ile Asp His Leu
    290                 295                 300

Ser Lys Asp Lys Pro Glu Leu Glu Val Val Leu Thr Glu Asp Ala Leu
305                 310                 315                 320

Lys Ser Leu Glu Asn Gln Thr Tyr Phe Lys Ser Phe Glu Glu Asn Gly
                325                 330                 335

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

Thr Val Ser Ala Lys Asp Leu Glu Leu Thr Gln Cys Tyr Lys Gln Ile
        355                 360                 365

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

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

Cys Gln Asp Asn Gln Thr Ile Ser Ser Glu Pro Glu Arg Thr Asn Ile
            420                 425                 430

Gln Asn Leu Asn Gln Leu Arg Glu Asp Glu Leu Gly Ser Asp Ile Ser
        435                 440                 445

Ala Leu Thr Leu Arg Ile Ser Glu Leu Glu Ser Gln Val Val Glu Met
    450                 455                 460

His Thr Ser Leu Ile Leu Glu Lys Glu Gln Val Glu Ile Ala Glu Lys
465                 470                 475                 480

Asn Val Leu Glu Lys Glu Lys Lys Leu Leu Glu Leu Gln Lys Leu Leu
                485                 490                 495

Glu Gly Asn Glu Lys Lys Gln Arg Glu Lys Glu Lys Lys Arg Ser Pro
            500                 505                 510

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

Glu Glu Ser Gly Phe Phe Asn Glu Leu Glu Ala Leu Arg Ala Glu Ser
    530                 535                 540

Val Ala Thr Lys Ala Glu Leu Ala Ser Tyr Lys Glu Lys Ala Glu Lys
545                 550                 555                 560

Leu Gln Glu Glu Leu Leu Val Lys Glu Thr Asn Met Thr Ser Leu Gln
                565                 570                 575

Lys Asp Leu Ser Gln Val Arg Asp His Leu Ala Glu Ala Lys Glu Lys
            580                 585                 590

Leu Ser Ile Leu Glu Lys Glu Asp Glu Thr Glu Val Gln Glu Ser Lys
        595                 600                 605
```

```
Lys Ala Cys Met Phe Glu Pro Leu Pro Ile Lys Leu Ser Lys Ser Ile
    610                 615                 620

Ala Ser Gln Thr Asp Gly Thr Leu Lys Ile Ser Ser Ser Asn Gln Thr
625                 630                 635                 640

Pro Gln Ile Leu Val Lys Asn Ala Gly Ile Gln Ile Asn Leu Gln Ser
                645                 650                 655

Glu Cys Ser Ser Glu Glu Val Thr Glu Ile Ile Ser Gln Phe Thr Glu
            660                 665                 670

Lys Ile Glu Lys Met Gln Glu Leu His Ala Ala Glu Ile Leu Asp Met
        675                 680                 685

Glu Ser Arg His Ile Ser Glu Thr Glu Thr Leu Lys Arg Glu His Tyr
    690                 695                 700

Val Ala Val Gln Leu Leu Lys Glu Glu Cys Gly Thr Leu Lys Ala Val
705                 710                 715                 720

Ile Gln Cys Leu Arg Ser Lys Glu Gly Ser Ser Ile Pro Glu Leu Ala
                725                 730                 735

His Ser Asp Ala Tyr Gln Thr Arg Glu Ile Cys Ser Ser Asp Ser Gly
            740                 745                 750

Ser Asp Trp Gly Gln Gly Ile Tyr Leu Thr His Ser Gln Gly Phe Asp
        755                 760                 765

Ile Ala Ser Glu Gly Arg Gly Glu Glu Ser Glu Ser Ala Thr Asp Ser
    770                 775                 780

Phe Pro Lys Lys Ile Lys Gly Leu Leu Arg Ala Val His Asn Glu Gly
785                 790                 795                 800

Met Gln Val Leu Ser Leu Thr Glu Ser Pro Tyr Ser Asp Gly Glu Asp
                805                 810                 815

His Ser Ile Gln Gln Val Ser Glu Pro Trp Leu Glu Glu Arg Lys Ala
            820                 825                 830

Tyr Ile Asn Thr Ile Ser Ser Leu Lys Asp Leu Ile Thr Lys Met Gln
```

```
        835                 840                 845

Leu Gln Arg Glu Ala Glu Val Tyr Asp Ser Ser Gln Ser His Glu Ser
    850                 855                 860

Phe Ser Asp Trp Arg Gly Glu Leu Leu Leu Ala Leu Gln Gln Val Phe
865                 870                 875                 880

Leu Glu Glu Arg Ser Val Leu Leu Ala Ala Phe Arg Thr Glu Leu Thr
                885                 890                 895

Ala Leu Gly Thr Thr Asp Ala Val Gly Leu Leu Asn Cys Leu Glu Gln
            900                 905                 910

Arg Ile Gln Glu Gln Gly Val Glu Tyr Gln Ala Ala Met Glu Cys Leu
        915                 920                 925

Gln Lys Ala Asp Arg Arg Ser Leu Leu Ser Glu Ile Gln Ala Leu His
    930                 935                 940

Ala Gln Met Asn Gly Arg Lys Ile Thr Leu Lys Arg Glu Gln Glu Ser
945                 950                 955                 960

Glu Lys Pro Ser Gln Glu Leu Leu Glu Tyr Asn Ile Gln Gln Lys Gln
                965                 970                 975

Ser Gln Met Leu Glu Met Gln Val Glu Leu Ser Ser Met Lys Asp Arg
            980                 985                 990

Ala Thr Glu Leu Gln Glu Gln Leu  Ser Ser Glu Lys Met  Val Val
Ala
        995                 1000                1005

Glu Leu  Lys Ser Glu Leu Ala  Gln Thr Lys Leu Glu  Leu Glu Thr
    1010                1015                1020

Thr Leu  Lys Ala Gln His Lys  His Leu Lys Glu Leu  Glu Ala Phe
    1025                1030                1035

Arg Leu  Glu Val Lys Asp Lys  Thr Asp Glu Val His  Leu Leu Asn
    1040                1045                1050

Asp Thr  Leu Ala Ser Glu Gln  Lys Lys Ser Arg Glu  Leu Gln Trp
```

1055 1060 1065

Ala Leu Glu Lys Glu Lys Ala Lys Leu Gly Arg Ser Glu Glu Arg
1070 1075 1080

Asp Lys Glu Glu Leu Glu Asp Leu Lys Phe Ser Leu Glu Ser Gln
1085 1090 1095

Lys Gln Arg Asn Leu Gln Leu Asn Leu Leu Leu Glu Gln Gln Lys
1100 1105 1110

Gln Leu Leu Asn Glu Ser Gln Gln Lys Ile Glu Ser Gln Arg Met
1115 1120 1125

Leu Tyr Asp Ala Gln Leu Ser Glu Glu Gln Gly Arg Asn Leu Glu
1130 1135 1140

Leu Gln Val Leu Leu Glu Ser Glu Lys Val Arg Ile Arg Glu Met
1145 1150 1155

Ser Ser Thr Leu Asp Arg Glu Arg Glu Leu His Ala Gln Leu Gln
1160 1165 1170

Ser Ser Asp Gly Thr Gly Gln Ser Arg Pro Pro Leu Pro Ser Glu
1175 1180 1185

Asp Leu Leu Lys Glu Leu Gln Lys Gln Leu Glu Glu Lys His Ser
1190 1195 1200

Arg Ile Val Glu Leu Leu Asn Glu Thr Glu Lys Tyr Lys Leu Asp
1205 1210 1215

Ser Leu Gln Thr Arg Gln Gln Met Glu Lys Asp Arg Gln Val His
1220 1225 1230

Arg Lys Thr Leu Gln Thr Glu Gln Glu Ala Asn Thr Glu Gly Gln
1235 1240 1245

Lys Lys Met His Glu Leu Gln Ser Lys Val Glu Asp Leu Gln Arg
1250 1255 1260

Gln Leu Glu Glu Lys Arg Gln Gln Val Tyr Lys Leu Asp Leu Glu
1265 1270 1275

```
Gly Gln  Arg Leu Gln Gly Ile  Met Gln Glu Phe Gln  Lys Gln Glu
    1280                1285                1290

Leu Glu  Arg Glu Glu Lys Arg  Glu Ser Arg Arg Ile  Leu Tyr Gln
    1295                1300                1305

Asn Leu  Asn Glu Pro Thr Thr  Trp Ser Leu Thr Ser  Asp Arg Thr
    1310                1315                1320

Arg Asn  Trp Val Leu Gln Gln  Lys Ile Glu Gly Glu  Thr Lys Glu
    1325                1330                1335

Ser Asn  Tyr Ala Lys Leu Ile  Glu Met Asn Gly Gly  Gly Thr Gly
    1340                1345                1350

Cys Asn  His Glu Leu Glu Met  Ile Arg Gln Lys Leu  Gln Cys Val
    1355                1360                1365

Ala Ser  Lys Leu Gln Val Leu  Pro Gln Lys Ala Ser  Glu Arg Leu
    1370                1375                1380

Gln Phe  Glu Thr Ala Asp Asp  Glu Asp Phe Ile Trp  Val Gln Glu
    1385                1390                1395

Asn Ile  Asp Glu Ile Ile Leu  Gln Leu Gln Lys Leu  Thr Gly Gln
    1400                1405                1410

Gln Gly  Glu Glu Pro Ser Leu  Val Ser Pro Ser Thr  Ser Cys Gly
    1415                1420                1425

Ser Leu  Thr Glu Arg Leu Leu  Arg Gln Asn Ala Glu  Leu Thr Gly
    1430                1435                1440

His Ile  Ser Gln Leu Thr Glu  Glu Lys Asn Asp Leu  Arg Asn Met
    1445                1450                1455

Val Met  Lys Leu Glu Glu Gln  Ile Arg Trp Tyr Arg  Gln Thr Gly
    1460                1465                1470

Ala Gly  Arg Asp Asn Ser Ser  Arg Phe Ser Leu Asn  Gly Gly Ala
    1475                1480                1485
```

```
Asn Ile  Glu Ala Ile Ile Ala  Ser Glu Lys Glu Val  Trp Asn Arg
    1490                 1495                 1500

Glu Lys  Leu Thr Leu Gln Lys  Ser Leu Lys Arg Ala  Glu Ala Glu
    1505                 1510                 1515

Val Tyr  Lys Leu Lys Ala Glu  Leu Arg Asn Asp Ser  Leu Leu Gln
    1520                 1525                 1530

Thr Leu  Ser Pro Asp Ser Glu  His Val Thr Leu Lys  Arg Ile Tyr
    1535                 1540                 1545

Gly Lys  Tyr Leu Arg Ala Glu  Ser Phe Arg Lys Ala  Leu Ile Tyr
    1550                 1555                 1560

Gln Lys  Lys Tyr Leu Leu Leu  Leu Leu Gly Gly Phe  Gln Glu Cys
    1565                 1570                 1575

Glu Asp  Ala Thr Leu Ala Leu  Leu Ala Arg Met Gly  Gly Gln Pro
    1580                 1585                 1590

Ala Phe  Thr Asp Leu Glu Val  Ile Thr Asn Arg Pro  Lys Gly Phe
    1595                 1600                 1605

Thr Arg  Phe Arg Ser Ala Val  Arg Val Ser Ile Ala  Ile Ser Arg
    1610                 1615                 1620

Met Lys  Phe Leu Val Arg Arg  Trp His Arg Val Thr  Gly Ser Val
    1625                 1630                 1635

Ser Ile  Asn Ile Asn Arg Asp  Gly Phe Gly Leu Asn  Gln Gly Ala
    1640                 1645                 1650

Glu Lys  Thr Asp Ser Phe Tyr  His Ser Ser Gly Gly  Leu Glu Leu
    1655                 1660                 1665

Tyr Gly  Glu Pro Arg His Thr  Thr Tyr Arg Ser Arg  Ser Asp Leu
    1670                 1675                 1680

Asp Tyr  Ile Arg Ser Pro Leu  Pro Phe Gln Asn Arg  Tyr Pro Gly
    1685                 1690                 1695
```

```
Thr Pro  Ala Asp Phe Asn Pro  Gly Ser Leu Ala Cys  Ser Gln Leu
    1700                1705                1710

Gln Asn  Tyr Asp Pro Asp Arg  Ala Leu Thr Asp Tyr  Ile Thr Arg
    1715                1720                1725

Leu Glu  Ala Leu Gln Arg Arg  Leu Gly Thr Ile Gln  Ser Gly Ala
    1730                1735                1740

Leu Ser  Leu Thr Thr Ser Trp  Gln His His Ser Ala  Arg Pro Thr
    1745                1750                1755

Ala Pro  Leu Ser Leu Lys Phe  Phe His Thr His
    1760                1765


<210> 683
<211> 314
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AKAP9; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA) anchor prt 9; "

<220>
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<400> 683
Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
1               5                  10                  15

Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
            20                  25                  30

Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
        35                  40                  45

Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
    50                  55                  60
```

```
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
65                  70                  75                  80

Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
                85                  90                  95

Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
            100                 105                 110

Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
        115                 120                 125

Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
    130                 135                 140

Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145                 150                 155                 160

Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
                165                 170                 175

Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
            180                 185                 190

Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
        195                 200                 205

Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
    210                 215                 220

Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225                 230                 235                 240

Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
                245                 250                 255

Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
            260                 265                 270

His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
        275                 280                 285
```

Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
290 295 300

Ile Lys Val Tyr Glu Met Val Cys Leu Phe
305 310

<210> 684
<211> 232
<212> PRT
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<220>
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<220>
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A kinase (PRKA) anchor prt 9; "

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<400> 684
Pro Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His
1 5 10 15

Asp Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn
20 25 30

Glu Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro
35 40 45

Glu Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His
50 55 60

Glu Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala
65 70 75 80

Asp Asp Cys Ser Ser Glu Glu Glu Glu Phe Gly Val Asp Asp Ser Tyr
85 90 95

Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met Glu

```
            100                 105                 110

Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg Glu
        115                 120                 125

Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln Leu
    130                 135                 140

Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr Gln
145                 150                 155                 160

Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr Met
                165                 170                 175

Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile Gln
            180                 185                 190

Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His Ser
        195                 200                 205

Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr His
    210                 215                 220

Gln Gln Gln Leu Glu Glu Gln Asp
225                 230


<210> 685
<211> 318
<212> PRT
<213> Homo sapiens

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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 685
Xaa His Tyr Val Ala Val Gln Leu Leu Lys Glu Glu Cys Gly Thr Leu
1 5 10 15

Lys Ala Val Ile Gln Cys Leu Arg Ser Lys Glu Gly Ser Ser Ile Pro
20 25 30

Glu Leu Ala His Ser Asp Ala Tyr Gln Thr Arg Glu Ile Cys Ser Ser
35 40 45

Asp Ser Gly Ser Asp Trp Gly Gln Gly Ile Tyr Leu Thr His Ser Gln
50 55 60

Gly Phe Asp Ile Ala Ser Glu Gly Arg Gly Glu Glu Ser Glu Ser Ala
65 70 75 80

Thr Asp Ser Phe Pro Lys Lys Ile Lys Gly Leu Leu Arg Ala Val His
85 90 95

Asn Glu Gly Met Gln Val Leu Ser Leu Thr Glu Ser Pro Tyr Ser Asp
100 105 110

Gly Glu Asp His Ser Ile Gln Gln Val Ser Glu Pro Trp Leu Glu Glu
115 120 125

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

Lys Met Gln Leu Gln Arg Glu Ala Glu Val Tyr Asp Ser Ser Gln Ser
145 150 155 160

His Glu Ser Phe Ser Asp Trp Arg Gly Glu Leu Leu Leu Ala Leu Gln
165 170 175

Gln Val Phe Leu Glu Glu Arg Ser Val Leu Leu Ala Ala Phe Arg Thr
180 185 190

Glu Leu Thr Ala Leu Gly Thr Thr Asp Ala Val Gly Leu Leu Asn Cys
195 200 205

```
Leu Glu Gln Arg Ile Gln Glu Gln Gly Val Glu Tyr Gln Ala Ala Met
    210                 215                 220

Glu Cys Leu Gln Lys Ala Asp Arg Arg Ser Leu Leu Ser Glu Ile Gln
225                 230                 235                 240

Ala Leu His Ala Gln Met Asn Gly Arg Lys Ile Thr Leu Lys Arg Glu
                245                 250                 255

Gln Glu Ser Glu Lys Pro Ser Gln Gly Met Leu Tyr Asp Lys Leu Ile
            260                 265                 270

Trp Leu His Lys Gln Val Lys Arg Phe His Phe Val Phe Phe Leu Ile
        275                 280                 285

Ile Ile Lys Leu Lys His Ile Phe Leu Val Thr Phe Ser Ser His Ser
    290                 295                 300

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


<210> 686
<211> 1637
<212> PRT
<213> Homo sapiens

<220>
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<400> 686
Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
1               5                   10                  15
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```
Val Gly Glu Leu Ile Phe Phe Phe Leu Ala Gln Phe Arg Gln Arg Lys
            20                  25                  30

Ala Gln Ser Asp Gly Gln Ser Pro Ser Lys Lys Gln Lys Lys Lys Arg
        35                  40                  45

Lys Thr Ser Ser Ser Lys His Asp Val Ser Ala His His Asp Leu Asn
    50                  55                  60

Ile Asp Gln Ser Gln Cys Asn Glu Met Tyr Ile Asn Ser Ser Gln Arg
65                  70                  75                  80

Val Glu Ser Thr Val Ile Pro Glu Ser Thr Ile Met Arg Thr Leu His
                85                  90                  95

Ser Gly Glu Ile Thr Ser His Glu Gln Gly Phe Ser Val Glu Leu Glu
            100                 105                 110

Ser Glu Ile Ser Thr Thr Ala Asp Asp Cys Ser Ser Glu Val Asn Gly
        115                 120                 125

Cys Ser Phe Val Met Arg Thr Gly Lys Pro Thr Asn Leu Leu Arg Glu
    130                 135                 140

Glu Glu Phe Gly Val Asp Asp Ser Tyr Ser Glu Gln Gly Ala Gln Asp
145                 150                 155                 160

Ser Pro Thr His Leu Glu Met Met Glu Ser Glu Leu Ala Gly Lys Gln
                165                 170                 175

His Glu Ile Glu Glu Leu Asn Arg Glu Leu Glu Glu Met Arg Val Thr
            180                 185                 190

Tyr Gly Thr Glu Gly Leu Gln Gln Leu Gln Glu Phe Glu Ala Ala Ile
        195                 200                 205

Lys Gln Arg Asp Gly Ile Ile Thr Gln Leu Thr Ala Asn Leu Gln Gln
    210                 215                 220

Ala Arg Arg Glu Lys Asp Glu Thr Met Arg Glu Phe Leu Glu Leu Thr
225                 230                 235                 240

Glu Gln Ser Gln Lys Leu Gln Ile Gln Phe Gln Gln Leu Gln Ala Ser
```

245 250 255

Glu Thr Leu Arg Asn Ser Thr His Ser Ser Thr Ala Ala Asp Leu Leu
260 265 270

Gln Ala Lys Gln Gln Ile Leu Thr His Gln Gln Gln Leu Glu Glu Gln
275 280 285

Asp His Leu Leu Glu Asp Tyr Gln Lys Lys Lys Glu Asp Phe Thr Met
290 295 300

Gln Ile Ser Phe Leu Gln Glu Lys Ile Lys Val Tyr Glu Met Glu Gln
305 310 315 320

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

Thr Ile Ile Glu Glu Leu Asn Thr Lys Ile Ile Glu Glu Glu Lys Lys
340 345 350

Thr Leu Glu Leu Lys Asp Lys Leu Thr Thr Ala Asp Lys Leu Leu Gly
355 360 365

Glu Leu Gln Glu Gln Ile Val Gln Lys Asn Gln Glu Ile Lys Asn Met
370 375 380

Lys Leu Glu Leu Thr Asn Ser Lys Gln Lys Glu Arg Gln Ser Ser Glu
385 390 395 400

Glu Ile Lys Gln Leu Met Gly Thr Val Glu Glu Leu Gln Lys Arg Asn
405 410 415

His Lys Asp Ser Gln Phe Glu Thr Asp Ile Val Gln Arg Met Glu Gln
420 425 430

Glu Thr Gln Arg Lys Leu Glu Gln Leu Arg Ala Glu Leu Asp Glu Met
435 440 445

Tyr Gly Gln Gln Ile Val Gln Met Lys Gln Glu Leu Ile Arg Gln His
450 455 460

Met Ala Gln Met Glu Glu Met Lys Thr Arg His Lys Gly Glu Met Glu
465 470 475 480

```
Asn Ala Leu Arg Ser Tyr Ser Asn Ile Thr Val Asn Glu Asp Gln Ile
                485                 490                 495

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

Thr Asn Ser Gln Lys Glu Lys Leu Lys Glu Glu Leu Gly Leu Ile Leu
        515                 520                 525

Glu Glu Lys Cys Ala Leu Gln Arg Gln Leu Glu Asp Leu Val Glu Glu
    530                 535                 540

Leu Ser Phe Ser Arg Glu Gln Ile Gln Arg Ala Arg Gln Thr Ile Ala
545                 550                 555                 560

Glu Gln Glu Ser Lys Leu Asn Glu Ala His Lys Ser Leu Ser Thr Val
                565                 570                 575

Glu Asp Leu Lys Ala Glu Ile Val Ser Ala Ser Glu Ser Arg Lys Glu
            580                 585                 590

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

Glu Met Leu Glu Lys Glu Lys Asn Ala Val Leu Asp Arg Met Ala Glu
    610                 615                 620

Ser Gln Glu Ala Glu Leu Glu Arg Leu Arg Thr Gln Leu Leu Phe Ser
625                 630                 635                 640

His Glu Glu Glu Leu Ser Lys Leu Lys Glu Asp Leu Glu Ile Glu His
                645                 650                 655

Arg Ile Asn Ile Glu Lys Leu Lys Asp Asn Leu Gly Ile His Tyr Lys
            660                 665                 670

Gln Gln Ile Asp Gly Leu Gln Asn Glu Met Ser Gln Lys Ile Glu Thr
        675                 680                 685

Met Gln Phe Glu Lys Asp Asn Leu Ile Thr Lys Gln Asn Gln Leu Ile
    690                 695                 700
```

```
Leu Glu Ile Ser Lys Leu Lys Asp Leu Gln Gln Ser Leu Val Asn Ser
705                 710                 715                 720

Lys Ser Glu Glu Met Thr Leu Gln Ile Asn Glu Leu Gln Lys Glu Ile
                725                 730                 735

Glu Ile Leu Arg Gln Glu Glu Lys Glu Lys Gly Thr Leu Glu Gln Glu
            740                 745                 750

Val Gln Glu Leu Gln Leu Lys Thr Glu Leu Leu Glu Lys Gln Met Lys
        755                 760                 765

Glu Lys Glu Asn Asp Leu Gln Glu Lys Phe Ala Gln Leu Glu Ala Glu
    770                 775                 780

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

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

Ile Lys Ser Lys Ser Lys Asp Ser Val Trp Glu Lys Glu Ile Glu Ile
            820                 825                 830

Leu Ile Glu Glu Asn Glu Asp Leu Lys Gln Gln Cys Ile Gln Leu Asn
        835                 840                 845

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

Phe Glu Val Asn Tyr Gln Glu Leu Gln Glu Glu Tyr Ala Cys Leu Leu
865                 870                 875                 880

Lys Val Lys Asp Asp Leu Glu Asp Ser Lys Asn Lys Gln Glu Leu Glu
                885                 890                 895

Tyr Lys Ser Lys Leu Lys Ala Leu Asn Glu Glu Leu His Leu Gln Arg
            900                 905                 910

Ile Asn Pro Thr Thr Val Lys Met Lys Ser Ser Val Phe Asp Glu Asp
        915                 920                 925
```

```
Lys Thr Phe Val Ala Glu Thr Leu Glu Met Gly Glu Val Val Glu Lys
    930                 935                 940

Asp Thr Thr Glu Leu Met Glu Lys Leu Glu Val Thr Lys Arg Glu Lys
945                 950                 955                 960

Leu Glu Leu Ser Gln Arg Leu Ser Asp Leu Ser Glu Gln Leu Lys Gln
                965                 970                 975

Lys His Gly Glu Ile Ser Phe Leu Asn Glu Glu Val Lys Ser Leu Lys
            980                 985                 990

Gln Glu Lys Glu Gln Val Ser Leu  Arg Cys Arg Glu Leu  Glu Ile
Ile
        995                 1000                1005

Ile Asn  His Asn Arg Ala Glu  Asn Val Gln Ser Cys  Asp Thr Gln
    1010                1015                1020

Val Ser  Ser Leu Leu Asp Gly  Val Val Thr Met Thr  Ser Arg Gly
    1025                1030                1035

Ala Glu  Gly Ser Val Ser Lys  Val Asn Lys Ser Phe  Gly Glu Glu
    1040                1045                1050

Ser Lys  Ile Met Val Glu Asp  Lys Val Ser Phe Glu  Asn Met Thr
    1055                1060                1065

Val Gly  Glu Glu Ser Lys Gln  Glu Gln Leu Ile Leu  Asp His Leu
    1070                1075                1080

Pro Ser  Val Thr Lys Glu Ser  Ser Leu Arg Ala Thr  Gln Pro Ser
    1085                1090                1095

Glu Asn  Asp Lys Leu Gln Lys  Glu Leu Asn Val Leu  Lys Ser Glu
    1100                1105                1110

Gln Asn  Asp Leu Arg Leu Gln  Met Glu Ala Gln Arg  Ile Cys Leu
    1115                1120                1125

Ser Leu  Val Tyr Ser Thr His  Val Asp Gln Val Arg  Glu Tyr Met
    1130                1135                1140
```

Glu Asn Glu Lys Asp Lys Ala Leu Cys Ser Leu Lys Glu Glu Leu
1145 1150 1155

Ile Phe Ala Gln Glu Glu Lys Ile Lys Glu Leu Gln Lys Ile His
1160 1165 1170

Gln Leu Glu Leu Gln Thr Met Lys Thr Gln Glu Thr Gly Asp Glu
1175 1180 1185

Gly Lys Pro Leu His Leu Leu Ile Gly Lys Leu Gln Lys Ala Val
1190 1195 1200

Ser Glu Glu Cys Ser Tyr Phe Leu Gln Thr Leu Cys Ser Val Leu
1205 1210 1215

Gly Glu Tyr Tyr Thr Pro Ala Leu Lys Cys Glu Val Asn Ala Glu
1220 1225 1230

Asp Lys Glu Asn Ser Gly Asp Tyr Ile Ser Glu Asn Glu Asp Pro
1235 1240 1245

Glu Leu Gln Asp Tyr Arg Tyr Glu Val Gln Asp Phe Gln Glu Asn
1250 1255 1260

Met His Thr Leu Leu Asn Lys Val Thr Glu Glu Tyr Asn Lys Leu
1265 1270 1275

Leu Val Leu Gln Thr Arg Leu Ser Lys Ile Trp Gly Gln Gln Thr
1280 1285 1290

Asp Gly Met Lys Leu Glu Phe Gly Glu Glu Asn Leu Pro Lys Glu
1295 1300 1305

Glu Thr Glu Phe Leu Ser Ile His Ser Gln Met Thr Asn Leu Glu
1310 1315 1320

Asp Ile Asp Val Asn His Lys Ser Lys Leu Ser Ser Leu Gln Asp
1325 1330 1335

Leu Glu Lys Thr Lys Leu Glu Glu Gln Val Gln Glu Leu Glu Ser
1340 1345 1350

Leu Ile Ser Ser Leu Gln Gln Gln Leu Lys Glu Thr Glu Gln Asn

```
    1355                1360                1365

Tyr Glu  Ala Glu Ile His Cys  Leu Gln Lys Arg Leu  Gln Ala Val
    1370                1375                1380

Ser Glu  Ser Thr Val Pro Pro  Ser Leu Pro Val Asp  Ser Val Val
    1385                1390                1395

Ile Thr  Glu Ser Asp Ala Gln  Arg Thr Met Tyr Pro  Gly Ser Cys
    1400                1405                1410

Val Lys  Lys Asn Ile Asp Gly  Thr Ile Glu Phe Ser  Gly Glu Phe
    1415                1420                1425

Gly Val  Lys Glu Glu Thr Asn  Ile Val Lys Leu Leu  Glu Lys Gln
    1430                1435                1440

Tyr Gln  Glu Gln Leu Glu Glu  Glu Val Ala Lys Val  Ile Val Ser
    1445                1450                1455

Met Ser  Ile Ala Phe Ala Gln  Gln Thr Glu Leu Ser  Arg Ile Ser
    1460                1465                1470

Gly Gly  Lys Glu Asn Thr Ala  Ser Ser Lys Gln Ala  His Ala Val
    1475                1480                1485

Cys Gln  Gln Glu Gln His Tyr  Phe Asn Glu Met Lys  Leu Ser Gln
    1490                1495                1500

Asp Gln  Ile Gly Phe Gln Thr  Phe Glu Thr Val Asp  Val Lys Phe
    1505                1510                1515

Lys Glu  Glu Phe Lys Pro Leu  Ser Lys Glu Leu Gly  Glu His Gly
    1520                1525                1530

Lys Glu  Ile Leu Leu Ser Asn  Ser Asp Pro His Asp  Ile Pro Glu
    1535                1540                1545

Ser Lys  Asp Cys Val Leu Thr  Ile Ser Glu Glu Met  Phe Ser Lys
    1550                1555                1560

Asp Lys  Thr Phe Ile Val Arg  Gln Ser Ile His Asp  Glu Ile Ser
    1565                1570                1575
```

```
Val Ser  Ser Met Asp Ala Ser  Arg Gln Leu Met Leu  Asn Glu Glu
    1580                1585                1590


Gln Leu  Glu Asp Met Arg Gln  Glu Leu Val Arg Gln  Tyr Gln Glu
    1595                1600                1605


His Gln  Gln Ala Thr Glu Leu  Leu Arg Gln Ala His  Met Arg Gln
    1610                1615                1620


Met Glu  Arg Gln Arg Glu Asp  Gln Glu Gln Thr Arg  Arg Asp
    1625                1630                1635


<210> 687
<211> 183
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      interacting prt 1; "

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<223> /note="Uniprot ID:  Q9NQ31; "

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<400> 687
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1               5                  10                  15


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


Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35                  40                  45
```

```
Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50                  55                  60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Lys Tyr Tyr Ser Ser Val
65                  70                  75                  80

Pro Glu Glu Gly Gly Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu
                85                  90                  95

Ser Lys Leu His Met Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp
            100                 105                 110

Arg Lys Lys Thr Ser Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu
        115                 120                 125

His Ala Pro Glu Ala Ser Gln Pro Ala Glu Asn Ile Ser Lys Asp Leu
    130                 135                 140

Tyr Ile Glu Val Tyr Pro Gly Thr Tyr Ser Val Thr Val Gly Ser Asn
145                 150                 155                 160

Asp Leu Thr Lys Lys Thr His Val Val Ala Val Asp Ser Gly Gln Ser
                165                 170                 175

Val Asp Leu Val Phe Pro Val
            180


<210> 688
<211> 210
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<221> source
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<220>
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<400> 688
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1   5   10   15

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

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35   40   45

Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50   55   60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
65   70   75   80

Thr Leu Ser Ala Ser Phe Arg Thr Met Ala Glu Phe Met Asp Tyr Thr
                85   90   95

Ser Ser Gln Cys Gly Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
            100   105   110

Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
        115   120   125

Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp Arg Lys Lys Thr Ser
    130   135   140

Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu His Ala Pro Glu Ala
145   150   155   160

Ser Gln Pro Ala Glu Asn Ile Ser Lys Asp Leu Tyr Ile Glu Val Tyr
                165   170   175

Pro Gly Thr Tyr Ser Val Thr Val Gly Ser Asn Asp Leu Thr Lys Lys
            180   185   190

Thr His Val Val Ala Val Asp Ser Gly Gln Ser Val Asp Leu Val Phe

195 200 205

Pro Val
210

<210> 689
<211> 183
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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interacting prt 1; "

<220>
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<223> /note="Uniprot ID: Q9NQ31; "

<220>
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<400> 689
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1 5 10 15

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

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
35 40 45

Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
50 55 60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
65 70 75 80

Thr Leu Ser Ala Ser Phe Arg Thr Met Ala Glu Phe Met Asp Tyr Thr
85 90 95

```
Ser Ser Gln Cys Gly Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
            100                 105                 110

Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
        115                 120                 125

Cys Leu Asp Ile Gly Asn Gly Gln Ala Glu Asn Ile Ser Lys Asp Leu
    130                 135                 140

Tyr Ile Glu Val Tyr Pro Gly Thr Tyr Ser Val Thr Val Gly Ser Asn
145                 150                 155                 160

Asp Leu Thr Lys Lys Thr His Val Val Ala Val Asp Ser Gly Gln Ser
                165                 170                 175

Val Asp Leu Val Phe Pro Val
            180


<210> 690
<211> 183
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000379885"

<400> 690
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1               5                   10                  15
```

```
Ser Leu Gln Arg Ser Ala Arg Leu Ala Leu Glu Val Leu Glu Arg Ala
            20                  25                  30

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35                  40                  45

Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50                  55                  60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Lys Tyr Tyr Ser Ser Val
65                  70                  75                  80

Pro Glu Glu Gly Gly Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu
                85                  90                  95

Ser Lys Leu His Met Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp
            100                 105                 110

Arg Lys Lys Thr Ser Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu
        115                 120                 125

His Ala Pro Glu Ala Ser Gln Pro Ala Glu Asn Ile Ser Lys Asp Leu
    130                 135                 140

Tyr Ile Glu Val Tyr Pro Gly Thr Tyr Ser Val Thr Val Gly Ser Asn
145                 150                 155                 160

Asp Leu Thr Lys Lys Thr His Val Val Ala Val Asp Ser Gly Gln Ser
                165                 170                 175

Val Asp Leu Val Phe Pro Val
            180


<210> 691
<211> 210
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 117; "

<220>
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<223> /note="Gene Symbol: AKIP1; "
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<220>
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A kinase (PRKA)
interacting prt 1; "

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<223> /note="Uniprot ID: Q9NQ31; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431331"

<400> 691
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1   5   10   15

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

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35   40   45

Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50   55   60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
65   70   75   80

Thr Leu Ser Ala Ser Phe Arg Thr Met Ala Glu Phe Met Asp Tyr Thr
                85   90   95

Ser Ser Gln Cys Gly Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
            100   105   110

Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
        115   120   125

Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp Arg Lys Lys Thr Ser
    130   135   140

Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu His Ala Pro Glu Ala
145   150   155   160

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

```
                165                 170                 175

Pro Gly Thr Tyr Ser Val Thr Val Gly Ser Asn Asp Leu Thr Lys Lys
            180                 185                 190

Thr His Val Val Ala Val Asp Ser Gly Gln Ser Val Asp Leu Val Phe
        195                 200                 205

Pro Val
    210


<210> 692
<211> 151
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 117; "

<220>
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<220>
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000431602"

<400> 692
Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg Ser Leu Gln Arg Ser
1               5                   10                  15

Ala Arg Leu Ala Leu Glu Val Leu Glu Arg Ala Lys Arg Arg Ala Val
            20                  25                  30

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

Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala Ala Gly Pro Gln Arg
    50                  55                  60

Val Leu Pro Gly Glu Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
65                  70                  75                  80
```

```
Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
                85                  90                  95

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

Tyr Ile Glu Val Tyr Pro Gly Thr Tyr Ser Val Thr Val Gly Ser Asn
        115                 120                 125

Asp Leu Thr Lys Lys Thr His Val Val Ala Val Asp Ser Gly Gln Ser
    130                 135                 140

Val Asp Leu Val Phe Pro Val
145                 150


<210> 693
<211> 195
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 117; "

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      interacting prt 1; "

<220>
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<223> /note="ENSP ID: ENSP00000433510"

<400> 693
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1               5                   10                  15

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

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35                  40                  45
```

```
Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50                  55                  60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
65                  70                  75                  80

Thr Leu Ser Ala Ser Phe Arg Thr Met Ala Glu Phe Met Asp Tyr Thr
                85                  90                  95

Ser Ser Gln Cys Gly Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
            100                 105                 110

Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
        115                 120                 125

Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp Arg Lys Lys Thr Ser
    130                 135                 140

Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu His Ala Pro Glu Ala
145                 150                 155                 160

Ser Gln Pro Val Ser Thr Glu Leu Leu Thr His Trp Val Ser Pro Pro
                165                 170                 175

Leu Gln Leu His Glu Pro Val Asp Met Val Leu Arg Gly Leu Phe Glu
            180                 185                 190

Leu Ser Leu
        195


<210> 694
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 117; "

<220>
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<223> /note="Gene Symbol: AKIP1; "

<220>
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<223> /note="Gene Name:
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A kinase (PRKA)
interacting prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434726"

<400> 694
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1 5 10 15

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

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
35 40 45

Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
50 55 60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Lys Tyr Tyr Ser Ser Val
65 70 75 80

Pro Glu Glu Gly Gly Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu
85 90 95

Ser Lys Leu His Met Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp
100 105 110

Arg Lys Lys Thr Ser Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu
115 120 125

His Ala Pro Glu Ala Ser Gln Pro Val Ser Thr Glu Leu Leu Thr His
130 135 140

Trp Val Ser Pro Pro Leu Gln Leu His Glu Pro Val Asp Met Val Leu
145 150 155 160

Arg Gly Leu Phe Glu Leu Ser Leu
165

<210> 695
<211> 179
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AKIP1; "

<220>
<221> source
<223> /note="Gene Name:
A kinase (PRKA)
interacting prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434785"

<400> 695
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1 5 10 15

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

Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
35 40 45

Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
50 55 60

Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
65 70 75 80

Thr Leu Ser Ala Ser Phe Arg Thr Met Ala Glu Phe Met Asp Tyr Thr
85 90 95

Ser Ser Gln Cys Gly Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
100 105 110

Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
115 120 125

Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp Arg Lys Lys Thr Ser
130 135 140

Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu His Ala Pro Glu Ala
145 150 155 160

```
Ser Gln Pro Val Ser Thr Glu Leu Leu Thr His Trp Val Ser Pro Pro
                165                 170                 175


Leu Gln Leu



<210> 696
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 117; "

<220>
<221> source
<223> /note="Gene Symbol: AKIP1; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA)
      interacting prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434820"

<400> 696
Met Asp Asn Cys Leu Ala Ala Ala Ala Leu Asn Gly Val Asp Arg Arg
1               5                   10                  15


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


Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35                  40                  45


Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50                  55                  60


Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Lys Tyr Tyr Ser Ser Val
65                  70                  75                  80


Pro Glu Glu Gly Gly Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu
                85                  90                  95
```

```
Ser Lys Leu His Met Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp
            100                 105                 110

Arg Lys Lys Thr Ser Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu
        115                 120                 125

His Ala Pro Glu Ala Ser Gln Pro Val Ser Thr Glu Leu Leu Thr His
    130                 135                 140

Trp Val Ser Pro Pro Leu Gln Leu His Glu Pro Val Asp Met Val Leu
145                 150                 155                 160

Arg Gly Leu Phe Glu Leu Ser Leu
                165

<210> 697
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 117; "

<220>
<221> source
<223> /note="Gene Symbol: AKIP1; "

<220>
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<223> /note="Gene Name:
      A kinase (PRKA)
      interacting prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436989"

<400> 697
Met Ala Glu Phe Met Asp Tyr Thr Ser Ser Gln Cys Gly Lys Tyr Tyr
1               5                   10                  15

Ser Ser Val Pro Glu Glu Gly Gly Ala Thr His Val Tyr Arg Tyr His
            20                  25                  30

Arg Gly Glu Ser Lys Leu His Met Cys Leu Asp Ile Gly Asn Gly Gln
        35                  40                  45
```

```
Arg Lys Asp Arg Lys Lys Thr Ser Leu Gly Pro Gly Gly Ser Tyr Gln
    50                  55                  60

Ile Ser Glu His Ala Pro Glu Ala Ser Gln Pro Ala Glu Asn Ile Ser
65                  70                  75                  80

Lys Asp Leu Tyr Ile Glu Val Tyr Pro Gly Thr Tyr Ser Val Thr Val
                85                  90                  95

Gly Ser Asn Asp Leu
            100


<210> 698
<211> 384
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 118; "

<220>
<221> source
<223> /note="Gene Symbol: AAR2; "

<220>
<221> source
<223> /note="Gene Name:
      AAR2 splicing  factor
      homolog; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9Y312; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000313674"

<400> 698
Met Ala Ala Val Gln Met Asp Pro Glu Leu Ala Lys Arg Leu Phe Phe
1               5                   10                  15

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

Gly Ile Asp Tyr Asn Ser Trp Glu Val Gly Pro Lys Phe Arg Gly Val
        35                  40                  45

Lys Met Ile Pro Pro Gly Ile His Phe Leu His Tyr Ser Ser Val Asp
```

```
    50                  55                  60

Lys Ala Asn Pro Lys Glu Val Gly Pro Arg Met Gly Phe Phe Leu Ser
65                  70                  75                  80

Leu His Gln Arg Gly Leu Thr Val Leu Arg Trp Ser Thr Leu Arg Glu
                85                  90                  95

Glu Val Asp Leu Ser Pro Ala Pro Glu Ser Glu Val Glu Ala Met Arg
            100                 105                 110

Ala Asn Leu Gln Glu Leu Asp Gln Phe Leu Gly Pro Tyr Pro Tyr Ala
        115                 120                 125

Thr Leu Lys Lys Trp Ile Ser Leu Thr Asn Phe Ile Ser Glu Ala Thr
    130                 135                 140

Val Glu Lys Leu Gln Pro Glu Asn Arg Gln Ile Cys Ala Phe Ser Asp
145                 150                 155                 160

Val Leu Pro Val Leu Ser Met Lys His Thr Lys Asp Arg Val Gly Gln
                165                 170                 175

Asn Leu Pro Arg Cys Gly Ile Glu Cys Lys Ser Tyr Gln Glu Gly Leu
            180                 185                 190

Ala Arg Leu Pro Glu Met Lys Pro Arg Ala Gly Thr Glu Ile Arg Phe
        195                 200                 205

Ser Glu Leu Pro Thr Gln Met Phe Pro Glu Gly Ala Thr Pro Ala Glu
    210                 215                 220

Ile Thr Lys His Ser Met Asp Leu Ser Tyr Ala Leu Glu Thr Val Leu
225                 230                 235                 240

Asn Lys Gln Phe Pro Ser Ser Pro Gln Asp Val Leu Gly Glu Leu Gln
                245                 250                 255

Phe Ala Phe Val Cys Phe Leu Leu Gly Asn Val Tyr Glu Ala Phe Glu
            260                 265                 270

His Trp Lys Arg Leu Leu Asn Leu Leu Cys Arg Ser Glu Ala Ala Met
        275                 280                 285
```

```
Met Lys His His Thr Leu Tyr Ile Asn Leu Ile Ser Ile Leu Tyr His
    290                 295                 300

Gln Leu Gly Glu Ile Pro Ala Asp Phe Phe Val Asp Ile Val Ser Gln
305                 310                 315                 320

Asp Asn Phe Leu Thr Ser Thr Leu Gln Val Phe Phe Ser Ser Ala Cys
                325                 330                 335

Ser Ile Ala Val Asp Ala Thr Leu Arg Lys Lys Ala Glu Lys Phe Gln
            340                 345                 350

Ala His Leu Thr Lys Lys Phe Arg Trp Asp Phe Ala Ala Glu Pro Glu
        355                 360                 365

Asp Cys Ala Pro Val Val Val Glu Leu Pro Glu Gly Ile Glu Met Gly
    370                 375                 380
```

<210> 699
<211> 384
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 118; "

<220>
<221> source
<223> /note="Gene Symbol: AAR2; "

<220>
<221> source
<223> /note="Gene Name:
AAR2 splicing factor
homolog; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y312; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000363043"

<400> 699

```
Met Ala Ala Val Gln Met Asp Pro Glu Leu Ala Lys Arg Leu Phe Phe
1               5                   10                  15
```

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

Gly Ile Asp Tyr Asn Ser Trp Glu Val Gly Pro Lys Phe Arg Gly Val
        35                  40                  45

Lys Met Ile Pro Pro Gly Ile His Phe Leu His Tyr Ser Ser Val Asp
    50                  55                  60

Lys Ala Asn Pro Lys Glu Val Gly Pro Arg Met Gly Phe Phe Leu Ser
65                  70                  75                  80

Leu His Gln Arg Gly Leu Thr Val Leu Arg Trp Ser Thr Leu Arg Glu
                85                  90                  95

Glu Val Asp Leu Ser Pro Ala Pro Glu Ser Glu Val Glu Ala Met Arg
            100                 105                 110

Ala Asn Leu Gln Glu Leu Asp Gln Phe Leu Gly Pro Tyr Pro Tyr Ala
        115                 120                 125

Thr Leu Lys Lys Trp Ile Ser Leu Thr Asn Phe Ile Ser Glu Ala Thr
    130                 135                 140

Val Glu Lys Leu Gln Pro Glu Asn Arg Gln Ile Cys Ala Phe Ser Asp
145                 150                 155                 160

Val Leu Pro Val Leu Ser Met Lys His Thr Lys Asp Arg Val Gly Gln
                165                 170                 175

Asn Leu Pro Arg Cys Gly Ile Glu Cys Lys Ser Tyr Gln Glu Gly Leu
            180                 185                 190

Ala Arg Leu Pro Glu Met Lys Pro Arg Ala Gly Thr Glu Ile Arg Phe
        195                 200                 205

Ser Glu Leu Pro Thr Gln Met Phe Pro Glu Gly Ala Thr Pro Ala Glu
    210                 215                 220

Ile Thr Lys His Ser Met Asp Leu Ser Tyr Ala Leu Glu Thr Val Leu
225                 230                 235                 240
```

```
Asn Lys Gln Phe Pro Ser Ser Pro Gln Asp Val Leu Gly Glu Leu Gln
                245                 250                 255

Phe Ala Phe Val Cys Phe Leu Leu Gly Asn Val Tyr Glu Ala Phe Glu
            260                 265                 270

His Trp Lys Arg Leu Leu Asn Leu Leu Cys Arg Ser Glu Ala Ala Met
        275                 280                 285

Met Lys His His Thr Leu Tyr Ile Asn Leu Ile Ser Ile Leu Tyr His
    290                 295                 300

Gln Leu Gly Glu Ile Pro Ala Asp Phe Phe Val Asp Ile Val Ser Gln
305                 310                 315                 320

Asp Asn Phe Leu Thr Ser Thr Leu Gln Val Phe Phe Ser Ser Ala Cys
                325                 330                 335

Ser Ile Ala Val Asp Ala Thr Leu Arg Lys Lys Ala Glu Lys Phe Gln
            340                 345                 350

Ala His Leu Thr Lys Lys Phe Arg Trp Asp Phe Ala Ala Glu Pro Glu
        355                 360                 365

Asp Cys Ala Pro Val Val Val Glu Leu Pro Glu Gly Ile Glu Met Gly
    370                 375                 380


<210> 700
<211> 398
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 118; "

<220>
<221> source
<223> /note="Gene Symbol: AAR2; "

<220>
<221> source
<223> /note="Gene Name:
      AAR2 splicing  factor
      homolog; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000380455"

<400> 700

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Met Ala Ala Val Gln Met Asp Pro Glu Leu Ala Lys Arg Leu Phe Phe
1               5                  10                  15

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

Gly Ile Asp Tyr Asn Ser Trp Glu Val Gly Pro Lys Phe Arg Gly Val
        35                  40                  45

Lys Met Ile Pro Pro Gly Ile His Phe Leu His Tyr Ser Ser Val Asp
    50                  55                  60

Lys Ala Asn Pro Lys Glu Val Gly Pro Arg Met Gly Phe Phe Leu Ser
65                  70                  75                  80

Leu His Gln Arg Gly Leu Thr Val Leu Arg Trp Ser Thr Leu Arg Glu
                85                  90                  95

Glu Val Asp Leu Ser Pro Ala Pro Glu Ser Glu Val Glu Ala Met Arg
            100                 105                 110

Ala Asn Leu Gln Glu Leu Asp Gln Phe Leu Gly Pro Tyr Pro Tyr Ala
        115                 120                 125

Thr Leu Lys Lys Trp Ile Ser Leu Thr Asn Phe Ile Ser Glu Ala Thr
    130                 135                 140

Val Glu Lys Leu Gln Pro Glu Asn Arg Gln Ile Cys Ala Phe Ser Asp
145                 150                 155                 160

Val Leu Pro Val Leu Ser Met Lys His Thr Lys Asp Arg Val Gly Gln
                165                 170                 175

Asn Leu Pro Arg Cys Gly Ile Glu Cys Lys Ser Tyr Gln Glu Gly Leu
            180                 185                 190

Ala Arg Leu Pro Glu Met Lys Pro Arg Ala Gly Thr Glu Ile Arg Phe
        195                 200                 205

Ser Glu Leu Pro Thr Gln Met Phe Pro Glu Gly Ala Thr Pro Ala Glu
    210                 215                 220
```

```
Ile Thr Lys His Ser Met Asp Leu Ser Tyr Ala Leu Glu Thr Val Leu
225                 230                 235                 240

Asn Lys Gln Phe Pro Ser Ser Pro Gln Asp Val Leu Gly Glu Leu Gln
                245                 250                 255

Phe Ala Phe Val Cys Phe Leu Leu Gly Asn Val Tyr Glu Ala Phe Glu
            260                 265                 270

His Trp Lys Arg Leu Leu Asn Leu Leu Cys Arg Ser Glu Ala Ala Met
        275                 280                 285

Met Lys His His Thr Leu Tyr Ile Asn Leu Ile Ser Ile Leu Tyr His
    290                 295                 300

Gln Leu Gly Glu Ile Pro Ala Asp Phe Phe Val Asp Ile Val Ser Gln
305                 310                 315                 320

Asp Asn Phe Leu Thr Ser Thr Leu Gln Arg Gln Ser Leu Ala Val Ser
                325                 330                 335

Pro Arg Leu Lys Cys Ser Asp Leu Ile Ile Ala Arg Cys Ser Leu Glu
            340                 345                 350

Leu Leu Gly Ser Tyr Asp Pro Pro Thr Ser Ala Ser Arg Val Ala Gly
        355                 360                 365

Thr Thr Gly Arg Tyr His His Thr Arg Leu Ile Asn Asn Asn Lys Lys
    370                 375                 380

Asn Cys Arg Asp Lys Val Phe Leu Cys Cys Pro Gly Trp Ser
385                 390                 395


<210> 701
<211> 523
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 119; "

<220>
<221> source
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<223> /note="Gene Symbol: ADCK1; "

<220>
<221> source
<223> /note="Gene Name:
aarF
domain containing kinase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q86TW2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000238561"

<400> 701

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Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1               5                  10                  15

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

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
        35                  40                  45

Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
    50                  55                  60

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
65                  70                  75                  80

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

Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr
            100                 105                 110

Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln
        115                 120                 125

Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Ile His Asp
    130                 135                 140

Leu Phe Gln Ser Phe Asp Asp Thr Pro Leu Gly Thr Ala Ser Leu Ala
145                 150                 155                 160
```

```
Gln Val His Lys Ala Val Leu His Asp Gly Arg Thr Val Ala Val Lys
                165                 170                 175

Val Gln His Pro Lys Val Arg Ala Gln Ser Ser Lys Asp Ile Leu Leu
            180                 185                 190

Met Glu Val Leu Val Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu
        195                 200                 205

Phe Met Trp Leu Val Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu
    210                 215                 220

Asp Phe Leu Asn Glu Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu
225                 230                 235                 240

Arg His Phe Asp Phe Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser
                245                 250                 255

Thr Glu Arg Val Leu Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn
            260                 265                 270

Asp Arg Asp Tyr Met Glu Arg Asn Lys Ile Asp Val Asn Glu Ile Ser
        275                 280                 285

Arg His Leu Gly Lys Met Tyr Ser Glu Met Ile Phe Val Asn Gly Phe
    290                 295                 300

Val His Cys Asp Pro His Pro Gly Asn Val Leu Val Arg Lys His Pro
305                 310                 315                 320

Gly Thr Gly Lys Ala Glu Ile Val Leu Leu Asp His Gly Leu Tyr Gln
                325                 330                 335

Met Leu Thr Glu Glu Phe Arg Leu Asn Tyr Cys His Leu Trp Gln Ser
            340                 345                 350

Leu Ile Trp Thr Asp Met Lys Arg Val Lys Glu Tyr Ser Gln Arg Leu
        355                 360                 365

Gly Ala Gly Asp Leu Tyr Pro Leu Phe Ala Cys Met Leu Thr Ala Arg
    370                 375                 380

Ser Trp Asp Ser Val Asn Arg Gly Ile Ser Gln Ala Pro Val Thr Ala
```

```
385                 390                 395                 400

Thr Glu Asp Leu Glu Ile Arg Asn Asn Ala Ala Asn Tyr Leu Pro Gln
                405                 410                 415

Ile Ser His Leu Leu Asn His Val Pro Arg Gln Met Leu Leu Ile Leu
            420                 425                 430

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

Ala Ser Ala Ser Ser Phe Leu Asn Met Ser Arg Cys Cys Ile Arg Ala
    450                 455                 460

Leu Ala Glu His Lys Lys Lys Asn Thr Cys Ser Phe Phe Arg Arg Thr
465                 470                 475                 480

Gln Ile Ser Phe Ser Glu Ala Phe Asn Leu Trp Gln Ile Asn Leu His
                485                 490                 495

Glu Leu Ile Leu Arg Val Lys Gly Leu Lys Leu Ala Asp Arg Val Leu
            500                 505                 510

Ala Leu Ile Cys Trp Leu Phe Pro Ala Pro Leu
        515                 520


<210> 702
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 119; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK1; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing kinase 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q86TW2; "
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<220>
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<400> 702
Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1   5   10   15

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

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
        35   40   45

Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
    50   55   60

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Ile His Asp Leu Phe Gln Ser
65   70   75   80

Phe Asp Asp Thr Pro Leu Gly Thr Ala Ser Leu Ala Gln Val His Lys
                85   90   95

Ala Val Leu His Asp Gly Arg Thr Val Ala Val Lys Val Gln His Pro
            100   105   110

Lys Val Arg Ala Gln Ser Ser Lys Asp Ile Leu Leu Met Glu Val Leu
        115   120   125

Val Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu
    130   135   140

Val Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn
145   150   155   160

Glu Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp
                165   170   175

Phe Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser Thr Glu Arg Val
            180   185   190

Leu Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn Asp Arg Asp Tyr
        195   200   205

```
Met Glu Arg Asn Lys Ile Asp Val Asn Glu Ile Ser Arg His Leu Gly
    210                 215                 220

Lys Met Tyr Ser Glu Met Ile Phe Val Asn Gly Phe Val His Cys Asp
225                 230                 235                 240

Pro His Pro Gly Asn Val Leu Val Arg Lys His Pro Gly Thr Gly Lys
                245                 250                 255

Ala Glu Ile Val Leu Leu Asp His Gly Leu Tyr Gln Met Leu Thr Glu
            260                 265                 270

Glu Phe Arg Leu Asn Tyr Cys His Leu Trp Gln Ser Leu Ile Trp Thr
        275                 280                 285

Asp Met Lys Arg Val Lys Glu Tyr Ser Gln Arg Leu Gly Ala Gly Asp
    290                 295                 300

Leu Tyr Pro Leu Phe Ala Cys Met Leu Thr Ala Arg Ser Trp Asp Ser
305                 310                 315                 320

Val Asn Arg Gly Ile Ser Gln Ala Pro Val Thr Ala Thr Glu Asp Leu
                325                 330                 335

Glu Ile Arg Asn Asn Ala Ala Asn Tyr Leu Pro Gln Ile Ser His Leu
            340                 345                 350

Leu Asn His Val Pro Arg Gln Met Leu Leu Ile Leu Lys Thr Asn Asp
        355                 360                 365

Leu Leu Arg Gly Ile Glu Ala Ala Leu Gly Thr Arg Ala Ser Ala Ser
    370                 375                 380

Ser Phe Leu Asn Met Ser Arg Cys Cys Ile Arg Ala Leu Ala Glu His
385                 390                 395                 400

Lys Lys Lys Asn Thr Cys Ser Phe Phe Arg Arg Thr Gln Ile Ser Phe
                405                 410                 415

Ser Glu Ala Phe Asn Leu Trp Gln Ile Asn Leu His Glu Leu Ile Leu
            420                 425                 430
```

Arg Val Lys Gly Leu Lys Leu Ala Asp Arg Val Leu Ala Leu Ile Cys
        435   440   445

Trp Leu Phe Pro Ala Pro Leu
    450   455

<210> 703
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 119; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK1; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377256"

<400> 703
Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1   5   10   15

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

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
        35   40   45

Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
    50   55   60

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
65   70   75   80

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

Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr

```
            100                 105                 110

Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln
        115                 120                 125

Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Val Leu Val
    130                 135                 140

Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu Val
145                 150                 155                 160

Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn Glu
                165                 170                 175

Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp Phe
            180                 185                 190

Leu Lys Pro Gly Gln Gln Ser Glu Thr Ala Ser Gln Gly Thr Thr Thr
        195                 200                 205

Thr Thr Lys Lys Lys Trp Asp Arg Lys Leu
    210                 215


<210> 704
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 119; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK1; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451271"

<400> 704
Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1               5                   10                  15
```

```
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
            20                  25                  30

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
        35                  40                  45

Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
    50                  55                  60

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Ser Leu Ala Val Ser Pro Arg
65                  70                  75                  80

Leu Glu Cys Ile Gly Val Ile Ser Ala His Cys Asn Leu Tyr Leu Leu
                85                  90                  95

Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr
            100                 105                 110

Gly Ala Pro Ser Leu Cys Gln Ala Ser Leu
        115                 120


<210> 705
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 119; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK1; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451549"

<400> 705
Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1               5                   10                  15
```

```
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
            20                  25                  30

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
        35                  40                  45

Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
    50                  55                  60

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
65                  70                  75                  80

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

Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr
            100                 105                 110

Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln
        115                 120                 125

Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Ile His Asp
    130                 135                 140

Leu Phe Gln Ser Phe Asp Asp Thr Pro Leu Gly Thr Ala Ser Leu Ala
145                 150                 155                 160

Gln Val His Lys Ala Val Leu His Asp Gly Arg Thr Val Ala Val Lys
                165                 170                 175

Val Gln His Pro Lys Val Arg Ala Gln Ser Ser Lys Asp Ile Leu Leu
            180                 185                 190

Met Glu Val Leu Val Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu
        195                 200                 205

Phe Met Trp Leu Val Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu
    210                 215                 220

Asp Phe Leu Asn Glu Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu
225                 230                 235                 240
```

```
Arg His Phe Asp Phe Leu Lys Ile Ser Arg His Leu Gly Lys Met Tyr
                245                 250                 255


Ser Glu Met Ile Phe Val Asn Gly Phe
            260                 265


<210> 706
<211> 626
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 120; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK2; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q7Z695; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000072869"

<400> 706
Met Val Ala Pro Trp Arg Val Ser Val Arg Val Cys Leu Ser His Leu
1               5                   10                  15


Arg Cys Phe Glu Leu Arg Gln Gly Leu Ser Leu Leu Arg Pro Ser Glu
            20                  25                  30


Cys Pro Arg Asp Ala Arg Leu Cys Trp Leu Leu Leu Gly Thr Leu Pro
        35                  40                  45


Lys Val Val Ser Leu Cys Gly Asp Val Gly Glu Gly Ala Pro Asp Val
    50                  55                  60


Leu Ser Arg Arg Arg Val Arg Cys Ser Gly Ala Ala Gly Ala Gly Pro
65                  70                  75                  80


Ala Glu Ser Leu Pro Arg Ala Gly Pro Leu Gly Gly Val Phe Leu His
```

```
                85                  90                  95

Leu Arg Leu Trp Leu Arg Ala Gly Ala Leu Leu Val Lys Phe Phe Pro
            100                 105                 110

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

Leu Trp Leu His Leu Leu Leu Lys Ala Thr Glu Thr Ser Gly Pro Thr
    130                 135                 140

Tyr Ile Lys Leu Gly Gln Trp Ala Ser Thr Arg Arg Asp Leu Phe Ser
145                 150                 155                 160

Glu Ala Phe Cys Ala Gln Phe Ser Lys Leu His Val Arg Val Thr Pro
                165                 170                 175

His Pro Trp Thr His Thr Glu Arg Phe Leu Arg Gln Ala Phe Gly Asp
            180                 185                 190

Asp Trp Gly Ser Ile Leu Ser Phe Glu Asn Arg Glu Pro Val Gly Ser
        195                 200                 205

Gly Cys Val Ala Gln Val Tyr Lys Ala Tyr Ala Asn Thr Ala Phe Leu
    210                 215                 220

Glu Thr Asp Ser Val Gln Arg Leu Gly Arg Ala Ser Cys Leu Pro Pro
225                 230                 235                 240

Phe Ser His Thr Gly Ala Val Gly Gly Leu Arg Glu Leu Phe Gly Tyr
                245                 250                 255

Leu Gly Asn Gly Arg Lys Pro Pro Glu Asn Leu Ala Asp Gln Ser Phe
            260                 265                 270

Leu Glu Arg Leu Leu Leu Pro Lys Ala Asp Leu Val Gly Ser Asn Ala
        275                 280                 285

Gly Val Ser Arg Ala Gln Val Pro Gly His Gln Pro Glu Ala Thr Asn
    290                 295                 300

Leu Ile Ser Val Ala Val Lys Val Leu His Pro Gly Leu Leu Ala Gln
305                 310                 315                 320
```

```
Val His Met Asp Leu Leu Leu Met Lys Ile Gly Ser Arg Val Leu Gly
                325                 330                 335

Val Leu Pro Gly Ile Lys Trp Leu Ser Leu Pro Glu Ile Val Glu Glu
            340                 345                 350

Phe Glu Lys Leu Met Val Gln Gln Ile Asp Leu Arg Tyr Glu Ala Gln
        355                 360                 365

Asn Leu Glu His Phe Gln Val Asn Phe Arg Asn Val Lys Ala Val Lys
    370                 375                 380

Phe Pro Thr Pro Leu Arg Pro Phe Val Thr Arg Glu Val Leu Val Glu
385                 390                 395                 400

Thr Tyr Glu Glu Ser Val Pro Val Ser Ser Tyr Gln Gln Ala Gly Ile
                405                 410                 415

Pro Val Asp Leu Lys Arg Lys Ile Ala Arg Leu Gly Ile Asn Met Leu
            420                 425                 430

Leu Lys Met Ile Phe Val Asp Asn Phe Val His Ala Asp Leu His Pro
        435                 440                 445

Gly Asn Ile Leu Val Gln Gly Ala Asn Gly Leu Ser Ser Ser Gln Glu
    450                 455                 460

Ala Gln Leu Gln Gln Ala Asp Ile Cys Asp Thr Leu Val Val Ala Val
465                 470                 475                 480

Pro Ser Ser Leu Cys Pro Leu Arg Leu Val Leu Leu Asp Ala Gly Ile
                485                 490                 495

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

Met Ala Val Val Met Gly Gln Gly Gln Arg Val Ala Glu Leu Ile Leu
        515                 520                 525

His His Ala Arg Ala Ser Glu Cys Arg Asp Val Glu Gly Phe Lys Thr
    530                 535                 540
```

```
Glu Met Ala Met Leu Val Thr Gln Ala Arg Lys Asn Thr Ile Thr Leu
545                 550                 555                 560

Glu Lys Leu His Val Ser Ser Leu Leu Ser Ser Val Phe Lys Leu Leu
                565                 570                 575

Met Thr His Lys Val Lys Leu Glu Ser Asn Phe Ala Ser Ile Val Phe
            580                 585                 590

Ala Ile Met Val Leu Glu Gly Leu Gly Arg Ser Leu Asp Pro Lys Leu
        595                 600                 605

Asp Ile Leu Glu Ala Ala Arg Pro Phe Leu Leu Thr Gly Pro Val Cys
    610                 615                 620

Pro Pro
625
```

<210> 707
<211> 470
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 120; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK2; "

<220>
<221> source
<223> /note="Gene Name:
aarF
domain containing kinase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417367"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 707

```
Xaa Cys Ala Gln Phe Ser Lys Leu His Val Arg Val Thr Pro His Pro
1               5                   10                  15
```

```
Trp Thr His Thr Glu Arg Phe Leu Arg Gln Ala Phe Gly Asp Asp Trp
            20                  25                  30

Gly Ser Ile Leu Ser Phe Glu Asn Arg Glu Pro Val Gly Ser Gly Cys
        35                  40                  45

Val Ala Gln Val Tyr Lys Ala Tyr Ala Asn Thr Ala Phe Leu Glu Thr
    50                  55                  60

Asp Ser Val Gln Arg Leu Gly Arg Ala Ser Cys Leu Pro Pro Phe Ser
65                  70                  75                  80

His Thr Gly Ala Val Gly Gly Leu Arg Glu Leu Phe Gly Tyr Leu Gly
                85                  90                  95

Asn Gly Arg Lys Pro Pro Glu Asn Leu Ala Asp Gln Ser Phe Leu Glu
            100                 105                 110

Arg Leu Leu Leu Pro Lys Ala Asp Leu Val Gly Ser Asn Ala Gly Val
        115                 120                 125

Ser Arg Ala Gln Val Pro Gly His Gln Pro Glu Ala Thr Asn Leu Ile
    130                 135                 140

Ser Val Ala Val Lys Val Leu His Pro Gly Leu Leu Ala Gln Val His
145                 150                 155                 160

Met Asp Leu Leu Leu Met Lys Ile Gly Ser Arg Val Leu Gly Val Leu
                165                 170                 175

Pro Gly Ile Lys Trp Leu Ser Leu Pro Glu Ile Val Glu Glu Phe Glu
            180                 185                 190

Lys Leu Met Val Gln Gln Ile Asp Leu Arg Tyr Glu Ala Gln Asn Leu
        195                 200                 205

Glu His Phe Gln Val Asn Phe Arg Asn Val Lys Ala Val Lys Phe Pro
    210                 215                 220

Thr Pro Leu Arg Pro Phe Val Thr Arg Glu Val Leu Val Glu Thr Tyr
225                 230                 235                 240
```

```
Glu Glu Ser Val Pro Val Ser Ser Tyr Gln Gln Ala Gly Ile Pro Val
                245                 250                 255

Asp Leu Lys Arg Lys Ile Ala Arg Leu Gly Ile Asn Met Leu Leu Lys
            260                 265                 270

Met Ile Phe Val Asp Asn Phe Val His Ala Asp Leu His Pro Gly Asn
        275                 280                 285

Ile Leu Val Gln Gly Ala Asn Gly Leu Ser Ser Ser Gln Glu Ala Gln
    290                 295                 300

Leu Gln Gln Ala Asp Ile Cys Asp Thr Leu Val Val Ala Val Pro Ser
305                 310                 315                 320

Ser Leu Cys Pro Leu Arg Leu Val Leu Leu Asp Ala Gly Ile Val Ala
                325                 330                 335

Glu Leu Gln Ala Pro Asp Leu Arg Asn Phe Arg Ala Val Phe Met Ala
            340                 345                 350

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

Ala Arg Ala Ser Glu Cys Arg Asp Val Glu Gly Phe Lys Thr Glu Met
    370                 375                 380

Ala Met Leu Val Thr Gln Ala Arg Lys Asn Thr Ile Thr Leu Glu Lys
385                 390                 395                 400

Leu His Val Ser Ser Leu Leu Ser Ser Val Phe Lys Leu Leu Met Thr
                405                 410                 415

His Lys Val Leu Arg Gly His Ser Lys Gln Ala Glu Arg Gly Trp Asp
            420                 425                 430

Gly Ser Arg Trp Leu Gly Gly Arg Thr Pro Ala Gly His Ala Ala Pro
        435                 440                 445

Arg Ala Ser Ala His Gln Val Gln Cys Gly Gly Gly Lys Gly Thr Lys
    450                 455                 460
```

```
Arg Arg Gln Ser Leu Pro
465                 470


<210> 708
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 120; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK2; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420288"

<400> 708
Ile Asp Leu Arg Tyr Glu Ala Gln Asn Leu Glu His Phe Gln Val Asn
1               5                   10                  15


Phe Arg Asn Val Lys Ala Val Lys Phe Pro Thr Pro Leu Arg Pro Phe
            20                  25                  30


Val Thr Arg Glu Val Leu Val Glu Thr Tyr Glu Glu Ser Val Pro Val
        35                  40                  45


Ser Ser Tyr Gln Gln Ala Gly Ile Pro Val Asp Leu Lys Arg Lys Ile
    50                  55                  60


Ala Arg Leu Gly Ile Asn Met Leu Leu Lys Met Ile Phe Val Asp Asn
65                  70                  75                  80


Phe Val His Ala Asp Leu His Pro Gly Asn Ile Leu Val Gln Gly Ala
                85                  90                  95


Asn Gly Leu Ser Ser Ser Gln Glu Ala Gln Leu Gln Gln Ala Asp Ile
            100                 105                 110


Cys Asp Thr Leu Val Val Ala Val Pro Ser Ser Leu Cys Pro Leu Arg
```

```
        115                 120                 125

Leu Val Leu Leu Asp Ala Gly Ile Val Ala Glu Leu Gln Ala Pro Asp
    130                 135                 140

Leu Arg Asn Phe Arg Ala Val Phe Met Ala Val Val Met Gly Gln Leu
145                 150                 155                 160

His Val Ser Ser Leu Leu Ser Ser Val Phe Lys Leu Leu Met Thr His
                165                 170                 175

Lys Val Lys Leu Glu Ser Asn Phe Ala Ser Ile Val Phe Ala Ile Met
            180                 185                 190

Val Leu Glu Gly Leu Gly Arg Ser Leu Asp Pro Lys Leu Asp Ile Leu
        195                 200                 205

Glu Ala Ala Arg Pro Phe Leu Leu Thr Gly Pro Val Cys Pro Pro
    210                 215                 220


<210> 709
<211> 590
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 120; "

<220>
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<223> /note="Gene Symbol: ADCK2; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420512"

<400> 709
Met Val Ala Pro Trp Arg Val Ser Val Arg Val Cys Leu Ser His Leu
1               5                   10                  15

Arg Cys Phe Glu Leu Arg Gln Gly Leu Ser Leu Leu Arg Pro Ser Glu
            20                  25                  30
```

```
Cys Pro Arg Asp Ala Arg Leu Cys Trp Leu Leu Leu Gly Thr Leu Pro
        35                  40                  45

Lys Val Val Ser Leu Cys Gly Asp Val Gly Glu Gly Ala Pro Asp Val
    50                  55                  60

Leu Ser Arg Arg Arg Val Arg Cys Ser Gly Ala Ala Gly Ala Gly Pro
65                  70                  75                  80

Ala Glu Ser Leu Pro Arg Ala Gly Pro Leu Gly Gly Val Phe Leu His
                85                  90                  95

Leu Arg Leu Trp Leu Arg Ala Gly Ala Leu Leu Val Lys Phe Phe Pro
            100                 105                 110

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

Leu Trp Leu His Leu Leu Leu Lys Ala Thr Glu Thr Ser Gly Pro Thr
    130                 135                 140

Tyr Ile Lys Leu Gly Gln Trp Ala Ser Thr Arg Arg Asp Leu Phe Ser
145                 150                 155                 160

Glu Ala Phe Cys Ala Gln Phe Ser Lys Leu His Val Arg Val Thr Pro
                165                 170                 175

His Pro Trp Thr His Thr Glu Arg Phe Leu Arg Gln Ala Phe Gly Asp
            180                 185                 190

Asp Trp Gly Ser Ile Leu Ser Phe Glu Asn Arg Glu Pro Val Gly Ser
        195                 200                 205

Gly Cys Val Ala Gln Val Tyr Lys Ala Tyr Ala Asn Thr Ala Phe Leu
    210                 215                 220

Glu Thr Asp Ser Val Gln Arg Leu Gly Arg Ala Ser Cys Leu Pro Pro
225                 230                 235                 240

Phe Ser His Thr Gly Ala Val Gly Gly Leu Arg Glu Leu Phe Gly Tyr
                245                 250                 255
```

```
Leu Gly Asn Gly Arg Lys Pro Pro Glu Asn Leu Ala Asp Gln Ser Phe
            260                 265                 270

Leu Glu Arg Leu Leu Leu Pro Lys Ala Asp Leu Val Gly Ser Asn Ala
        275                 280                 285

Gly Val Ser Arg Ala Gln Val Pro Gly His Gln Pro Glu Ala Thr Asn
    290                 295                 300

Leu Ile Ser Val Ala Val Lys Val Leu His Pro Gly Leu Leu Ala Gln
305                 310                 315                 320

Val His Met Asp Leu Leu Leu Met Lys Ile Gly Ser Arg Val Leu Gly
                325                 330                 335

Val Leu Pro Gly Ile Lys Trp Leu Ser Leu Pro Glu Ile Val Glu Glu
            340                 345                 350

Phe Glu Lys Leu Met Val Gln Gln Ile Asp Leu Arg Tyr Glu Ala Gln
        355                 360                 365

Asn Leu Glu His Phe Gln Val Asn Phe Arg Asn Val Lys Ala Val Lys
    370                 375                 380

Phe Pro Thr Pro Leu Arg Pro Phe Val Thr Arg Glu Val Leu Val Glu
385                 390                 395                 400

Thr Tyr Glu Glu Ser Val Pro Val Ser Ser Tyr Gln Gln Ala Gly Ile
                405                 410                 415

Pro Val Asp Leu Lys Arg Lys Ile Ala Arg Leu Gly Ile Asn Met Leu
            420                 425                 430

Leu Lys Met Ile Phe Val Asp Asn Phe Val His Ala Asp Leu His Pro
        435                 440                 445

Gly Asn Ile Leu Val Gln Gly Ala Asn Gly Leu Ser Ser Ser Gln Glu
    450                 455                 460

Ala Gln Leu Gln Gln Ala Asp Ile Cys Asp Thr Leu Val Val Ala Val
465                 470                 475                 480
```

```
Pro Ser Ser Leu Cys Pro Leu Arg Leu Val Leu Leu Asp Ala Gly Ile
                485                 490                 495

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

Met Ala Val Val Met Gly Gln Gly Gln Arg Val Ala Glu Leu Ile Leu
        515                 520                 525

His His Ala Arg Ala Ser Glu Cys Arg Asp Val Glu Gly Phe Lys Thr
    530                 535                 540

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

Glu Lys Leu His Val Ser Ser Leu Leu Ser Ser Val Phe Lys Leu Leu
                565                 570                 575

Met Thr His Lys Val Lys Ser Gln Phe Ile Pro Ala Pro Ser
            580                 585                 590


<210> 710
<211> 407
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 120; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK2; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480996"

<400> 710
Met Val Ala Pro Trp Arg Val Ser Val Arg Val Cys Leu Ser His Leu
1               5                   10                  15

Arg Cys Phe Glu Leu Arg Gln Gly Leu Ser Leu Leu Arg Pro Ser Glu
```

```
            20                  25                  30

Cys Pro Arg Asp Ala Arg Leu Cys Trp Leu Leu Leu Gly Thr Leu Pro
        35                  40                  45

Lys Val Val Ser Leu Cys Gly Asp Val Gly Glu Gly Ala Pro Asp Val
    50                  55                  60

Leu Ser Arg Arg Arg Val Arg Cys Ser Gly Ala Ala Gly Ala Gly Pro
65                  70                  75                  80

Ala Glu Ser Leu Pro Arg Ala Gly Pro Leu Gly Gly Val Phe Leu His
                85                  90                  95

Leu Arg Leu Trp Leu Arg Ala Gly Ala Leu Leu Val Lys Phe Phe Pro
            100                 105                 110

Leu Leu Leu Leu Tyr Pro Leu Thr Tyr Leu Ala Pro Ser Val Ser Thr
        115                 120                 125

Leu Trp Leu His Leu Leu Leu Lys Ala Thr Glu Thr Ser Gly Pro Thr
    130                 135                 140

Tyr Ile Lys Leu Gly Gln Trp Ala Ser Thr Arg Arg Asp Leu Phe Ser
145                 150                 155                 160

Glu Ala Phe Cys Ala Gln Phe Ser Lys Leu His Val Arg Val Thr Pro
                165                 170                 175

His Pro Trp Thr His Thr Glu Arg Phe Leu Arg Gln Ala Phe Gly Asp
            180                 185                 190

Asp Trp Gly Ser Ile Leu Ser Phe Glu Asn Arg Glu Pro Val Gly Ser
        195                 200                 205

Gly Cys Val Ala Gln Val Tyr Lys Ala Tyr Ala Asn Thr Ala Phe Leu
    210                 215                 220

Glu Thr Asp Ser Val Gln Arg Leu Gly Arg Ala Ser Cys Leu Pro Pro
225                 230                 235                 240

Phe Ser His Thr Gly Ala Val Gly Gly Leu Arg Glu Leu Phe Gly Tyr
                245                 250                 255
```

```
Leu Gly Asn Gly Arg Lys Pro Pro Glu Asn Leu Ala Asp Gln Ser Phe
            260                 265                 270

Leu Glu Arg Leu Leu Leu Pro Lys Ala Asp Leu Val Gly Ser Asn Ala
        275                 280                 285

Gly Val Ser Arg Ala Gln Val Pro Gly His Gln Pro Glu Ala Thr Asn
    290                 295                 300

Leu Ile Ser Val Ala Val Lys Val Leu His Pro Gly Leu Leu Ala Gln
305                 310                 315                 320

Val His Met Asp Leu Leu Leu Met Lys Ile Gly Ser Arg Val Leu Gly
                325                 330                 335

Val Leu Pro Gly Ile Lys Trp Leu Ser Leu Pro Glu Ile Val Glu Glu
            340                 345                 350

Phe Glu Lys Leu Met Val Gln Gln Ile Asp Leu Arg Tyr Glu Ala Gln
        355                 360                 365

Asn Leu Glu His Phe Gln Val Asn Phe Arg Asn Val Lys Ala Val Lys
    370                 375                 380

Phe Pro Thr Pro Leu Arg Pro Ser Tyr Gly Ser Trp Asp Val Leu Lys
385                 390                 395                 400

Leu Gly His Gln Phe Gln Met
                405
```

<210> 711
<211> 647
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 121; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK3; "

<220>
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<223> /note="Gene Name:
aarF
domain containing kinase 3; "

<220>
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<223> /note="Uniprot ID: Q8NI60; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355739"

<400> 711

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Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1               5                   10                  15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
            20                  25                  30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
        35                  40                  45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
    50                  55                  60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65                  70                  75                  80

Phe Ser Val Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala
                85                  90                  95

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
            100                 105                 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
        115                 120                 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
    130                 135                 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145                 150                 155                 160

Arg Phe Phe His Gln Asp Gln Ser Pro Val Gly Gly Leu Thr Ala Glu
                165                 170                 175
```

```
Asp Ile Glu Lys Ala Arg Gln Ala Lys Ala Arg Pro Glu Asn Lys Gln
            180                 185                 190

His Lys Gln Thr Leu Ser Glu His Ala Arg Glu Arg Lys Val Pro Val
        195                 200                 205

Thr Arg Ile Gly Arg Leu Ala Asn Phe Gly Gly Leu Ala Val Gly Leu
    210                 215                 220

Gly Phe Gly Ala Leu Ala Glu Val Ala Lys Lys Ser Leu Arg Ser Glu
225                 230                 235                 240

Asp Pro Ser Gly Lys Lys Ala Val Leu Gly Ser Ser Pro Phe Leu Ser
                245                 250                 255

Glu Ala Asn Ala Glu Arg Ile Val Arg Thr Leu Cys Lys Val Arg Gly
            260                 265                 270

Ala Ala Leu Lys Leu Gly Gln Met Leu Ser Ile Gln Asp Asp Ala Phe
        275                 280                 285

Ile Asn Pro His Leu Ala Lys Ile Phe Glu Arg Val Arg Gln Ser Ala
    290                 295                 300

Asp Phe Met Pro Leu Lys Gln Met Met Lys Thr Leu Asn Asn Asp Leu
305                 310                 315                 320

Gly Pro Asn Trp Arg Asp Lys Leu Glu Tyr Phe Glu Glu Arg Pro Phe
                325                 330                 335

Ala Ala Ala Ser Ile Gly Gln Val His Leu Ala Arg Met Lys Gly Gly
            340                 345                 350

Arg Glu Val Ala Met Lys Ile Gln Tyr Pro Gly Val Ala Gln Ser Ile
        355                 360                 365

Asn Ser Asp Val Asn Asn Leu Met Ala Val Leu Asn Met Ser Asn Met
    370                 375                 380

Leu Pro Glu Gly Leu Phe Pro Glu His Leu Ile Asp Val Leu Arg Arg
385                 390                 395                 400

Glu Leu Ala Leu Glu Cys Asp Tyr Gln Arg Glu Ala Ala Cys Ala Arg
```

405 410 415

Lys Phe Arg Asp Leu Leu Lys Gly His Pro Phe Phe Tyr Val Pro Glu
420 425 430

Ile Val Asp Glu Leu Cys Ser Pro His Val Leu Thr Thr Glu Leu Val
435 440 445

Ser Gly Phe Pro Leu Asp Gln Ala Glu Gly Leu Ser Gln Glu Ile Arg
450 455 460

Asn Glu Ile Cys Tyr Asn Ile Leu Val Leu Cys Leu Arg Glu Leu Phe
465 470 475 480

Glu Phe His Phe Met Gln Thr Asp Pro Asn Trp Ser Asn Phe Phe Tyr
485 490 495

Asp Pro Gln Gln His Lys Val Ala Leu Leu Asp Phe Gly Ala Thr Arg
500 505 510

Glu Tyr Asp Arg Ser Phe Thr Asp Leu Tyr Ile Gln Ile Ile Arg Ala
515 520 525

Ala Ala Asp Arg Asp Arg Glu Thr Val Arg Ala Lys Ser Ile Glu Met
530 535 540

Lys Phe Leu Thr Gly Tyr Glu Val Lys Val Met Glu Asp Ala His Leu
545 550 555 560

Asp Ala Ile Leu Ile Leu Gly Glu Ala Phe Ala Ser Asp Glu Pro Phe
565 570 575

Asp Phe Gly Thr Gln Ser Thr Thr Glu Lys Ile His Asn Leu Ile Pro
580 585 590

Val Met Leu Arg His Arg Leu Val Pro Pro Pro Glu Glu Thr Tyr Ser
595 600 605

Leu His Arg Lys Met Gly Gly Ser Phe Leu Ile Cys Ser Lys Leu Lys
610 615 620

Ala Arg Phe Pro Cys Lys Ala Met Phe Glu Glu Ala Tyr Ser Asn Tyr
625 630 635 640

```
Cys Lys Arg Gln Ala Gln Gln
                645


<210> 712
<211> 595
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 121; "

<220>
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<223> /note="Gene Symbol: ADCK3; "

<220>
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<223> /note="Gene Name:
      aarF
      domain containing kinase 3; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8NI60; "

<220>
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<223> /note="ENSP ID: ENSP00000355740"

<400> 712
Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe
1               5                  10                  15


Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro
            20                  25                  30


His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp
        35                  40                  45


Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser Glu Gly Pro Ala
    50                  55                  60


Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly
65                  70                  75                  80


Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn
                85                  90                  95
```

```
Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg Arg Phe Phe His
            100                 105                 110

Gln Asp Gln Ser Pro Val Gly Gly Leu Thr Ala Glu Asp Ile Glu Lys
        115                 120                 125

Ala Arg Gln Ala Lys Ala Arg Pro Glu Asn Lys Gln His Lys Gln Thr
    130                 135                 140

Leu Ser Glu His Ala Arg Glu Arg Lys Val Pro Val Thr Arg Ile Gly
145                 150                 155                 160

Arg Leu Ala Asn Phe Gly Gly Leu Ala Val Gly Leu Gly Phe Gly Ala
                165                 170                 175

Leu Ala Glu Val Ala Lys Lys Ser Leu Arg Ser Glu Asp Pro Ser Gly
            180                 185                 190

Lys Lys Ala Val Leu Gly Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala
        195                 200                 205

Glu Arg Ile Val Arg Thr Leu Cys Lys Val Arg Gly Ala Ala Leu Lys
    210                 215                 220

Leu Gly Gln Met Leu Ser Ile Gln Asp Asp Ala Phe Ile Asn Pro His
225                 230                 235                 240

Leu Ala Lys Ile Phe Glu Arg Val Arg Gln Ser Ala Asp Phe Met Pro
                245                 250                 255

Leu Lys Gln Met Met Lys Thr Leu Asn Asn Asp Leu Gly Pro Asn Trp
            260                 265                 270

Arg Asp Lys Leu Glu Tyr Phe Glu Glu Arg Pro Phe Ala Ala Ala Ser
        275                 280                 285

Ile Gly Gln Val His Leu Ala Arg Met Lys Gly Gly Arg Glu Val Ala
    290                 295                 300

Met Lys Ile Gln Tyr Pro Gly Val Ala Gln Ser Ile Asn Ser Asp Val
305                 310                 315                 320
```

```
Asn Asn Leu Met Ala Val Leu Asn Met Ser Asn Met Leu Pro Glu Gly
                325                 330                 335

Leu Phe Pro Glu His Leu Ile Asp Val Leu Arg Arg Glu Leu Ala Leu
            340                 345                 350

Glu Cys Asp Tyr Gln Arg Glu Ala Ala Cys Ala Arg Lys Phe Arg Asp
        355                 360                 365

Leu Leu Lys Gly His Pro Phe Phe Tyr Val Pro Glu Ile Val Asp Glu
    370                 375                 380

Leu Cys Ser Pro His Val Leu Thr Thr Glu Leu Val Ser Gly Phe Pro
385                 390                 395                 400

Leu Asp Gln Ala Glu Gly Leu Ser Gln Glu Ile Arg Asn Glu Ile Cys
                405                 410                 415

Tyr Asn Ile Leu Val Leu Cys Leu Arg Glu Leu Phe Glu Phe His Phe
            420                 425                 430

Met Gln Thr Asp Pro Asn Trp Ser Asn Phe Phe Tyr Asp Pro Gln Gln
        435                 440                 445

His Lys Val Ala Leu Leu Asp Phe Gly Ala Thr Arg Glu Tyr Asp Arg
    450                 455                 460

Ser Phe Thr Asp Leu Tyr Ile Gln Ile Ile Arg Ala Ala Ala Asp Arg
465                 470                 475                 480

Asp Arg Glu Thr Val Arg Ala Lys Ser Ile Glu Met Lys Phe Leu Thr
                485                 490                 495

Gly Tyr Glu Val Lys Val Met Glu Asp Ala His Leu Asp Ala Ile Leu
            500                 505                 510

Ile Leu Gly Glu Ala Phe Ala Ser Asp Glu Pro Phe Asp Phe Gly Thr
        515                 520                 525

Gln Ser Thr Thr Glu Lys Ile His Asn Leu Ile Pro Val Met Leu Arg
    530                 535                 540

His Arg Leu Val Pro Pro Pro Glu Glu Thr Tyr Ser Leu His Arg Lys
```

545 550 555 560

Met Gly Gly Ser Phe Leu Ile Cys Ser Lys Leu Lys Ala Arg Phe Pro
565 570 575

Cys Lys Ala Met Phe Glu Glu Ala Tyr Ser Asn Tyr Cys Lys Arg Gln
580 585 590

Ala Gln Gln
595

<210> 713
<211> 647
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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aarF
domain containing kinase 3; "

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<223> /note="Uniprot ID: Q8NI60; "

<220>
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<223> /note="ENSP ID: ENSP00000355741"

<400> 713
Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1 5 10 15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
20 25 30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
35 40 45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
50 55 60

```
Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65                  70                  75                  80

Phe Ser Val Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala
                85                  90                  95

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
            100                 105                 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
        115                 120                 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
    130                 135                 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145                 150                 155                 160

Arg Phe Phe His Gln Asp Gln Ser Pro Val Gly Gly Leu Thr Ala Glu
                165                 170                 175

Asp Ile Glu Lys Ala Arg Gln Ala Lys Ala Arg Pro Glu Asn Lys Gln
            180                 185                 190

His Lys Gln Thr Leu Ser Glu His Ala Arg Glu Arg Lys Val Pro Val
        195                 200                 205

Thr Arg Ile Gly Arg Leu Ala Asn Phe Gly Gly Leu Ala Val Gly Leu
    210                 215                 220

Gly Phe Gly Ala Leu Ala Glu Val Ala Lys Lys Ser Leu Arg Ser Glu
225                 230                 235                 240

Asp Pro Ser Gly Lys Lys Ala Val Leu Gly Ser Ser Pro Phe Leu Ser
                245                 250                 255

Glu Ala Asn Ala Glu Arg Ile Val Arg Thr Leu Cys Lys Val Arg Gly
            260                 265                 270

Ala Ala Leu Lys Leu Gly Gln Met Leu Ser Ile Gln Asp Asp Ala Phe
        275                 280                 285
```

```
Ile Asn Pro His Leu Ala Lys Ile Phe Glu Arg Val Arg Gln Ser Ala
    290                 295                 300

Asp Phe Met Pro Leu Lys Gln Met Met Lys Thr Leu Asn Asn Asp Leu
305                 310                 315                 320

Gly Pro Asn Trp Arg Asp Lys Leu Glu Tyr Phe Glu Glu Arg Pro Phe
                325                 330                 335

Ala Ala Ala Ser Ile Gly Gln Val His Leu Ala Arg Met Lys Gly Gly
            340                 345                 350

Arg Glu Val Ala Met Lys Ile Gln Tyr Pro Gly Val Ala Gln Ser Ile
        355                 360                 365

Asn Ser Asp Val Asn Asn Leu Met Ala Val Leu Asn Met Ser Asn Met
    370                 375                 380

Leu Pro Glu Gly Leu Phe Pro Glu His Leu Ile Asp Val Leu Arg Arg
385                 390                 395                 400

Glu Leu Ala Leu Glu Cys Asp Tyr Gln Arg Glu Ala Ala Cys Ala Arg
                405                 410                 415

Lys Phe Arg Asp Leu Leu Lys Gly His Pro Phe Phe Tyr Val Pro Glu
            420                 425                 430

Ile Val Asp Glu Leu Cys Ser Pro His Val Leu Thr Thr Glu Leu Val
        435                 440                 445

Ser Gly Phe Pro Leu Asp Gln Ala Glu Gly Leu Ser Gln Glu Ile Arg
    450                 455                 460

Asn Glu Ile Cys Tyr Asn Ile Leu Val Leu Cys Leu Arg Glu Leu Phe
465                 470                 475                 480

Glu Phe His Phe Met Gln Thr Asp Pro Asn Trp Ser Asn Phe Phe Tyr
                485                 490                 495

Asp Pro Gln Gln His Lys Val Ala Leu Leu Asp Phe Gly Ala Thr Arg
            500                 505                 510
```

```
Glu Tyr Asp Arg Ser Phe Thr Asp Leu Tyr Ile Gln Ile Ile Arg Ala
        515                 520                 525

Ala Ala Asp Arg Asp Arg Glu Thr Val Arg Ala Lys Ser Ile Glu Met
    530                 535                 540

Lys Phe Leu Thr Gly Tyr Glu Val Lys Val Met Glu Asp Ala His Leu
545                 550                 555                 560

Asp Ala Ile Leu Ile Leu Gly Glu Ala Phe Ala Ser Asp Glu Pro Phe
                565                 570                 575

Asp Phe Gly Thr Gln Ser Thr Thr Glu Lys Ile His Asn Leu Ile Pro
            580                 585                 590

Val Met Leu Arg His Arg Leu Val Pro Pro Pro Glu Glu Thr Tyr Ser
        595                 600                 605

Leu His Arg Lys Met Gly Gly Ser Phe Leu Ile Cys Ser Lys Leu Lys
    610                 615                 620

Ala Arg Phe Pro Cys Lys Ala Met Phe Glu Glu Ala Tyr Ser Asn Tyr
625                 630                 635                 640

Cys Lys Arg Gln Ala Gln Gln
                645


<210> 714
<211> 503
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 122; "

<220>
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<223> /note="Gene Symbol: ADCK4; "

<220>
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<223> /note="Gene Name:
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      domain containing kinase 4; "

<220>
<221> source
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<223> /note="Uniprot ID: Q96D53; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000243583"

<400> 714
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Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                  10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met Ala Lys
            100                 105                 110

Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Asp Asn Ser Phe Ile Ser
        115                 120                 125

Pro Gln Leu Gln His Ile Phe Glu Arg Val Arg Gln Ser Ala Asp Phe
    130                 135                 140

Met Pro Arg Trp Gln Met Leu Arg Val Leu Glu Glu Glu Leu Gly Arg
145                 150                 155                 160

Asp Trp Gln Ala Lys Val Ala Ser Leu Glu Glu Val Pro Phe Ala Ala
                165                 170                 175

Ala Ser Ile Gly Gln Val His Gln Gly Leu Leu Arg Asp Gly Thr Glu
            180                 185                 190

Val Ala Val Lys Ile Gln Tyr Pro Gly Ile Ala Gln Ser Ile Gln Ser
        195                 200                 205
```

```
Asp Val Gln Asn Leu Leu Ala Val Leu Lys Met Ser Ala Ala Leu Pro
    210                 215                 220

Ala Gly Leu Phe Ala Glu Gln Ser Leu Gln Ala Leu Gln Gln Glu Leu
225                 230                 235                 240

Ala Trp Glu Cys Asp Tyr Arg Arg Glu Ala Ala Cys Ala Gln Asn Phe
                245                 250                 255

Arg Gln Leu Leu Ala Asn Asp Pro Phe Phe Arg Val Pro Ala Val Val
            260                 265                 270

Lys Glu Leu Cys Thr Thr Arg Val Leu Gly Met Glu Leu Ala Gly Gly
        275                 280                 285

Val Pro Leu Asp Gln Cys Gln Gly Leu Ser Gln Asp Leu Arg Asn Gln
    290                 295                 300

Ile Cys Phe Gln Leu Leu Thr Leu Cys Leu Arg Glu Leu Phe Glu Phe
305                 310                 315                 320

Arg Phe Met Gln Thr Asp Pro Asn Trp Ala Asn Phe Leu Tyr Asp Ala
                325                 330                 335

Ser Ser His Gln Val Thr Leu Leu Asp Phe Gly Ala Ser Arg Glu Phe
            340                 345                 350

Gly Thr Glu Phe Thr Asp His Tyr Ile Glu Val Val Lys Ala Ala Ala
        355                 360                 365

Asp Gly Asp Arg Asp Cys Val Leu Gln Lys Ser Arg Asp Leu Lys Phe
    370                 375                 380

Leu Thr Gly Phe Glu Thr Lys Ala Phe Ser Asp Ala His Val Glu Ala
385                 390                 395                 400

Val Met Ile Leu Gly Glu Pro Phe Ala Thr Gln Gly Pro Tyr Asp Phe
                405                 410                 415

Gly Ser Gly Glu Thr Ala Arg Arg Ile Gln Asp Leu Ile Pro Val Leu
            420                 425                 430
```

```
Leu Arg His Arg Leu Cys Pro Pro Pro Glu Glu Thr Tyr Ala Leu His
        435                 440                 445

Arg Lys Leu Ala Gly Ala Phe Leu Ala Cys Ala His Leu Arg Ala His
    450                 455                 460

Ile Ala Cys Arg Asp Leu Phe Gln Asp Thr Tyr His Arg Tyr Trp Ala
465                 470                 475                 480

Ser Arg Gln Pro Asp Ala Ala Thr Ala Gly Ser Leu Pro Thr Lys Gly
                485                 490                 495

Asp Ser Trp Val Asp Pro Ser
            500


<210> 715
<211> 544
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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      domain containing kinase 4; "

<220>
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<223> /note="Uniprot ID:  Q96D53; "

<220>
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<223> /note="ENSP ID: ENSP00000315118"

<400> 715
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                   10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30
```

```
Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met Ala Lys
            100                 105                 110

Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Glu Gly Gly Ser Gly Leu
        115                 120                 125

Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg Ile Val Gln
    130                 135                 140

Thr Leu Cys Thr Val Arg Gly Ala Ala Leu Lys Val Gly Gln Met Leu
145                 150                 155                 160

Ser Ile Gln Asp Asn Ser Phe Ile Ser Pro Gln Leu Gln His Ile Phe
                165                 170                 175

Glu Arg Val Arg Gln Ser Ala Asp Phe Met Pro Arg Trp Gln Met Leu
            180                 185                 190

Arg Val Leu Glu Glu Glu Leu Gly Arg Asp Trp Gln Ala Lys Val Ala
        195                 200                 205

Ser Leu Glu Glu Val Pro Phe Ala Ala Ala Ser Ile Gly Gln Val His
    210                 215                 220

Gln Gly Leu Leu Arg Asp Gly Thr Glu Val Ala Val Lys Ile Gln Tyr
225                 230                 235                 240

Pro Gly Ile Ala Gln Ser Ile Gln Ser Asp Val Gln Asn Leu Leu Ala
                245                 250                 255

Val Leu Lys Met Ser Ala Ala Leu Pro Ala Gly Leu Phe Ala Glu Gln
```

```
            260                 265                 270

Ser Leu Gln Ala Leu Gln Gln Glu Leu Ala Trp Glu Cys Asp Tyr Arg
        275                 280                 285

Arg Glu Ala Ala Cys Ala Gln Asn Phe Arg Gln Leu Leu Ala Asn Asp
    290                 295                 300

Pro Phe Phe Arg Val Pro Ala Val Val Lys Glu Leu Cys Thr Thr Arg
305                 310                 315                 320

Val Leu Gly Met Glu Leu Ala Gly Gly Val Pro Leu Asp Gln Cys Gln
                325                 330                 335

Gly Leu Ser Gln Asp Leu Arg Asn Gln Ile Cys Phe Gln Leu Leu Thr
            340                 345                 350

Leu Cys Leu Arg Glu Leu Phe Glu Phe Arg Phe Met Gln Thr Asp Pro
        355                 360                 365

Asn Trp Ala Asn Phe Leu Tyr Asp Ala Ser Ser His Gln Val Thr Leu
    370                 375                 380

Leu Asp Phe Gly Ala Ser Arg Glu Phe Gly Thr Glu Phe Thr Asp His
385                 390                 395                 400

Tyr Ile Glu Val Val Lys Ala Ala Ala Asp Gly Asp Arg Asp Cys Val
                405                 410                 415

Leu Gln Lys Ser Arg Asp Leu Lys Phe Leu Thr Gly Phe Glu Thr Lys
            420                 425                 430

Ala Phe Ser Asp Ala His Val Glu Ala Val Met Ile Leu Gly Glu Pro
        435                 440                 445

Phe Ala Thr Gln Gly Pro Tyr Asp Phe Gly Ser Gly Glu Thr Ala Arg
    450                 455                 460

Arg Ile Gln Asp Leu Ile Pro Val Leu Leu Arg His Arg Leu Cys Pro
465                 470                 475                 480

Pro Pro Glu Glu Thr Tyr Ala Leu His Arg Lys Leu Ala Gly Ala Phe
                485                 490                 495
```

```
Leu Ala Cys Ala His Leu Arg Ala His Ile Ala Cys Arg Asp Leu Phe
            500                 505                 510

Gln Asp Thr Tyr His Arg Tyr Trp Ala Ser Arg Gln Pro Asp Ala Ala
        515                 520                 525

Thr Ala Gly Ser Leu Pro Thr Lys Gly Asp Ser Trp Val Asp Pro Ser
    530                 535                 540
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<210> 716
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 122; "

<220>
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<223> /note="Gene Symbol: ADCK4; "

<220>
<221> source
<223> /note="Gene Name:
aarF
domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470876"

<400> 716

```
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                  10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80
```

```
Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met Ala Lys
            100                 105                 110

Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Glu Gly Gly Ser Gly Leu
        115                 120                 125

Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg Ile Val Gln
    130                 135                 140

Thr Leu Cys Thr Val
145
```

<210> 717
<211> 204
<212> PRT
<213> Homo sapiens

<220>
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<220>
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aarF
domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470894"

<400> 717

```
Met Ala Lys Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Glu Gly Gly
1               5                   10                  15

Ser Gly Leu Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg
            20                  25                  30

Ile Val Gln Thr Leu Cys Thr Val Arg Gly Ala Ala Leu Lys Val Gly
        35                  40                  45
```

```
Gln Met Leu Ser Ile Gln Asp Asn Ser Phe Ile Ser Pro Gln Leu Gln
    50                  55                  60

His Ile Phe Glu Arg Val Arg Gln Ser Ala Asp Phe Met Pro Arg Trp
65                  70                  75                  80

Gln Met Leu Arg Val Leu Glu Glu Glu Leu Gly Arg Asp Trp Gln Ala
                85                  90                  95

Lys Val Ala Ser Leu Glu Glu Val Pro Phe Ala Ala Ala Ser Ile Gly
            100                 105                 110

Gln Val His Gln Gly Leu Leu Arg Asp Gly Thr Glu Val Ala Val Lys
        115                 120                 125

Ile Gln Tyr Pro Gly Ile Ala Gln Ser Ile Gln Ser Asp Val Gln Asn
    130                 135                 140

Leu Leu Ala Val Leu Lys Met Ser Ala Ala Leu Pro Ala Gly Leu Phe
145                 150                 155                 160

Ala Glu Gln Ser Leu Gln Ala Leu Gln Gln Glu Leu Ala Trp Glu Cys
                165                 170                 175

Asp Tyr Arg Arg Glu Ala Ala Cys Ala Gln Asn Phe Arg Gln Leu Leu
            180                 185                 190

Ala Asn Asp Pro Phe Phe Arg Val Pro Ala Val Val
        195                 200
```

<210> 718
<211> 230
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 122; "

<220>
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<223> /note="Gene Symbol: ADCK4; "

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<221> source
<223> /note="Gene Name:
aarF

domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470916"

<400> 718

```
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                  10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met Ala Lys
            100                 105                 110

Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Glu Gly Gly Ser Gly Leu
        115                 120                 125

Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg Ile Val Gln
    130                 135                 140

Thr Leu Cys Thr Val Arg Gly Ala Ala Leu Lys Val Gly Gln Met Leu
145                 150                 155                 160

Ser Ile Gln Asp Asn Ser Phe Ile Ser Pro Gln Leu Gln His Ile Phe
                165                 170                 175

Glu Arg Val Arg Gln Ser Ala Asp Phe Met Pro Arg Trp Gln Met Leu
            180                 185                 190

Arg Val Leu Glu Glu Glu Leu Gly Arg Asp Trp Gln Ala Lys Val Ala
        195                 200                 205
```

```
Ser Leu Glu Glu Val Pro Phe Ala Ala Ala Ser Ile Gly Gln Val His
    210                 215                 220


Gln Gly Leu Leu Arg Asp
225                 230


<210> 719
<211> 115
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      domain containing kinase 4; "

<220>
<221> source
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<400> 719
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                   10                  15


Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30


Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45


Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60


Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80


Glu Arg Lys Thr Thr Ala Ser Ser Ala Leu Ser Cys Ser Thr Ser Leu
                85                  90                  95
```

Ser Gly Ser Ala Arg Ala Pro Thr Ser Cys Pro Ala Gly Arg Cys Cys
100 105 110

Thr Pro Ala
115

<210> 720
<211> 134
<212> PRT
<213> Homo sapiens

<220>
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<220>
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aarF
domain containing kinase 4; "

<220>
<221> source
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<400> 720
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1 5 10 15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
20 25 30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
35 40 45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
50 55 60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65 70 75 80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
85 90 95

```
Glu Gly Gly Ser Gly Leu Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn
            100                 105                 110

Ala Glu Arg Ile Val Gln Thr Leu Cys Thr Val Arg Gly Ala Ala Leu
        115                 120                 125

Lys Val Gly Gln Met Leu
    130


<210> 721
<211> 81
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      aarF
      domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472519"

<400> 721
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                   10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Thr Leu Ser Pro Phe Pro
65                  70                  75                  80

Ser
```

<210> 722
<211> 10
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
aarF
domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472775"

<400> 722
Met Trp Leu Lys Val Gly Gly Leu Leu Arg
1 5 10

<210> 723
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 122; "

<220>
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<223> /note="Gene Symbol: ADCK4; "

<220>
<221> source
<223> /note="Gene Name:
aarF
domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472925"

<400> 723
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1 5 10 15

```
Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met
            100                 105                 110


<210> 724
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 122; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK4; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472978"

<400> 724
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                   10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30
```

```
Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met Ala Lys
            100                 105                 110

Lys Ser Met Pro Gly Gly Arg Leu Gln
        115                 120


<210> 725
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 122; "

<220>
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<223> /note="Gene Symbol: ADCK4; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000473017"

<400> 725
Met Ala Lys Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Glu Gly Gly
1               5                   10                  15

Ser Gly Leu Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg
            20                  25                  30
```

```
Ile Val Gln Thr Leu Cys Thr Val Arg Gly Ala Ala Leu Lys Val Gly
        35                  40                  45

Gln Met Leu Ser Ile Gln Ala Ser Ser Ala Leu Ser Cys Ser Thr Ser
    50                  55                  60

Leu Ser Gly Ser Ala Arg Ala Pro Thr
65                  70


<210> 726
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 122; "

<220>
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<223> /note="Gene Symbol: ADCK4; "

<220>
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<223> /note="Gene Name:
      aarF
      domain containing kinase 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000473189"

<400> 726
Met Trp Leu Lys Val Gly Gly Leu Leu Arg Gly Thr Gly Gly Gln Leu
1               5                   10                  15

Gly Gln Thr Val Gly Trp Pro Cys Gly Ala Leu Gly Pro Gly Pro His
            20                  25                  30

Arg Trp Gly Pro Cys Gly Gly Ser Trp Ala Gln Lys Phe Tyr Gln Asp
        35                  40                  45

Gly Pro Gly Arg Gly Leu Gly Glu Glu Asp Ile Arg Arg Ala Arg Glu
    50                  55                  60

Ala Arg Pro Arg Lys Thr Pro Arg Pro Gln Leu Ser Asp Arg Ser Arg
65                  70                  75                  80

Glu Arg Lys Val Pro Ala Ser Arg Ile Ser Arg Leu Ala Asn Phe Gly
```

```
                85                  90                  95

Gly Leu Ala Val Gly Leu Gly Leu Gly Val Leu Ala Glu Met Ala Lys
            100                 105                 110

Lys Ser Met Pro Gly Gly Arg Leu Gln Ser Glu Gly Gly Ser Gly Leu
        115                 120                 125

Asp Ser Ser Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg Ile Val Gln
    130                 135                 140

Thr Leu Cys Thr Val Arg Gly Ala Ala Leu Lys Val Gly
145                 150                 155


<210> 727
<211> 580
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 123; "

<220>
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<223> /note="Gene Symbol: ADCK5; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q3MIX3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000310547"

<400> 727
Met Trp Arg Pro Val Gln Leu Cys His Phe His Ser Ala Leu Leu His
1               5                   10                  15

Ser Arg Gln Lys Pro Trp Pro Ser Pro Ala Val Phe Phe Arg Arg Asn
            20                  25                  30

Val Arg Gly Leu Pro Pro Arg Phe Ser Ser Pro Thr Pro Leu Trp Arg
        35                  40                  45
```

```
Lys Val Leu Ser Thr Ala Val Val Gly Ala Pro Leu Leu Leu Gly Ala
    50                  55                  60

Arg Tyr Val Met Ala Glu Ala Arg Glu Lys Arg Arg Met Arg Leu Val
65                  70                  75                  80

Val Asp Gly Met Gly Arg Phe Gly Arg Ser Leu Lys Val Gly Leu Gln
                85                  90                  95

Ile Ser Leu Asp Tyr Trp Trp Cys Thr Asn Val Val Leu Arg Gly Val
            100                 105                 110

Glu Glu Asn Ser Pro Gly Tyr Leu Glu Val Met Ser Ala Cys His Gln
        115                 120                 125

Arg Ala Ala Asp Ala Leu Val Ala Gly Ala Ile Ser Asn Gly Gly Leu
    130                 135                 140

Tyr Val Lys Leu Gly Gln Gly Leu Cys Ser Phe Asn His Leu Leu Pro
145                 150                 155                 160

Pro Glu Tyr Thr Arg Thr Leu Arg Val Leu Glu Asp Arg Ala Leu Lys
                165                 170                 175

Arg Gly Phe Gln Glu Val Asp Glu Leu Phe Leu Glu Asp Phe Gln Ala
            180                 185                 190

Leu Pro His Glu Leu Phe Gln Glu Phe Asp Tyr Gln Pro Ile Ala Ala
        195                 200                 205

Ala Ser Leu Ala Gln Val His Arg Ala Lys Leu His Asp Gly Thr Ser
    210                 215                 220

Val Ala Val Lys Val Gln Tyr Ile Asp Leu Arg Asp Arg Phe Asp Gly
225                 230                 235                 240

Asp Ile His Thr Leu Glu Leu Leu Leu Arg Leu Val Glu Val Met His
                245                 250                 255

Pro Ser Phe Gly Phe Ser Trp Val Leu Gln Asp Leu Lys Gly Thr Leu
            260                 265                 270
```

```
Ala Gln Glu Leu Asp Phe Glu Asn Glu Gly Arg Asn Ala Glu Arg Cys
        275                 280                 285

Ala Arg Glu Leu Ala His Phe Pro Tyr Val Val Val Pro Arg Val His
    290                 295                 300

Trp Asp Lys Ser Ser Lys Arg Val Leu Thr Ala Asp Phe Cys Ala Gly
305                 310                 315                 320

Cys Lys Val Asn Asp Val Glu Ala Ile Arg Ser Gln Gly Leu Ala Val
                325                 330                 335

His Asp Ile Ala Glu Lys Leu Ile Lys Ala Phe Ala Glu Gln Ile Phe
            340                 345                 350

Tyr Thr Gly Phe Ile His Ser Asp Pro His Pro Gly Asn Val Leu Val
        355                 360                 365

Arg Lys Gly Pro Asp Gly Lys Ala Glu Leu Val Leu Leu Asp His Gly
    370                 375                 380

Leu Tyr Gln Phe Leu Glu Glu Lys Asp Arg Ala Ala Leu Cys Gln Leu
385                 390                 395                 400

Trp Arg Ala Ile Ile Leu Arg Asp Asp Ala Ala Met Arg Ala His Ala
                405                 410                 415

Ala Ala Leu Gly Val Gln Asp Tyr Leu Leu Phe Ala Glu Met Leu Met
            420                 425                 430

Gln Arg Pro Val Arg Leu Gly Gln Leu Trp Gly Ser His Leu Leu Ser
        435                 440                 445

Arg Glu Glu Ala Ala Tyr Met Val Asp Met Ala Arg Glu Arg Phe Glu
    450                 455                 460

Ala Val Met Ala Val Leu Arg Glu Leu Pro Arg Pro Met Leu Leu Val
465                 470                 475                 480

Leu Arg Asn Ile Asn Thr Val Arg Ala Ile Asn Val Ala Leu Gly Ala
                485                 490                 495
```

```
Pro Val Asp Arg Tyr Phe Leu Met Ala Lys Arg Ala Val Arg Gly Trp
            500                 505                 510

Ser Arg Leu Ala Gly Ala Thr Tyr Arg Gly Val Tyr Gly Thr Ser Leu
        515                 520                 525

Leu Arg His Ala Lys Val Val Trp Glu Met Leu Lys Phe Glu Val Ala
    530                 535                 540

Leu Arg Leu Glu Thr Leu Ala Met Arg Leu Thr Ala Leu Leu Ala Arg
545                 550                 555                 560

Ala Leu Val His Leu Ser Leu Val Pro Pro Ala Glu Glu Leu Tyr Gln
                565                 570                 575

Tyr Leu Glu Thr
            580
```

<210> 728
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 123; "

<220>
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<223> /note="Gene Symbol: ADCK5; "

<220>
<221> source
<223> /note="Gene Name:
aarF
domain containing kinase 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431875"

<400> 728

```
Met Trp Arg Pro Val Gln Leu Cys His Phe His Ser Ala Leu Leu His
1               5                   10                  15

Ser Arg Gln Lys Pro Trp Pro Ser Pro Ala Val Phe Phe Arg Arg Asn
            20                  25                  30

Val Arg Gly Leu Pro Pro Arg Phe Ser Ser Pro Thr Pro Leu Trp Arg
```

```
        35                  40                  45

Lys Val Leu Ser Thr Ala Val Val Gly Ala Pro Leu Leu Leu Gly Ala
    50                  55                  60

Arg Tyr Val Met Ala Glu Ala Arg Glu Lys Arg Arg Met Arg Leu Val
65                  70                  75                  80

Val Asp Gly Met Gly Arg Phe Gly Arg Ser Leu Lys Val Gly Leu Gln
                85                  90                  95

Ile Ser Leu Asp Tyr Trp Trp Cys Thr Asn Val Val Leu Arg Gly Val
            100                 105                 110

Glu Glu Pro Arg Leu Leu Gly Gly Asp Val Cys Val Ser Pro Ala Gly
        115                 120                 125

Gly
```

<210> 729
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 123; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK5; "

<220>
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<223> /note="Gene Name:
aarF
domain containing kinase 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436484"

<400> 729

```
Met Trp Arg Pro Val Gln Leu Cys His Phe His Ser Ala Leu Leu His
1               5                   10                  15

Ser Arg Gln Lys Pro Trp Pro Ser Pro Ala Val Phe Phe Arg Arg Asn
            20                  25                  30
```

```
Val Arg Gly Leu Pro Pro Arg Phe Ser Ser Pro Thr Pro Leu Trp Arg
        35                  40                  45

Lys Val Leu Ser Thr Ala Val Val Gly Ala Pro Leu Leu Leu Gly Ala
    50                  55                  60

Arg Tyr Val Met Ala Glu Ala Arg Glu Lys Arg Arg Met Arg Leu Val
65                  70                  75                  80

Val Asp Gly Met Gly Arg Phe Gly Arg Pro Cys Leu Pro Arg Pro Trp
                85                  90                  95

Arg Pro Thr Leu Leu Val Ser Ser Ser Leu Pro Ser Gly Pro Gln Ala
            100                 105                 110

Ala Gly Leu
        115


<210> 730
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 123; "

<220>
<221> source
<223> /note="Gene Symbol: ADCK5; "

<220>
<221> source
<223> /note="Gene Name:
      aarF
      domain containing kinase 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000473494"

<400> 730
Met Trp Arg Pro Ala Gly Val Gln Cys Leu Asn Leu Gly Ser Leu Gln
1               5                   10                  15

Ser Pro Pro Thr Lys Ile Lys Arg Phe Ser Cys Leu Ser Leu Pro Thr
            20                  25                  30
```

```
Thr Trp Asp Tyr Arg Cys Ser Ser Val Ile Ser Thr Leu Leu Cys Cys
        35                  40                  45

Thr Ala Gly Arg Ser Pro Gly Arg Pro Leu Leu Cys Ser Ser Gly Glu
    50                  55                  60

Thr Ser Gly Ala Phe Leu Gln Gly Ser Pro Ala Pro His Pro Cys Gly
65                  70                  75                  80

Gly Arg Cys Ser Pro Pro Arg
                85
```

<210> 731
<211> 1196
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
Abelson helper integration site 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N157; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000265602"

<400> 731

```
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                   10                  15

Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30

Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Pro Asp Thr
        35                  40                  45

Ile Arg Ser Asn Leu His Tyr Met Lys Glu Thr Thr Ser Asp Asp Pro
```

```
    50                  55                  60

Asp Thr Ile Arg Ser Asn Leu Pro His Ile Lys Glu Thr Thr Ser Asp
65                  70                  75                  80

Asp Val Ser Ala Ala Asn Thr Asn Asn Leu Lys Lys Ser Thr Arg Val
                85                  90                  95

Thr Lys Asn Lys Leu Arg Asn Thr Gln Leu Ala Thr Glu Asn Pro Asn
            100                 105                 110

Gly Asp Ala Ser Val Glu Glu Asp Lys Gln Gly Lys Pro Asn Lys Lys
        115                 120                 125

Val Ile Lys Thr Val Pro Gln Leu Thr Thr Gln Asp Leu Lys Pro Glu
    130                 135                 140

Thr Pro Glu Asn Lys Val Asp Ser Thr His Gln Lys Thr His Thr Lys
145                 150                 155                 160

Pro Gln Pro Gly Val Asp His Gln Lys Ser Glu Lys Ala Asn Glu Gly
                165                 170                 175

Arg Glu Glu Thr Asp Leu Glu Glu Asp Glu Glu Leu Met Gln Ala Tyr
            180                 185                 190

Gln Cys His Val Thr Glu Glu Met Ala Lys Glu Ile Lys Arg Lys Ile
        195                 200                 205

Arg Lys Lys Leu Lys Glu Gln Leu Thr Tyr Phe Pro Ser Asp Thr Leu
    210                 215                 220

Phe His Asp Asp Lys Leu Ser Ser Glu Lys Arg Lys Lys Lys Lys Glu
225                 230                 235                 240

Val Pro Val Phe Ser Lys Ala Glu Thr Ser Thr Leu Thr Ile Ser Gly
                245                 250                 255

Asp Thr Val Glu Gly Glu Gln Lys Lys Glu Ser Ser Val Arg Ser Val
            260                 265                 270

Ser Ser Asp Ser His Gln Asp Asp Glu Ile Ser Ser Met Glu Gln Ser
        275                 280                 285
```

```
Thr Glu Asp Ser Met Gln Asp Asp Thr Lys Pro Lys Pro Lys Lys Thr
    290                 295                 300

Lys Lys Lys Thr Lys Ala Val Ala Asp Asn Asn Glu Asp Val Asp Gly
305                 310                 315                 320

Asp Gly Val His Glu Ile Thr Ser Arg Asp Ser Pro Val Tyr Pro Lys
                325                 330                 335

Cys Leu Leu Asp Asp Asp Leu Val Leu Gly Val Tyr Ile His Arg Thr
            340                 345                 350

Asp Arg Leu Lys Ser Asp Phe Met Ile Ser His Pro Met Val Lys Ile
        355                 360                 365

His Val Val Asp Glu His Thr Gly Gln Tyr Val Lys Lys Asp Asp Ser
    370                 375                 380

Gly Arg Pro Val Ser Ser Tyr Tyr Glu Lys Glu Asn Val Asp Tyr Ile
385                 390                 395                 400

Leu Pro Ile Met Thr Gln Pro Tyr Asp Phe Lys Gln Leu Lys Ser Arg
                405                 410                 415

Leu Pro Glu Trp Glu Glu Gln Ile Val Phe Asn Glu Asn Phe Pro Tyr
            420                 425                 430

Leu Leu Arg Gly Ser Asp Glu Ser Pro Lys Val Ile Leu Phe Phe Glu
        435                 440                 445

Ile Leu Asp Phe Leu Ser Val Asp Glu Ile Lys Asn Asn Ser Glu Val
    450                 455                 460

Gln Asn Gln Glu Cys Gly Phe Arg Lys Ile Ala Trp Ala Phe Leu Lys
465                 470                 475                 480

Leu Leu Gly Ala Asn Gly Asn Ala Asn Ile Asn Ser Lys Leu Arg Leu
                485                 490                 495

Gln Leu Tyr Tyr Pro Pro Thr Lys Pro Arg Ser Pro Leu Ser Val Val
            500                 505                 510
```

```
Glu Ala Phe Glu Trp Trp Ser Lys Cys Pro Arg Asn His Tyr Pro Ser
        515                 520                 525

Thr Leu Tyr Val Thr Val Arg Gly Leu Lys Val Pro Asp Cys Ile Lys
    530                 535                 540

Pro Ser Tyr Arg Ser Met Met Ala Leu Gln Glu Glu Lys Gly Lys Pro
545                 550                 555                 560

Val His Cys Glu Arg His His Glu Ser Ser Ser Val Asp Thr Glu Pro
                565                 570                 575

Gly Leu Glu Glu Ser Lys Glu Val Ile Lys Trp Lys Arg Leu Pro Gly
            580                 585                 590

Gln Ala Cys Arg Ile Pro Asn Lys His Leu Phe Ser Leu Asn Ala Gly
        595                 600                 605

Glu Arg Gly Cys Phe Cys Leu Asp Phe Ser His Asn Gly Arg Ile Leu
    610                 615                 620

Ala Ala Ala Cys Ala Ser Arg Asp Gly Tyr Pro Ile Ile Leu Tyr Glu
625                 630                 635                 640

Ile Pro Ser Gly Arg Phe Met Arg Glu Leu Cys Gly His Leu Asn Ile
                645                 650                 655

Ile Tyr Asp Leu Ser Trp Ser Lys Asp Asp His Tyr Ile Leu Thr Ser
            660                 665                 670

Ser Ser Asp Gly Thr Ala Arg Ile Trp Lys Asn Glu Ile Asn Asn Thr
        675                 680                 685

Asn Thr Phe Arg Val Leu Pro His Pro Ser Phe Val Tyr Thr Ala Lys
    690                 695                 700

Phe His Pro Ala Val Arg Glu Leu Val Val Thr Gly Cys Tyr Asp Ser
705                 710                 715                 720

Met Ile Arg Ile Trp Lys Val Glu Met Arg Glu Asp Ser Ala Ile Leu
                725                 730                 735
```

```
Val Arg Gln Phe Asp Val His Lys Ser Phe Ile Asn Ser Leu Cys Phe
            740                 745                 750

Asp Thr Glu Gly His His Met Tyr Ser Gly Asp Cys Thr Gly Val Ile
        755                 760                 765

Val Val Trp Asn Thr Tyr Val Lys Ile Asn Asp Leu Glu His Ser Val
    770                 775                 780

His His Trp Thr Ile Asn Lys Glu Ile Lys Glu Thr Glu Phe Lys Gly
785                 790                 795                 800

Ile Pro Ile Ser Tyr Leu Glu Ile His Pro Asn Gly Lys Arg Leu Leu
                805                 810                 815

Ile His Thr Lys Asp Ser Thr Leu Arg Ile Met Asp Leu Arg Ile Leu
            820                 825                 830

Val Ala Arg Lys Phe Val Gly Ala Ala Asn Tyr Arg Glu Lys Ile His
        835                 840                 845

Ser Thr Leu Thr Pro Cys Gly Thr Phe Leu Phe Ala Gly Ser Glu Asp
    850                 855                 860

Gly Ile Val Tyr Val Trp Asn Pro Glu Thr Gly Glu Gln Val Ala Met
865                 870                 875                 880

Tyr Ser Asp Leu Pro Phe Lys Ser Pro Ile Arg Asp Ile Ser Tyr His
                885                 890                 895

Pro Phe Glu Asn Met Val Ala Phe Cys Ala Phe Gly Gln Asn Glu Pro
            900                 905                 910

Ile Leu Leu Tyr Ile Tyr Asp Phe His Val Ala Gln Gln Glu Ala Glu
        915                 920                 925

Met Phe Lys Arg Tyr Asn Gly Thr Phe Pro Leu Pro Gly Ile His Gln
    930                 935                 940

Ser Gln Asp Ala Leu Cys Thr Cys Pro Lys Leu Pro His Gln Gly Ser
945                 950                 955                 960

Phe Gln Ile Asp Glu Phe Val His Thr Glu Ser Ser Ser Thr Lys Met
```

965 970 975

Gln Leu Val Lys Gln Arg Leu Glu Thr Val Thr Glu Val Ile Arg Ser
980 985 990

Cys Ala Ala Lys Val Asn Lys Asn Leu Ser Phe Thr Ser Pro Pro
Ala
995 1000 1005

Val Ser Ser Gln Gln Ser Lys Leu Lys Gln Ser Asn Met Leu Thr
1010 1015 1020

Ala Gln Glu Ile Leu His Gln Phe Gly Phe Thr Gln Thr Gly Ile
1025 1030 1035

Ile Ser Ile Glu Arg Lys Pro Cys Asn His Gln Val Asp Thr Ala
1040 1045 1050

Pro Thr Val Val Ala Leu Tyr Asp Tyr Thr Ala Asn Arg Ser Asp
1055 1060 1065

Glu Leu Thr Ile His Arg Gly Asp Ile Ile Arg Val Phe Phe Lys
1070 1075 1080

Asp Asn Glu Asp Trp Trp Tyr Gly Ser Ile Gly Lys Gly Gln Glu
1085 1090 1095

Gly Tyr Phe Pro Ala Asn His Val Ala Ser Glu Thr Leu Tyr Gln
1100 1105 1110

Glu Leu Pro Pro Glu Ile Lys Glu Arg Ser Pro Pro Leu Ser Pro
1115 1120 1125

Glu Glu Lys Thr Lys Ile Glu Lys Ser Pro Ala Pro Gln Lys Gln
1130 1135 1140

Ser Ile Asn Lys Asn Lys Ser Gln Asp Phe Arg Leu Gly Ser Glu
1145 1150 1155

Ser Met Thr His Ser Glu Met Arg Lys Glu Gln Ser His Glu Asp
1160 1165 1170

Gln Gly His Ile Met Asp Thr Arg Met Arg Lys Asn Lys Gln Ala

1175 1180 1185

Gly Arg Lys Val Thr Leu Ile Glu
1190 1195

<210> 732
<211> 1053
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<400> 732
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1 5 10 15

Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
20 25 30

Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Pro Asp Thr
35 40 45

Ile Arg Ser Asn Leu His Tyr Met Lys Glu Thr Thr Ser Asp Asp Pro
50 55 60

Asp Thr Ile Arg Ser Asn Leu Pro His Ile Lys Glu Thr Thr Ser Asp
65 70 75 80

Asp Val Ser Ala Ala Asn Thr Asn Asn Leu Lys Lys Ser Thr Arg Val
85 90 95

```
Thr Lys Asn Lys Leu Arg Asn Thr Gln Leu Ala Thr Glu Asn Pro Asn
            100                 105                 110

Gly Asp Ala Ser Val Glu Glu Asp Lys Gln Gly Lys Pro Asn Lys Lys
        115                 120                 125

Val Ile Lys Thr Val Pro Gln Leu Thr Thr Gln Asp Leu Lys Pro Glu
    130                 135                 140

Thr Pro Glu Asn Lys Val Asp Ser Thr His Gln Lys Thr His Thr Lys
145                 150                 155                 160

Pro Gln Pro Gly Val Asp His Gln Lys Ser Glu Lys Ala Asn Glu Gly
                165                 170                 175

Arg Glu Glu Thr Asp Leu Glu Glu Asp Glu Glu Leu Met Gln Ala Tyr
            180                 185                 190

Gln Cys His Val Thr Glu Glu Met Ala Lys Glu Ile Lys Arg Lys Ile
        195                 200                 205

Arg Lys Lys Leu Lys Glu Gln Leu Thr Tyr Phe Pro Ser Asp Thr Leu
    210                 215                 220

Phe His Asp Asp Lys Leu Ser Ser Glu Lys Arg Lys Lys Lys Lys Glu
225                 230                 235                 240

Val Pro Val Phe Ser Lys Ala Glu Thr Ser Thr Leu Thr Ile Ser Gly
                245                 250                 255

Asp Thr Val Glu Gly Glu Gln Lys Lys Glu Ser Ser Val Arg Ser Val
            260                 265                 270

Ser Ser Asp Ser His Gln Asp Asp Glu Ile Ser Ser Met Glu Gln Ser
        275                 280                 285

Thr Glu Asp Ser Met Gln Asp Asp Thr Lys Pro Lys Pro Lys Lys Thr
    290                 295                 300

Lys Lys Lys Thr Lys Ala Val Ala Asp Asn Asn Glu Asp Val Asp Gly
305                 310                 315                 320
```

```
Asp Gly Val His Glu Ile Thr Ser Arg Asp Ser Pro Val Tyr Pro Lys
                325                 330                 335

Cys Leu Leu Asp Asp Asp Leu Val Leu Gly Val Tyr Ile His Arg Thr
            340                 345                 350

Asp Arg Leu Lys Ser Asp Phe Met Ile Ser His Pro Met Val Lys Ile
        355                 360                 365

His Val Val Asp Glu His Thr Gly Gln Tyr Val Lys Lys Asp Asp Ser
    370                 375                 380

Gly Arg Pro Val Ser Ser Tyr Tyr Glu Lys Glu Asn Val Asp Tyr Ile
385                 390                 395                 400

Leu Pro Ile Met Thr Gln Pro Tyr Asp Phe Lys Gln Leu Lys Ser Arg
                405                 410                 415

Leu Pro Glu Trp Glu Glu Gln Ile Val Phe Asn Glu Asn Phe Pro Tyr
            420                 425                 430

Leu Leu Arg Gly Ser Asp Glu Ser Pro Lys Val Ile Leu Phe Phe Glu
        435                 440                 445

Ile Leu Asp Phe Leu Ser Val Asp Glu Ile Lys Asn Asn Ser Glu Val
    450                 455                 460

Gln Asn Gln Glu Cys Gly Phe Arg Lys Ile Ala Trp Ala Phe Leu Lys
465                 470                 475                 480

Leu Leu Gly Ala Asn Gly Asn Ala Asn Ile Asn Ser Lys Leu Arg Leu
                485                 490                 495

Gln Leu Tyr Tyr Pro Pro Thr Lys Pro Arg Ser Pro Leu Ser Val Val
            500                 505                 510

Glu Ala Phe Glu Trp Trp Ser Lys Cys Pro Arg Asn His Tyr Pro Ser
        515                 520                 525

Thr Leu Tyr Val Thr Val Arg Gly Leu Lys Val Pro Asp Cys Ile Lys
    530                 535                 540

Pro Ser Tyr Arg Ser Met Met Ala Leu Gln Glu Glu Lys Gly Lys Pro
```

545 550 555 560

Val His Cys Glu Arg His His Glu Ser Ser Ser Val Asp Thr Glu Pro
565 570 575

Gly Leu Glu Glu Ser Lys Glu Val Ile Lys Trp Lys Arg Leu Pro Gly
580 585 590

Gln Ala Cys Arg Ile Pro Asn Lys His Leu Phe Ser Leu Asn Ala Gly
595 600 605

Glu Arg Gly Cys Phe Cys Leu Asp Phe Ser His Asn Gly Arg Ile Leu
610 615 620

Ala Ala Ala Cys Ala Ser Arg Asp Gly Tyr Pro Ile Ile Leu Tyr Glu
625 630 635 640

Ile Pro Ser Gly Arg Phe Met Arg Glu Leu Cys Gly His Leu Asn Ile
645 650 655

Ile Tyr Asp Leu Ser Trp Ser Lys Asp Asp His Tyr Ile Leu Thr Ser
660 665 670

Ser Ser Asp Gly Thr Ala Arg Ile Trp Lys Asn Glu Ile Asn Asn Thr
675 680 685

Asn Thr Phe Arg Val Leu Pro His Pro Ser Phe Val Tyr Thr Ala Lys
690 695 700

Phe His Pro Ala Val Arg Glu Leu Val Val Thr Gly Cys Tyr Asp Ser
705 710 715 720

Met Ile Arg Ile Trp Lys Val Glu Met Arg Glu Asp Ser Ala Ile Leu
725 730 735

Val Arg Gln Phe Asp Val His Lys Ser Phe Ile Asn Ser Leu Cys Phe
740 745 750

Asp Thr Glu Gly His His Met Tyr Ser Gly Asp Cys Thr Gly Val Ile
755 760 765

Val Val Trp Asn Thr Tyr Val Lys Ile Asn Asp Leu Glu His Ser Val
770 775 780

```
His His Trp Thr Ile Asn Lys Glu Ile Lys Glu Thr Glu Phe Lys Gly
785                 790                 795                 800

Ile Pro Ile Ser Tyr Leu Glu Ile His Pro Asn Gly Lys Arg Leu Leu
                805                 810                 815

Ile His Thr Lys Asp Ser Thr Leu Arg Ile Met Asp Leu Arg Ile Leu
            820                 825                 830

Val Ala Arg Lys Phe Val Gly Ala Ala Asn Tyr Arg Glu Lys Ile His
        835                 840                 845

Ser Thr Leu Thr Pro Cys Gly Thr Phe Leu Phe Ala Gly Ser Glu Asp
    850                 855                 860

Gly Ile Val Tyr Val Trp Asn Pro Glu Thr Gly Glu Gln Val Ala Met
865                 870                 875                 880

Tyr Ser Asp Leu Pro Phe Lys Ser Pro Ile Arg Asp Ile Ser Tyr His
                885                 890                 895

Pro Phe Glu Asn Met Val Ala Phe Cys Ala Phe Gly Gln Asn Glu Pro
            900                 905                 910

Ile Leu Leu Tyr Ile Tyr Asp Phe His Val Ala Gln Gln Glu Ala Glu
        915                 920                 925

Met Phe Lys Arg Tyr Asn Gly Thr Phe Pro Leu Pro Gly Ile His Gln
    930                 935                 940

Ser Gln Asp Ala Leu Cys Thr Cys Pro Lys Leu Pro His Gln Gly Ser
945                 950                 955                 960

Phe Gln Ile Asp Glu Phe Val His Thr Glu Ser Ser Ser Thr Lys Met
                965                 970                 975

Gln Leu Val Lys Gln Arg Leu Glu Thr Val Thr Glu Val Ile Arg Ser
            980                 985                 990

Cys Ala Ala Lys Val Asn Lys Asn  Leu Ser Phe Thr Ser  Pro Pro
Ala
        995                 1000                1005
```

```
Val Ser  Ser Gln Gln Ser Lys  Leu Lys Gln Ser Asn  Met Leu Thr
    1010                1015                1020


Ala Gln  Glu Ile Leu His Gln  Phe Gly Phe Thr Gln  Thr Asp Ser
    1025                1030                1035


His Phe  Ala Glu Phe Asn Thr  Cys Ile Leu Trp Trp  Lys Lys His
    1040                1045                1050


<210> 733
<211> 668
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 733
Xaa Pro Thr Lys Pro Arg Ser Pro Leu Ser Val Val Glu Ala Phe Glu
1               5                  10                  15


Trp Trp Ser Lys Cys Pro Arg Asn His Tyr Pro Ser Thr Leu Tyr Val
            20                  25                  30


Thr Val Arg Gly Leu Lys Val Pro Asp Cys Ile Lys Pro Ser Tyr Arg
        35                  40                  45


Ser Met Met Ala Leu Gln Glu Glu Lys Gly Lys Pro Val His Cys Glu
    50                  55                  60
```

```
Arg His His Glu Ser Ser Ser Val Asp Thr Glu Pro Gly Leu Glu Glu
65                  70                  75                  80

Ser Lys Glu Val Ile Lys Trp Lys Arg Leu Pro Gly Gln Ala Cys Arg
                85                  90                  95

Ile Pro Asn Lys His Leu Phe Ser Leu Asn Ala Gly Glu Arg Gly Cys
            100                 105                 110

Phe Cys Leu Asp Phe Ser His Asn Gly Arg Ile Leu Ala Ala Ala Cys
        115                 120                 125

Ala Ser Arg Asp Gly Tyr Pro Ile Ile Leu Tyr Glu Ile Pro Ser Gly
    130                 135                 140

Arg Phe Met Arg Glu Leu Cys Gly His Leu Asn Ile Ile Tyr Asp Leu
145                 150                 155                 160

Ser Trp Ser Lys Asp Asp His Tyr Ile Leu Thr Ser Ser Ser Asp Gly
                165                 170                 175

Thr Ala Arg Ile Trp Lys Asn Glu Ile Asn Asn Thr Asn Thr Phe Arg
            180                 185                 190

Val Leu Pro His Pro Ser Phe Val Tyr Thr Ala Lys Phe His Pro Ala
        195                 200                 205

Val Arg Glu Leu Val Val Thr Gly Cys Tyr Asp Ser Met Ile Arg Ile
    210                 215                 220

Trp Lys Val Glu Met Arg Glu Asp Ser Ala Ile Leu Val Arg Gln Phe
225                 230                 235                 240

Asp Val His Lys Ser Phe Ile Asn Ser Leu Cys Phe Asp Thr Glu Gly
                245                 250                 255

His His Met Tyr Ser Gly Asp Cys Thr Gly Val Ile Val Val Trp Asn
            260                 265                 270

Thr Tyr Val Lys Ile Asn Asp Leu Glu His Ser Val His His Trp Thr
        275                 280                 285
```

```
Ile Asn Lys Glu Ile Lys Glu Thr Glu Phe Lys Gly Ile Pro Ile Ser
    290                 295                 300

Tyr Leu Glu Ile His Pro Asn Gly Lys Arg Leu Leu Ile His Thr Lys
305                 310                 315                 320

Asp Ser Thr Leu Arg Ile Met Asp Leu Arg Ile Leu Val Ala Arg Lys
                325                 330                 335

Phe Val Gly Ala Ala Asn Tyr Arg Glu Lys Ile His Ser Thr Leu Thr
            340                 345                 350

Pro Cys Gly Thr Phe Leu Phe Ala Gly Ser Glu Asp Gly Ile Val Tyr
        355                 360                 365

Val Trp Asn Pro Glu Thr Gly Glu Gln Val Ala Met Tyr Ser Asp Leu
    370                 375                 380

Pro Phe Lys Ser Pro Ile Arg Asp Ile Ser Tyr His Pro Phe Glu Asn
385                 390                 395                 400

Met Val Ala Phe Cys Ala Phe Gly Gln Asn Glu Pro Ile Leu Leu Tyr
                405                 410                 415

Ile Tyr Asp Phe His Val Ala Gln Gln Glu Ala Glu Met Phe Lys Arg
            420                 425                 430

Tyr Asn Gly Thr Phe Pro Leu Pro Gly Ile His Gln Ser Gln Asp Ala
        435                 440                 445

Leu Cys Thr Cys Pro Lys Leu Pro His Gln Gly Ser Phe Gln Ile Asp
    450                 455                 460

Glu Phe Val His Thr Glu Ser Ser Ser Thr Lys Met Gln Leu Val Lys
465                 470                 475                 480

Gln Arg Leu Glu Thr Val Thr Glu Val Ile Arg Ser Cys Ala Ala Lys
                485                 490                 495

Val Asn Lys Asn Leu Ser Phe Thr Ser Pro Pro Ala Val Ser Ser Gln
            500                 505                 510
```

```
Gln Ser Lys Leu Lys Gln Ser Asn Met Leu Thr Ala Gln Glu Ile Leu
        515                 520                 525

His Gln Phe Gly Phe Thr Gln Thr Gly Ile Ile Ser Ile Glu Arg Lys
    530                 535                 540

Pro Cys Asn His Gln Val Asp Thr Ala Pro Thr Val Val Ala Leu Tyr
545                 550                 555                 560

Asp Tyr Thr Ala Asn Arg Ser Asp Glu Leu Thr Ile His Arg Gly Asp
                565                 570                 575

Ile Ile Arg Val Phe Phe Lys Asp Asn Glu Asp Trp Trp Tyr Gly Ser
            580                 585                 590

Ile Gly Lys Gly Gln Glu Gly Tyr Phe Pro Ala Asn His Val Ala Ser
        595                 600                 605

Glu Thr Leu Tyr Gln Glu Leu Pro Pro Glu Ile Lys Glu Arg Ser Pro
    610                 615                 620

Pro Leu Ser Pro Glu Glu Lys Thr Lys Ile Glu Lys Ser Pro Ala Pro
625                 630                 635                 640

Gln Lys Gln Ser Ile Asn Lys Asn Lys Ser Gln Asp Phe Arg Leu Gly
                645                 650                 655

Ser Glu Ser Met Thr His Lys Glu Leu Lys Lys Ser
            660                 665


<210> 734
<211> 1196
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 124; "

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<400> 734
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1   5   10   15

Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20   25   30

Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Pro Asp Thr
        35   40   45

Ile Arg Ser Asn Leu His Tyr Met Lys Glu Thr Thr Ser Asp Asp Pro
    50   55   60

Asp Thr Ile Arg Ser Asn Leu Pro His Ile Lys Glu Thr Thr Ser Asp
65   70   75   80

Asp Val Ser Ala Ala Asn Thr Asn Asn Leu Lys Lys Ser Thr Arg Val
                85   90   95

Thr Lys Asn Lys Leu Arg Asn Thr Gln Leu Ala Thr Glu Asn Pro Asn
            100   105   110

Gly Asp Ala Ser Val Glu Glu Asp Lys Gln Gly Lys Pro Asn Lys Lys
        115   120   125

Val Ile Lys Thr Val Pro Gln Leu Thr Thr Gln Asp Leu Lys Pro Glu
    130   135   140

Thr Pro Glu Asn Lys Val Asp Ser Thr His Gln Lys Thr His Thr Lys
145   150   155   160

Pro Gln Pro Gly Val Asp His Gln Lys Ser Glu Lys Ala Asn Glu Gly
                165   170   175

Arg Glu Glu Thr Asp Leu Glu Glu Asp Glu Glu Leu Met Gln Ala Tyr
            180   185   190

```
Gln Cys His Val Thr Glu Glu Met Ala Lys Glu Ile Lys Arg Lys Ile
        195                 200                 205

Arg Lys Lys Leu Lys Glu Gln Leu Thr Tyr Phe Pro Ser Asp Thr Leu
    210                 215                 220

Phe His Asp Asp Lys Leu Ser Ser Glu Lys Arg Lys Lys Lys Lys Glu
225                 230                 235                 240

Val Pro Val Phe Ser Lys Ala Glu Thr Ser Thr Leu Thr Ile Ser Gly
                245                 250                 255

Asp Thr Val Glu Gly Glu Gln Lys Lys Glu Ser Ser Val Arg Ser Val
            260                 265                 270

Ser Ser Asp Ser His Gln Asp Asp Glu Ile Ser Ser Met Glu Gln Ser
        275                 280                 285

Thr Glu Asp Ser Met Gln Asp Asp Thr Lys Pro Lys Pro Lys Lys Thr
    290                 295                 300

Lys Lys Lys Thr Lys Ala Val Ala Asp Asn Asn Glu Asp Val Asp Gly
305                 310                 315                 320

Asp Gly Val His Glu Ile Thr Ser Arg Asp Ser Pro Val Tyr Pro Lys
                325                 330                 335

Cys Leu Leu Asp Asp Asp Leu Val Leu Gly Val Tyr Ile His Arg Thr
            340                 345                 350

Asp Arg Leu Lys Ser Asp Phe Met Ile Ser His Pro Met Val Lys Ile
        355                 360                 365

His Val Val Asp Glu His Thr Gly Gln Tyr Val Lys Lys Asp Asp Ser
    370                 375                 380

Gly Arg Pro Val Ser Ser Tyr Tyr Glu Lys Glu Asn Val Asp Tyr Ile
385                 390                 395                 400

Leu Pro Ile Met Thr Gln Pro Tyr Asp Phe Lys Gln Leu Lys Ser Arg
                405                 410                 415
```

```
Leu Pro Glu Trp Glu Glu Gln Ile Val Phe Asn Glu Asn Phe Pro Tyr
            420                 425                 430

Leu Leu Arg Gly Ser Asp Glu Ser Pro Lys Val Ile Leu Phe Phe Glu
        435                 440                 445

Ile Leu Asp Phe Leu Ser Val Asp Glu Ile Lys Asn Asn Ser Glu Val
    450                 455                 460

Gln Asn Gln Glu Cys Gly Phe Arg Lys Ile Ala Trp Ala Phe Leu Lys
465                 470                 475                 480

Leu Leu Gly Ala Asn Gly Asn Ala Asn Ile Asn Ser Lys Leu Arg Leu
                485                 490                 495

Gln Leu Tyr Tyr Pro Pro Thr Lys Pro Arg Ser Pro Leu Ser Val Val
            500                 505                 510

Glu Ala Phe Glu Trp Trp Ser Lys Cys Pro Arg Asn His Tyr Pro Ser
        515                 520                 525

Thr Leu Tyr Val Thr Val Arg Gly Leu Lys Val Pro Asp Cys Ile Lys
    530                 535                 540

Pro Ser Tyr Arg Ser Met Met Ala Leu Gln Glu Glu Lys Gly Lys Pro
545                 550                 555                 560

Val His Cys Glu Arg His His Glu Ser Ser Ser Val Asp Thr Glu Pro
                565                 570                 575

Gly Leu Glu Glu Ser Lys Glu Val Ile Lys Trp Lys Arg Leu Pro Gly
            580                 585                 590

Gln Ala Cys Arg Ile Pro Asn Lys His Leu Phe Ser Leu Asn Ala Gly
        595                 600                 605

Glu Arg Gly Cys Phe Cys Leu Asp Phe Ser His Asn Gly Arg Ile Leu
    610                 615                 620

Ala Ala Ala Cys Ala Ser Arg Asp Gly Tyr Pro Ile Ile Leu Tyr Glu
625                 630                 635                 640

Ile Pro Ser Gly Arg Phe Met Arg Glu Leu Cys Gly His Leu Asn Ile
```

645 650 655

Ile Tyr Asp Leu Ser Trp Ser Lys Asp Asp His Tyr Ile Leu Thr Ser
660 665 670

Ser Ser Asp Gly Thr Ala Arg Ile Trp Lys Asn Glu Ile Asn Asn Thr
675 680 685

Asn Thr Phe Arg Val Leu Pro His Pro Ser Phe Val Tyr Thr Ala Lys
690 695 700

Phe His Pro Ala Val Arg Glu Leu Val Val Thr Gly Cys Tyr Asp Ser
705 710 715 720

Met Ile Arg Ile Trp Lys Val Glu Met Arg Glu Asp Ser Ala Ile Leu
725 730 735

Val Arg Gln Phe Asp Val His Lys Ser Phe Ile Asn Ser Leu Cys Phe
740 745 750

Asp Thr Glu Gly His His Met Tyr Ser Gly Asp Cys Thr Gly Val Ile
755 760 765

Val Val Trp Asn Thr Tyr Val Lys Ile Asn Asp Leu Glu His Ser Val
770 775 780

His His Trp Thr Ile Asn Lys Glu Ile Lys Glu Thr Glu Phe Lys Gly
785 790 795 800

Ile Pro Ile Ser Tyr Leu Glu Ile His Pro Asn Gly Lys Arg Leu Leu
805 810 815

Ile His Thr Lys Asp Ser Thr Leu Arg Ile Met Asp Leu Arg Ile Leu
820 825 830

Val Ala Arg Lys Phe Val Gly Ala Ala Asn Tyr Arg Glu Lys Ile His
835 840 845

Ser Thr Leu Thr Pro Cys Gly Thr Phe Leu Phe Ala Gly Ser Glu Asp
850 855 860

Gly Ile Val Tyr Val Trp Asn Pro Glu Thr Gly Glu Gln Val Ala Met
865 870 875 880

```
Tyr Ser Asp Leu Pro Phe Lys Ser Pro Ile Arg Asp Ile Ser Tyr His
                885                 890                 895

Pro Phe Glu Asn Met Val Ala Phe Cys Ala Phe Gly Gln Asn Glu Pro
            900                 905                 910

Ile Leu Leu Tyr Ile Tyr Asp Phe His Val Ala Gln Gln Glu Ala Glu
        915                 920                 925

Met Phe Lys Arg Tyr Asn Gly Thr Phe Pro Leu Pro Gly Ile His Gln
    930                 935                 940

Ser Gln Asp Ala Leu Cys Thr Cys Pro Lys Leu Pro His Gln Gly Ser
945                 950                 955                 960

Phe Gln Ile Asp Glu Phe Val His Thr Glu Ser Ser Ser Thr Lys Met
                965                 970                 975

Gln Leu Val Lys Gln Arg Leu Glu Thr Val Thr Glu Val Ile Arg Ser
            980                 985                 990

Cys Ala Ala Lys Val Asn Lys Asn  Leu Ser Phe Thr Ser  Pro Pro
Ala
        995                 1000                1005

Val Ser  Ser Gln Gln Ser Lys  Leu Lys Gln Ser Asn  Met Leu Thr
    1010                1015                1020

Ala Gln  Glu Ile Leu His Gln  Phe Gly Phe Thr Gln  Thr Gly Ile
    1025                1030                1035

Ile Ser  Ile Glu Arg Lys Pro  Cys Asn His Gln Val  Asp Thr Ala
    1040                1045                1050

Pro Thr  Val Val Ala Leu Tyr  Asp Tyr Thr Ala Asn  Arg Ser Asp
    1055                1060                1065

Glu Leu  Thr Ile His Arg Gly  Asp Ile Ile Arg Val  Phe Phe Lys
    1070                1075                1080

Asp Asn  Glu Asp Trp Trp Tyr  Gly Ser Ile Gly Lys  Gly Gln Glu
    1085                1090                1095
```

```
Gly Tyr  Phe Pro Ala Asn His  Val Ala Ser Glu Thr  Leu Tyr Gln
    1100                1105                1110

Glu Leu  Pro Pro Glu Ile Lys  Glu Arg Ser Pro Pro  Leu Ser Pro
    1115                1120                1125

Glu Glu  Lys Thr Lys Ile Glu  Lys Ser Pro Ala Pro  Gln Lys Gln
    1130                1135                1140

Ser Ile  Asn Lys Asn Lys Ser  Gln Asp Phe Arg Leu  Gly Ser Glu
    1145                1150                1155

Ser Met  Thr His Ser Glu Met  Arg Lys Glu Gln Ser  His Glu Asp
    1160                1165                1170

Gln Gly  His Ile Met Asp Thr  Arg Met Arg Lys Asn  Lys Gln Ala
    1175                1180                1185

Gly Arg  Lys Val Thr Leu Ile  Glu
    1190                1195


<210> 735
<211> 1196
<212> PRT
<213> Homo sapiens

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      Abelson helper integration site 1; "

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<220>
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<400> 735
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Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                  10                  15

Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30

Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Pro Asp Thr
        35                  40                  45

Ile Arg Ser Asn Leu His Tyr Met Lys Glu Thr Thr Ser Asp Asp Pro
    50                  55                  60

Asp Thr Ile Arg Ser Asn Leu Pro His Ile Lys Glu Thr Thr Ser Asp
65                  70                  75                  80

Asp Val Ser Ala Ala Asn Thr Asn Asn Leu Lys Lys Ser Thr Arg Val
                85                  90                  95

Thr Lys Asn Lys Leu Arg Asn Thr Gln Leu Ala Thr Glu Asn Pro Asn
            100                 105                 110

Gly Asp Ala Ser Val Glu Glu Asp Lys Gln Gly Lys Pro Asn Lys Lys
        115                 120                 125

Val Ile Lys Thr Val Pro Gln Leu Thr Thr Gln Asp Leu Lys Pro Glu
    130                 135                 140

Thr Pro Glu Asn Lys Val Asp Ser Thr His Gln Lys Thr His Thr Lys
145                 150                 155                 160

Pro Gln Pro Gly Val Asp His Gln Lys Ser Glu Lys Ala Asn Glu Gly
                165                 170                 175

Arg Glu Glu Thr Asp Leu Glu Glu Asp Glu Glu Leu Met Gln Ala Tyr
            180                 185                 190

Gln Cys His Val Thr Glu Glu Met Ala Lys Glu Ile Lys Arg Lys Ile
        195                 200                 205

Arg Lys Lys Leu Lys Glu Gln Leu Thr Tyr Phe Pro Ser Asp Thr Leu
    210                 215                 220

Phe His Asp Asp Lys Leu Ser Ser Glu Lys Arg Lys Lys Lys Lys Glu
```

225 230 235 240

Val Pro Val Phe Ser Lys Ala Glu Thr Ser Thr Leu Thr Ile Ser Gly
245 250 255

Asp Thr Val Glu Gly Glu Gln Lys Lys Glu Ser Ser Val Arg Ser Val
260 265 270

Ser Ser Asp Ser His Gln Asp Asp Glu Ile Ser Ser Met Glu Gln Ser
275 280 285

Thr Glu Asp Ser Met Gln Asp Asp Thr Lys Pro Lys Pro Lys Lys Thr
290 295 300

Lys Lys Lys Thr Lys Ala Val Ala Asp Asn Asn Glu Asp Val Asp Gly
305 310 315 320

Asp Gly Val His Glu Ile Thr Ser Arg Asp Ser Pro Val Tyr Pro Lys
325 330 335

Cys Leu Leu Asp Asp Asp Leu Val Leu Gly Val Tyr Ile His Arg Thr
340 345 350

Asp Arg Leu Lys Ser Asp Phe Met Ile Ser His Pro Met Val Lys Ile
355 360 365

His Val Val Asp Glu His Thr Gly Gln Tyr Val Lys Lys Asp Asp Ser
370 375 380

Gly Arg Pro Val Ser Ser Tyr Tyr Glu Lys Glu Asn Val Asp Tyr Ile
385 390 395 400

Leu Pro Ile Met Thr Gln Pro Tyr Asp Phe Lys Gln Leu Lys Ser Arg
405 410 415

Leu Pro Glu Trp Glu Glu Gln Ile Val Phe Asn Glu Asn Phe Pro Tyr
420 425 430

Leu Leu Arg Gly Ser Asp Glu Ser Pro Lys Val Ile Leu Phe Phe Glu
435 440 445

Ile Leu Asp Phe Leu Ser Val Asp Glu Ile Lys Asn Asn Ser Glu Val
450 455 460

```
Gln Asn Gln Glu Cys Gly Phe Arg Lys Ile Ala Trp Ala Phe Leu Lys
465                 470                 475                 480

Leu Leu Gly Ala Asn Gly Asn Ala Asn Ile Asn Ser Lys Leu Arg Leu
                485                 490                 495

Gln Leu Tyr Tyr Pro Pro Thr Lys Pro Arg Ser Pro Leu Ser Val Val
            500                 505                 510

Glu Ala Phe Glu Trp Trp Ser Lys Cys Pro Arg Asn His Tyr Pro Ser
        515                 520                 525

Thr Leu Tyr Val Thr Val Arg Gly Leu Lys Val Pro Asp Cys Ile Lys
    530                 535                 540

Pro Ser Tyr Arg Ser Met Met Ala Leu Gln Glu Glu Lys Gly Lys Pro
545                 550                 555                 560

Val His Cys Glu Arg His His Glu Ser Ser Ser Val Asp Thr Glu Pro
                565                 570                 575

Gly Leu Glu Glu Ser Lys Glu Val Ile Lys Trp Lys Arg Leu Pro Gly
            580                 585                 590

Gln Ala Cys Arg Ile Pro Asn Lys His Leu Phe Ser Leu Asn Ala Gly
        595                 600                 605

Glu Arg Gly Cys Phe Cys Leu Asp Phe Ser His Asn Gly Arg Ile Leu
    610                 615                 620

Ala Ala Ala Cys Ala Ser Arg Asp Gly Tyr Pro Ile Ile Leu Tyr Glu
625                 630                 635                 640

Ile Pro Ser Gly Arg Phe Met Arg Glu Leu Cys Gly His Leu Asn Ile
                645                 650                 655

Ile Tyr Asp Leu Ser Trp Ser Lys Asp Asp His Tyr Ile Leu Thr Ser
            660                 665                 670

Ser Ser Asp Gly Thr Ala Arg Ile Trp Lys Asn Glu Ile Asn Asn Thr
        675                 680                 685
```

```
Asn Thr Phe Arg Val Leu Pro His Pro Ser Phe Val Tyr Thr Ala Lys
    690                 695                 700

Phe His Pro Ala Val Arg Glu Leu Val Val Thr Gly Cys Tyr Asp Ser
705                 710                 715                 720

Met Ile Arg Ile Trp Lys Val Glu Met Arg Glu Asp Ser Ala Ile Leu
                725                 730                 735

Val Arg Gln Phe Asp Val His Lys Ser Phe Ile Asn Ser Leu Cys Phe
            740                 745                 750

Asp Thr Glu Gly His His Met Tyr Ser Gly Asp Cys Thr Gly Val Ile
        755                 760                 765

Val Val Trp Asn Thr Tyr Val Lys Ile Asn Asp Leu Glu His Ser Val
    770                 775                 780

His His Trp Thr Ile Asn Lys Glu Ile Lys Glu Thr Glu Phe Lys Gly
785                 790                 795                 800

Ile Pro Ile Ser Tyr Leu Glu Ile His Pro Asn Gly Lys Arg Leu Leu
                805                 810                 815

Ile His Thr Lys Asp Ser Thr Leu Arg Ile Met Asp Leu Arg Ile Leu
            820                 825                 830

Val Ala Arg Lys Phe Val Gly Ala Ala Asn Tyr Arg Glu Lys Ile His
        835                 840                 845

Ser Thr Leu Thr Pro Cys Gly Thr Phe Leu Phe Ala Gly Ser Glu Asp
    850                 855                 860

Gly Ile Val Tyr Val Trp Asn Pro Glu Thr Gly Glu Gln Val Ala Met
865                 870                 875                 880

Tyr Ser Asp Leu Pro Phe Lys Ser Pro Ile Arg Asp Ile Ser Tyr His
                885                 890                 895

Pro Phe Glu Asn Met Val Ala Phe Cys Ala Phe Gly Gln Asn Glu Pro
            900                 905                 910
```

```
Ile Leu Leu Tyr Ile Tyr Asp Phe His Val Ala Gln Gln Glu Ala Glu
        915                 920                 925

Met Phe Lys Arg Tyr Asn Gly Thr Phe Pro Leu Pro Gly Ile His Gln
    930                 935                 940

Ser Gln Asp Ala Leu Cys Thr Cys Pro Lys Leu Pro His Gln Gly Ser
945                 950                 955                 960

Phe Gln Ile Asp Glu Phe Val His Thr Glu Ser Ser Ser Thr Lys Met
                965                 970                 975

Gln Leu Val Lys Gln Arg Leu Glu Thr Val Thr Glu Val Ile Arg Ser
            980                 985                 990

Cys Ala Ala Lys Val Asn Lys Asn  Leu Ser Phe Thr Ser  Pro Pro
Ala
        995                 1000                1005

Val Ser  Ser Gln Gln Ser Lys  Leu Lys Gln Ser Asn  Met Leu Thr
    1010                1015                1020

Ala Gln  Glu Ile Leu His Gln  Phe Gly Phe Thr Gln  Thr Gly Ile
    1025                1030                1035

Ile Ser  Ile Glu Arg Lys Pro  Cys Asn His Gln Val  Asp Thr Ala
    1040                1045                1050

Pro Thr  Val Val Ala Leu Tyr  Asp Tyr Thr Ala Asn  Arg Ser Asp
    1055                1060                1065

Glu Leu  Thr Ile His Arg Gly  Asp Ile Ile Arg Val  Phe Phe Lys
    1070                1075                1080

Asp Asn  Glu Asp Trp Trp Tyr  Gly Ser Ile Gly Lys  Gly Gln Glu
    1085                1090                1095

Gly Tyr  Phe Pro Ala Asn His  Val Ala Ser Glu Thr  Leu Tyr Gln
    1100                1105                1110

Glu Leu  Pro Pro Glu Ile Lys  Glu Arg Ser Pro Pro  Leu Ser Pro
    1115                1120                1125
```

```
Glu Glu  Lys Thr Lys Ile Glu  Lys Ser Pro Ala Pro  Gln Lys Gln
    1130                1135                1140


Ser Ile  Asn Lys Asn Lys Ser  Gln Asp Phe Arg Leu  Gly Ser Glu
    1145                1150                1155


Ser Met  Thr His Ser Glu Met  Arg Lys Glu Gln Ser  His Glu Asp
    1160                1165                1170


Gln Gly  His Ile Met Asp Thr  Arg Met Arg Lys Asn  Lys Gln Ala
    1175                1180                1185


Gly Arg  Lys Val Thr Leu Ile  Glu
    1190                1195


<210> 736
<211> 609
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
      Abelson helper integration site 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N157; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432167"

<400> 736
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                  10                  15


Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30


Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Pro Asp Thr
        35                  40                  45
```

```
Ile Arg Ser Asn Leu His Tyr Met Lys Glu Thr Thr Ser Asp Asp Pro
    50                  55                  60

Asp Thr Ile Arg Ser Asn Leu Pro His Ile Lys Glu Thr Thr Ser Asp
65                  70                  75                  80

Asp Val Ser Ala Ala Asn Thr Asn Asn Leu Lys Lys Ser Thr Arg Val
                85                  90                  95

Thr Lys Asn Lys Leu Arg Asn Thr Gln Leu Ala Thr Glu Asn Pro Asn
            100                 105                 110

Gly Asp Ala Ser Val Glu Glu Asp Lys Gln Gly Lys Pro Asn Lys Lys
        115                 120                 125

Val Ile Lys Thr Val Pro Gln Leu Thr Thr Gln Asp Leu Lys Pro Glu
    130                 135                 140

Thr Pro Glu Asn Lys Val Asp Ser Thr His Gln Lys Thr His Thr Lys
145                 150                 155                 160

Pro Gln Pro Gly Val Asp His Gln Lys Ser Glu Lys Ala Asn Glu Gly
                165                 170                 175

Arg Glu Glu Thr Asp Leu Glu Glu Asp Glu Glu Leu Met Gln Ala Tyr
            180                 185                 190

Gln Cys His Val Thr Glu Glu Met Ala Lys Glu Ile Lys Arg Lys Ile
        195                 200                 205

Arg Lys Lys Leu Lys Glu Gln Leu Thr Tyr Phe Pro Ser Asp Thr Leu
    210                 215                 220

Phe His Asp Asp Lys Leu Ser Ser Glu Lys Arg Lys Lys Lys Lys Glu
225                 230                 235                 240

Val Pro Val Phe Ser Lys Ala Glu Thr Ser Thr Leu Thr Ile Ser Gly
                245                 250                 255

Asp Thr Val Glu Gly Glu Gln Lys Lys Glu Ser Ser Val Arg Ser Val
            260                 265                 270
```

```
Ser Ser Asp Ser His Gln Asp Asp Glu Ile Ser Ser Met Glu Gln Ser
        275                 280                 285

Thr Glu Asp Ser Met Gln Asp Asp Thr Lys Pro Lys Pro Lys Lys Thr
    290                 295                 300

Lys Lys Lys Thr Lys Ala Val Ala Asp Asn Asn Glu Asp Val Asp Gly
305                 310                 315                 320

Asp Gly Val His Glu Ile Thr Ser Arg Asp Ser Pro Val Tyr Pro Lys
                325                 330                 335

Cys Leu Leu Asp Asp Asp Leu Val Leu Gly Val Tyr Ile His Arg Thr
            340                 345                 350

Asp Arg Leu Lys Ser Asp Phe Met Ile Ser His Pro Met Val Lys Ile
        355                 360                 365

His Val Val Asp Glu His Thr Gly Gln Tyr Val Lys Lys Asp Asp Ser
    370                 375                 380

Gly Arg Pro Val Ser Ser Tyr Tyr Glu Lys Glu Asn Val Asp Tyr Ile
385                 390                 395                 400

Leu Pro Ile Met Thr Gln Pro Tyr Asp Phe Lys Gln Leu Lys Ser Arg
                405                 410                 415

Leu Pro Glu Trp Glu Glu Gln Ile Val Phe Asn Glu Asn Phe Pro Tyr
            420                 425                 430

Leu Leu Arg Gly Ser Asp Glu Ser Pro Lys Val Ile Leu Phe Phe Glu
        435                 440                 445

Ile Leu Asp Phe Leu Ser Val Asp Glu Ile Lys Asn Asn Ser Glu Val
    450                 455                 460

Gln Asn Gln Glu Cys Gly Phe Arg Lys Ile Ala Trp Ala Phe Leu Lys
465                 470                 475                 480

Leu Leu Gly Ala Asn Gly Asn Ala Asn Ile Asn Ser Lys Leu Arg Leu
                485                 490                 495
```

```
Gln Leu Tyr Tyr Pro Pro Thr Lys Pro Arg Ser Pro Leu Ser Val Val
            500                 505                 510

Glu Ala Phe Glu Trp Trp Ser Lys Cys Pro Arg Asn His Tyr Pro Ser
        515                 520                 525

Thr Leu Tyr Val Thr Val Arg Gly Leu Lys Val Pro Asp Cys Ile Lys
    530                 535                 540

Pro Ser Tyr Arg Ser Met Met Ala Leu Gln Glu Glu Lys Gly Lys Pro
545                 550                 555                 560

Val His Cys Glu Arg His His Glu Ser Ser Ser Val Asp Thr Glu Pro
                565                 570                 575

Gly Leu Glu Glu Ser Lys Glu Val Ile Lys Trp Lys Arg Leu Pro Gly
            580                 585                 590

Gln Glu Asn Glu Asp Val Phe Val Leu Ile Ser Pro Thr Met Glu Glu
        595                 600                 605

Tyr
```

<210> 737
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433017"

<400> 737

```
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                   10                  15
```

```
Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30

Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Asn Gln Glu
        35                  40                  45

Lys Ser Met Ala Val Trp
    50


<210> 738
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
      Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433063"

<400> 738
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                   10                  15

Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30

Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Pro Asp Thr
        35                  40                  45

Ile Arg Ser Asn Leu Pro His Ile Lys Glu Thr Thr Ser Asp Asp Val
    50                  55                  60

Ser Ala Ala Asn Thr Asn Asn Leu Lys Lys Ser Thr Arg Val Thr Lys
65                  70                  75                  80
```

```
Asn Lys Leu Arg Asn Thr Gln Leu Ala Thr Glu Asn Pro Asn Gly Asp
                85                  90                  95

Ala Ser Val Glu Glu Asp Lys Gln Gly Lys Pro Asn Lys Lys Val Ile
            100                 105                 110

Lys Thr Val Pro Gln Leu Thr Thr Gln Asp Leu Lys Pro Glu Thr Pro
        115                 120                 125

Glu Asn Lys Val Asp Ser Thr His Gln Lys Thr His Thr Lys Pro Gln
    130                 135                 140

Pro Gly Val Asp His Gln Lys Ser Glu Lys Ala Asn Glu Gly Arg Glu
145                 150                 155                 160

Glu Thr Asp Leu Glu Glu Asp Glu Glu Leu Met Gln Ala Tyr Gln Cys
                165                 170                 175

His Val Thr Glu Glu Met Ala Lys Glu Ile Lys Arg Lys Ile Arg Lys
            180                 185                 190

Lys Leu Lys Glu Gln Leu Thr Tyr Phe Pro Ser Asp Thr Leu Phe His
        195                 200                 205

Asp Asp Lys Leu Ser Ser Glu Lys Arg Lys Lys Lys Lys Glu Val Pro
    210                 215                 220

Val Phe Ser Lys Ala Glu Thr Ser Thr Leu Thr Ile Ser Gly Asp Thr
225                 230                 235                 240

Val Glu Gly Glu Gln Lys Lys Glu Ser Ser Val Arg Ser Val Ser Ser
                245                 250                 255

Asp Ser His Gln Asp Asp Glu Ile Ser Ser Met Glu Gln Ser Thr Glu
            260                 265                 270

Asp Ser Met Gln Asp Asp Thr Lys Pro Lys Pro Lys Lys Thr Lys Lys
        275                 280                 285
```

<210> 739
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433864"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 739
Xaa Asp Phe Arg Leu Gly Ser Glu Ser Met Thr Gln Arg Glu Leu Asn
1 5 10 15

Glu Lys Ala Gly Gly Ile Cys Ile Ala Arg Glu Gly Leu
20 25

<210> 740
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434697"

<220>
<221> MOD_RES

<222> (1)..(1)
<223> Any amino acid

<400> 740
Xaa Gly Thr Phe Pro Leu Pro Gly Ile His Gln Ser Gln Asp Ala Leu
1 5 10 15

Cys Thr Cys Pro Lys Leu Pro His Gln Gly Ser Phe Gln Ile Asp Glu
20 25 30

Phe Val His Thr Glu Ser Ser Ser Thr Lys Met Gln Leu Val Lys Gln
35 40 45

Arg Leu Glu Thr Val Thr Glu Val Ile Arg Ser Cys Ala Ala Lys Val
50 55 60

Asn Lys Asn Leu Ser Phe Thr Ser Pro Pro Ala Val Ser Ser Gln Gln
65 70 75 80

Ser Lys Leu Lys Gln Ser Asn Met Leu Thr Ala Gln Glu Ile Leu His
85 90 95

Gln Phe Gly Phe Thr Gln Thr Gly Glu Pro Leu Ser Tyr Phe Asp Asn
100 105 110

Ser Phe Lys Cys Ser Asp Ala Cys Cys Val Asp Glu Tyr His Leu Phe
115 120 125

Leu

<210> 741
<211> 542
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435710"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 741
Xaa Ser Leu Asn Ala Gly Glu Arg Gly Cys Phe Cys Leu Asp Phe Ser
1 5 10 15

His Asn Gly Arg Ile Leu Ala Ala Ala Cys Ala Ser Arg Asp Gly Tyr
20 25 30

Pro Ile Ile Leu Tyr Glu Ile Pro Ser Gly Arg Phe Met Arg Glu Leu
35 40 45

Cys Gly His Leu Asn Ile Ile Tyr Asp Leu Ser Trp Ser Lys Asp Asp
50 55 60

His Tyr Ile Leu Thr Ser Ser Ser Asp Gly Thr Ala Arg Ile Trp Lys
65 70 75 80

Asn Glu Ile Asn Asn Thr Asn Thr Phe Arg Val Leu Pro His Pro Ser
85 90 95

Phe Val Tyr Thr Ala Lys Phe His Pro Ala Val Arg Glu Leu Val Val
100 105 110

Thr Gly Cys Tyr Asp Ser Met Ile Arg Ile Trp Lys Val Glu Met Arg
115 120 125

Glu Asp Ser Ala Ile Leu Val Arg Gln Phe Asp Val His Lys Ser Phe
130 135 140

Ile Asn Ser Leu Cys Phe Asp Thr Glu Gly His His Met Tyr Ser Gly
145 150 155 160

Asp Cys Thr Gly Val Ile Val Val Trp Asn Thr Tyr Val Lys Ile Asn
165 170 175

Asp Leu Glu His Ser Val His His Trp Thr Ile Asn Lys Glu Ile Lys

```
            180                 185                 190

Glu Thr Glu Phe Lys Gly Ile Pro Ile Ser Tyr Leu Glu Ile His Pro
        195                 200                 205

Asn Gly Lys Arg Leu Leu Ile His Thr Lys Asp Ser Thr Leu Arg Ile
    210                 215                 220

Met Asp Leu Arg Ile Leu Val Ala Arg Lys Phe Val Gly Ala Ala Asn
225                 230                 235                 240

Tyr Arg Glu Lys Ile His Ser Thr Leu Thr Pro Cys Gly Thr Phe Leu
                245                 250                 255

Phe Ala Gly Ser Glu Asp Gly Ile Val Tyr Val Trp Asn Pro Glu Thr
            260                 265                 270

Gly Glu Gln Val Ala Met Tyr Ser Asp Leu Pro Phe Lys Ser Pro Ile
        275                 280                 285

Arg Asp Ile Ser Tyr His Pro Phe Glu Asn Met Val Ala Phe Cys Ala
    290                 295                 300

Phe Gly Gln Asn Glu Pro Ile Leu Leu Tyr Ile Tyr Asp Phe His Val
305                 310                 315                 320

Ala Gln Gln Glu Ala Glu Met Phe Lys Arg Tyr Asn Gly Thr Phe Pro
                325                 330                 335

Leu Pro Gly Ile His Gln Ser Gln Asp Ala Leu Cys Thr Cys Pro Lys
            340                 345                 350

Leu Pro His Gln Gly Ser Phe Gln Ile Asp Glu Phe Val His Thr Glu
        355                 360                 365

Ser Ser Ser Thr Lys Met Gln Leu Val Lys Gln Arg Leu Glu Thr Val
    370                 375                 380

Thr Glu Val Ile Arg Ser Cys Ala Ala Lys Val Asn Lys Asn Leu Ser
385                 390                 395                 400

Phe Thr Ser Pro Pro Ala Val Ser Ser Gln Gln Ser Lys Leu Lys Gln
                405                 410                 415
```

```
Ser Asn Met Leu Thr Ala Gln Glu Ile Leu His Gln Phe Gly Phe Thr
            420                 425                 430

Gln Thr Gly Ile Ile Ser Ile Glu Arg Lys Pro Cys Asn His Gln Val
        435                 440                 445

Asp Thr Ala Pro Thr Val Val Ala Leu Tyr Asp Tyr Thr Ala Asn Arg
    450                 455                 460

Ser Asp Glu Leu Thr Ile His Arg Gly Asp Ile Ile Arg Val Phe Phe
465                 470                 475                 480

Lys Asp Asn Glu Asp Trp Trp Tyr Gly Ser Ile Gly Lys Gly Gln Glu
                485                 490                 495

Gly Tyr Phe Pro Ala Asn His Val Ala Ser Glu Thr Leu Tyr Gln Glu
            500                 505                 510

Leu Pro Pro Glu Ile Lys Glu Arg Ser Pro Pro Leu Ser Pro Glu Glu
        515                 520                 525

Lys Thr Lys Ile Glu Lys Ser Pro Ala Pro Gln Lys Val Lys
    530                 535                 540


<210> 742
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
      Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436071"

<400> 742
```

```
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                   10                  15


Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30


Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Val Ser Lys
        35                  40                  45


<210> 743
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 124; "

<220>
<221> source
<223> /note="Gene Symbol: AHI1; "

<220>
<221> source
<223> /note="Gene Name:
      Abelson helper integration site 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436516"

<400> 743
Met Pro Thr Ala Glu Ser Glu Ala Lys Val Lys Thr Lys Val Arg Phe
1               5                   10                  15


Glu Glu Leu Leu Lys Thr His Ser Asp Leu Met Arg Glu Lys Lys Lys
            20                  25                  30


Leu Lys Lys Lys Leu Val Arg Ser Glu Glu Asn Ile Ser Val Ser Lys
        35                  40                  45


<210> 744
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 125; "

<220>
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<221> source
<223> /note="Gene Symbol: ABHD14A-ACY1; "

<220>
<221> source
<223> /note="Gene Name:
ABHD14A-ACY1 readthrough; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417688"

<400> 744

```
Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu Gly Gly Ala Arg
1               5                  10                  15

Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr Ser Met Ser Arg
            20                  25                  30

Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu
        35                  40                  45

Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly
    50                  55                  60

Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro
65                  70                  75                  80

Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala His Arg Val Glu
                85                  90                  95

Val Val Leu Leu His Gly Lys Ala Phe Asn Ser His Thr Trp Glu Gln
            100                 105                 110

Leu Gly Thr Leu Gln Leu Leu Ser Gln Arg Gly Tyr Arg Ala Val Ala
        115                 120                 125

Leu Asp Leu Pro Ala His His Ala Gln Arg His Asp Gln Gln Gly Ser
    130                 135                 140

Arg Gly Gly Ala Pro Ile Gly Asp Ala Leu Pro Pro Val Pro Ala Tyr
145                 150                 155                 160

Pro His Cys Pro Ala Gln Ala
                165
```

<210> 745
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 125; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14A-ACY1; "

<220>
<221> source
<223> /note="Gene Name:
ABHD14A-ACY1 readthrough; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420395"

<400> 745
Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu Gly Gly Ala Arg
1 5 10 15

Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr Ser Met Ser Arg
20 25 30

Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu
35 40 45

Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly
50 55 60

Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro
65 70 75 80

Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala His Arg Val Glu
85 90 95

Val Val Leu Leu His Gly Lys Ala Phe Asn Ser His Thr Trp Glu Gln
100 105 110

Leu Gly Thr Leu Gln Leu Leu Ser Gln Arg Gly Tyr Arg Ala Val Ala
115 120 125

Leu Asp Leu Pro Ala His His Ala Gln Arg His Asp Gln Gln Gly Ser
130 135 140

```
Arg Gly Gly Ala Pro Ile Gly Asp Ala Leu Pro Pro Val Pro Ala Tyr
145                 150                 155                 160


Pro His Cys Pro Ala Gln Ala
                165


<210> 746
<211> 509
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 125; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14A-ACY1; "

<220>
<221> source
<223> /note="Gene Name:
      ABHD14A-ACY1 readthrough; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420487"

<400> 746
Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu Gly Gly Ala Arg
1               5                   10                  15


Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr Ser Met Ser Arg
            20                  25                  30


Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu
        35                  40                  45


Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly
    50                  55                  60


Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro
65                  70                  75                  80


Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala His Arg Val Glu
                85                  90                  95
```

```
Val Val Leu Leu His Gly Lys Ala Phe Asn Ser His Thr Trp Glu Gln
            100                 105                 110

Leu Gly Thr Leu Gln Leu Leu Ser Gln Arg Gly Tyr Arg Ala Val Ala
        115                 120                 125

Leu Asp Leu Pro Gly Ala Ala Val Ala Phe Phe Glu Glu Thr Ala Arg
    130                 135                 140

Gln Leu Gly Leu Gly Cys Gln Lys Val Glu Val Ala Pro Gly Tyr Val
145                 150                 155                 160

Val Thr Val Leu Thr Trp Pro Gly Thr Asn Pro Thr Leu Ser Ser Ile
                165                 170                 175

Leu Leu Asn Ser His Thr Asp Val Val Pro Val Phe Lys Glu His Trp
            180                 185                 190

Ser His Asp Pro Phe Glu Ala Phe Lys Asp Ser Glu Gly Tyr Ile Tyr
        195                 200                 205

Ala Arg Gly Ala Gln Asp Met Lys Cys Val Ser Ile Gln Tyr Leu Glu
    210                 215                 220

Ala Val Arg Arg Leu Lys Val Glu Gly His Arg Phe Pro Arg Thr Ile
225                 230                 235                 240

His Met Thr Phe Val Pro Asp Glu Glu Val Gly Gly His Gln Gly Met
                245                 250                 255

Glu Leu Phe Val Gln Arg Pro Glu Phe His Ala Leu Arg Ala Gly Phe
            260                 265                 270

Ala Leu Asp Glu Gly Ile Ala Asn Pro Thr Asp Ala Phe Thr Val Phe
        275                 280                 285

Tyr Ser Glu Arg Ser Pro Trp Trp Val Arg Val Thr Ser Thr Gly Arg
    290                 295                 300

Pro Gly His Ala Ser Arg Phe Met Glu Asp Thr Ala Ala Glu Lys Leu
305                 310                 315                 320

His Lys Val Val Asn Ser Ile Leu Ala Phe Arg Glu Lys Glu Trp Gln
```

```
                325                 330                 335

Arg Leu Gln Ser Asn Pro His Leu Lys Glu Gly Ser Val Thr Ser Val
            340                 345                 350

Asn Leu Thr Lys Leu Glu Gly Gly Val Ala Tyr Asn Val Ile Pro Ala
        355                 360                 365

Thr Met Ser Ala Ser Phe Asp Phe Arg Val Ala Pro Asp Val Asp Phe
    370                 375                 380

Lys Ala Phe Glu Glu Gln Leu Gln Ser Trp Cys Gln Ala Ala Gly Glu
385                 390                 395                 400

Gly Val Thr Leu Glu Phe Ala Gln Lys Trp Met His Pro Gln Val Thr
                405                 410                 415

Pro Thr Asp Asp Ser Asn Pro Trp Trp Ala Ala Phe Ser Arg Val Cys
            420                 425                 430

Lys Asp Met Asn Leu Thr Leu Glu Pro Glu Ile Met Pro Ala Ala Thr
        435                 440                 445

Asp Asn Arg Tyr Ile Arg Ala Val Gly Val Pro Ala Leu Gly Phe Ser
    450                 455                 460

Pro Met Asn Arg Thr Pro Val Leu Leu His Asp His Asp Glu Arg Leu
465                 470                 475                 480

His Glu Ala Val Phe Leu Arg Gly Val Asp Ile Tyr Thr Arg Leu Leu
                485                 490                 495

Pro Ala Leu Ala Ser Val Pro Ala Leu Pro Ser Asp Ser
            500                 505


<210> 747
<211> 405
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 126; "

<220>
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<221> source
<223> /note="Gene Symbol: ABHD1; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q96SE0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000326491"

<400> 747

```
Met Leu Ser Ser Phe Leu Ser Pro Gln Asn Gly Thr Trp Ala Asp Thr
1               5                  10                  15

Phe Ser Leu Leu Leu Ala Leu Ala Val Ala Leu Tyr Leu Gly Tyr Tyr
            20                  25                  30

Trp Ala Cys Val Leu Gln Arg Pro Arg Leu Val Ala Gly Pro Gln Phe
        35                  40                  45

Leu Ala Phe Leu Glu Pro His Cys Ser Ile Thr Thr Glu Thr Phe Tyr
    50                  55                  60

Pro Thr Leu Trp Cys Phe Glu Gly Arg Leu Gln Ser Ile Phe Gln Val
65                  70                  75                  80

Leu Leu Gln Ser Gln Pro Leu Val Leu Tyr Gln Ser Asp Ile Leu Gln
                85                  90                  95

Thr Pro Asp Gly Gly Gln Leu Leu Leu Asp Trp Ala Lys Gln Pro Asp
            100                 105                 110

Ser Ser Gln Asp Pro Asp Pro Thr Thr Gln Pro Ile Val Leu Leu Leu
        115                 120                 125

Pro Gly Ile Thr Gly Ser Ser Gln Glu Thr Tyr Val Leu His Leu Val
    130                 135                 140

Asn Gln Ala Leu Arg Asp Gly Tyr Gln Ala Val Val Phe Asn Asn Arg
145                 150                 155                 160
```

```
Gly Cys Arg Gly Glu Glu Leu Arg Thr His Arg Ala Phe Cys Ala Ser
                165                 170                 175

Asn Thr Glu Asp Leu Glu Thr Val Val Asn His Ile Lys His Arg Tyr
            180                 185                 190

Pro Gln Ala Pro Leu Leu Ala Val Gly Ile Ser Phe Gly Gly Ile Leu
        195                 200                 205

Val Leu Asn His Leu Ala Gln Ala Arg Gln Ala Ala Gly Leu Val Ala
    210                 215                 220

Ala Leu Thr Leu Ser Ala Cys Trp Asp Ser Phe Glu Thr Thr Arg Ser
225                 230                 235                 240

Leu Glu Thr Pro Leu Asn Ser Leu Leu Phe Asn Gln Pro Leu Thr Ala
                245                 250                 255

Gly Leu Cys Gln Leu Val Glu Arg Asn Arg Lys Val Ile Glu Lys Val
            260                 265                 270

Val Asp Ile Asp Phe Val Leu Gln Ala Arg Thr Ile Arg Gln Phe Asp
        275                 280                 285

Glu Arg Tyr Thr Ser Val Ala Phe Gly Tyr Gln Asp Cys Val Thr Tyr
    290                 295                 300

Tyr Lys Ala Ala Ser Pro Arg Thr Lys Ile Asp Ala Ile Arg Ile Pro
305                 310                 315                 320

Val Leu Tyr Leu Ser Ala Ala Asp Asp Pro Phe Ser Pro Val Cys Ala
                325                 330                 335

Leu Pro Ile Gln Ala Ala Gln His Ser Pro Tyr Val Ala Leu Leu Ile
            340                 345                 350

Thr Ala Arg Gly Gly His Ile Gly Phe Leu Glu Gly Leu Leu Pro Trp
        355                 360                 365

Gln His Trp Tyr Met Ser Arg Leu Leu His Gln Tyr Ala Lys Ala Ile
    370                 375                 380
```

```
Phe Gln Asp Pro Glu Gly Leu Pro Asp Leu Arg Ala Leu Leu Pro Ser
385                 390                 395                 400


Glu Asp Arg Asn Ser
                405


<210> 748
<211> 102
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 126; "

<220>
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<223> /note="Gene Symbol: ABHD1; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000390390"

<400> 748
Met Ala Pro Gly Gln Thr Pro Ser Leu Cys Ser Trp Leu Leu Pro Leu
1               5                   10                  15


Pro Ser Thr Trp Ala Thr Thr Gly His Val Cys Phe Ser Asp Ile Leu
            20                  25                  30


Gln Thr Pro Asp Gly Gly Gln Leu Leu Leu Asp Trp Ala Lys Gln Pro
        35                  40                  45


Asp Ser Ser Gln Asp Pro Asp Pro Thr Thr Gln Pro Ile Val Leu Leu
    50                  55                  60


Leu Pro Gly Ile Thr Gly Ser Ser Gln Glu Thr Tyr Val Leu His Leu
65                  70                  75                  80


Val Asn Gln Ala Leu Arg Asp Gly Tyr Gln Pro Thr Gly Leu Phe Val
                85                  90                  95


Pro Ala Ile Leu Lys Ile
```

100

<210> 749
<211> 177
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 126; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 1; "

<220>
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<223> /note="ENSP ID: ENSP00000397522"

<400> 749
Met Ala Pro Gly Gln Thr Pro Ser Leu Cys Ser Trp Leu Leu Pro Leu
1 5 10 15

Pro Ser Thr Trp Ala Thr Thr Gly His Val Cys Phe Ser Asp Ile Leu
20 25 30

Gln Thr Pro Asp Gly Gly Gln Leu Leu Leu Asp Trp Ala Lys Gln Pro
35 40 45

Asp Ser Ser Gln Asp Pro Asp Pro Thr Thr Gln Pro Ile Val Leu Leu
50 55 60

Leu Pro Gly Ile Thr Gly Ser Ser Gln Glu Thr Tyr Val Leu His Leu
65 70 75 80

Val Asn Gln Ala Leu Arg Asp Gly Tyr Gln Ala Val Val Phe Asn Asn
85 90 95

Arg Gly Cys Arg Gly Glu Glu Leu Arg Thr His Arg Ala Phe Cys Ala
100 105 110

Ser Asn Thr Glu Asp Leu Glu Thr Val Val Asn His Ile Lys His Arg
115 120 125

```
Tyr Pro Gln Ala Pro Leu Leu Ala Val Gly Ile Ser Phe Gly Gly Ile
    130                 135                 140

Leu Val Leu Asn His Leu Ala Gln Ala Arg Gln Ala Ala Gly Leu Val
145                 150                 155                 160

Ala Ala Leu Thr Leu Ser Ala Cys Trp Asp Ser Phe Glu Thr Thr Arg
                165                 170                 175

Ser
```

<210> 750
<211> 305
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ABHD1; "

<220>
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<223> /note="Gene Name:
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domain containing 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q96SE0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410756"

<400> 750

```
Met Leu Ser Ser Phe Leu Ser Pro Gln Asn Gly Thr Trp Ala Asp Thr
1               5                   10                  15

Phe Ser Leu Leu Leu Ala Leu Ala Val Ala Leu Tyr Leu Gly Tyr Tyr
            20                  25                  30

Trp Ala Cys Val Leu Gln Arg Pro Arg Leu Val Ala Gly Pro Gln Phe
        35                  40                  45
```

```
Leu Ala Phe Leu Glu Pro His Cys Ser Ile Thr Thr Glu Thr Phe Tyr
    50                  55                  60

Pro Thr Leu Trp Cys Phe Glu Gly Arg Leu Gln Ser Ile Phe Gln Val
65                  70                  75                  80

Leu Leu Gln Ser Gln Pro Leu Val Leu Tyr Gln Ser Asp Ile Leu Gln
                85                  90                  95

Thr Pro Asp Gly Gly Gln Leu Leu Leu Asp Trp Ala Lys Gln Pro Asp
            100                 105                 110

Ser Ser Gln Asp Pro Asp Pro Thr Thr Gln Pro Ile Val Leu Leu Leu
        115                 120                 125

Pro Gly Ile Thr Gly Ser Ser Gln Glu Thr Tyr Val Leu His Leu Val
    130                 135                 140

Asn Gln Ala Leu Arg Asp Gly Tyr Gln Ala Val Val Phe Asn Asn Arg
145                 150                 155                 160

Gly Cys Arg Gly Glu Glu Leu Arg Thr His Arg Ala Phe Cys Ala Ser
                165                 170                 175

Asn Thr Glu Asp Leu Glu Thr Val Val Asn His Ile Lys His Arg Tyr
            180                 185                 190

Pro Gln Ala Pro Leu Leu Ala Val Gly Ile Ser Phe Gly Gly Ile Leu
        195                 200                 205

Val Leu Asn His Leu Ala Gln Ala Arg Gln Ala Ala Gly Leu Val Ala
    210                 215                 220

Ala Leu Thr Leu Ser Ala Cys Trp Asp Ser Phe Glu Thr Thr Arg Ser
225                 230                 235                 240

Leu Glu Thr Pro Leu Asn Ser Leu Leu Phe Asn Gln Pro Leu Thr Ala
                245                 250                 255

Gly Leu Cys Gln Leu Val Glu Arg Leu Ser Tyr Gly Lys Thr Cys Arg
            260                 265                 270
```

```
Pro Val Gln Ser Ala Ser Leu Met Ser Ala Thr His Leu Trp Pro Leu
        275                 280                 285


Asp Ile Lys Thr Val Leu Pro Thr Thr Lys Gln Gln Ala Leu Glu Pro
    290                 295                 300


Arg
305


<210> 751
<211> 305
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 126; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD1; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96SE0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481238"

<400> 751
Met Leu Ser Ser Phe Leu Ser Pro Gln Asn Gly Thr Trp Ala Asp Thr
1               5                   10                  15


Phe Ser Leu Leu Leu Ala Leu Ala Val Ala Leu Tyr Leu Gly Tyr Tyr
            20                  25                  30


Trp Ala Cys Val Leu Gln Arg Pro Arg Leu Val Ala Gly Pro Gln Phe
        35                  40                  45


Leu Ala Phe Leu Glu Pro His Cys Ser Ile Thr Thr Glu Thr Phe Tyr
    50                  55                  60


Pro Thr Leu Trp Cys Phe Glu Gly Arg Leu Gln Ser Ile Phe Gln Val
```

```
65                  70                  75                  80

Leu Leu Gln Ser Gln Pro Leu Val Leu Tyr Gln Ser Asp Ile Leu Gln
                85                  90                  95

Thr Pro Asp Gly Gly Gln Leu Leu Leu Asp Trp Ala Lys Gln Pro Asp
            100                 105                 110

Ser Ser Gln Asp Pro Asp Pro Thr Thr Gln Pro Ile Val Leu Leu Leu
        115                 120                 125

Pro Gly Ile Thr Gly Ser Ser Gln Glu Thr Tyr Val Leu His Leu Val
    130                 135                 140

Asn Gln Ala Leu Arg Asp Gly Tyr Gln Ala Val Val Phe Asn Asn Arg
145                 150                 155                 160

Gly Cys Arg Gly Glu Glu Leu Arg Thr His Arg Ala Phe Cys Ala Ser
                165                 170                 175

Asn Thr Glu Asp Leu Glu Thr Val Val Asn His Ile Lys His Arg Tyr
            180                 185                 190

Pro Gln Ala Pro Leu Leu Ala Val Gly Ile Ser Phe Gly Gly Ile Leu
        195                 200                 205

Val Leu Asn His Leu Ala Gln Ala Arg Gln Ala Ala Gly Leu Val Ala
    210                 215                 220

Ala Leu Thr Leu Ser Ala Cys Trp Asp Ser Phe Glu Thr Thr Arg Ser
225                 230                 235                 240

Leu Glu Thr Pro Leu Asn Ser Leu Leu Phe Asn Gln Pro Leu Thr Ala
                245                 250                 255

Gly Leu Cys Gln Leu Val Glu Arg Leu Ser Tyr Gly Lys Thr Cys Arg
            260                 265                 270

Pro Val Gln Ser Ala Ser Leu Met Ser Ala Thr His Leu Trp Pro Leu
        275                 280                 285

Asp Ile Lys Thr Val Leu Pro Thr Thr Lys Gln Gln Ala Leu Glu Pro
    290                 295                 300
```

Arg
305

<210> 752
<211> 306
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 127; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD10; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 10; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUJ1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000273359"

<400> 752
Met Ala Val Ala Arg Leu Ala Ala Val Ala Ala Trp Val Pro Cys Arg
1   5   10   15

Ser Trp Gly Trp Ala Ala Val Pro Phe Gly Pro His Arg Gly Leu Ser
            20   25   30

Val Leu Leu Ala Arg Ile Pro Gln Arg Ala Pro Arg Trp Leu Pro Ala
        35   40   45

Cys Arg Gln Lys Thr Ser Leu Ser Phe Leu Asn Arg Pro Asp Leu Pro
    50   55   60

Asn Leu Ala Tyr Lys Lys Leu Lys Gly Lys Ser Pro Gly Ile Ile Phe
65   70   75   80

Ile Pro Gly Tyr Leu Ser Tyr Met Asn Gly Thr Lys Ala Leu Ala Ile
                85   90   95

```
Glu Glu Phe Cys Lys Ser Leu Gly His Ala Cys Ile Arg Phe Asp Tyr
            100                 105                 110

Ser Gly Val Gly Ser Ser Asp Gly Asn Ser Glu Glu Ser Thr Leu Gly
        115                 120                 125

Lys Trp Arg Lys Asp Val Leu Ser Ile Ile Asp Asp Leu Ala Asp Gly
    130                 135                 140

Pro Gln Ile Leu Val Gly Ser Ser Leu Gly Gly Trp Leu Met Leu His
145                 150                 155                 160

Ala Ala Ile Ala Arg Pro Glu Lys Val Val Ala Leu Ile Gly Val Ala
                165                 170                 175

Thr Ala Ala Asp Thr Leu Val Thr Lys Phe Asn Gln Leu Pro Val Glu
            180                 185                 190

Leu Lys Lys Glu Val Glu Met Lys Gly Val Trp Ser Met Pro Ser Lys
        195                 200                 205

Tyr Ser Glu Glu Gly Val Tyr Asn Val Gln Tyr Ser Phe Ile Lys Glu
    210                 215                 220

Ala Glu His His Cys Leu Leu His Ser Pro Ile Pro Val Asn Cys Pro
225                 230                 235                 240

Ile Arg Leu Leu His Gly Met Lys Asp Asp Ile Val Pro Trp His Thr
                245                 250                 255

Ser Met Gln Val Ala Asp Arg Val Leu Ser Thr Asp Val Asp Val Ile
            260                 265                 270

Leu Arg Lys His Ser Asp His Arg Met Arg Glu Lys Ala Asp Ile Gln
        275                 280                 285

Leu Leu Val Tyr Thr Ile Asp Asp Leu Ile Asp Lys Leu Ser Thr Ile
    290                 295                 300

Val Asn
305
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<210> 753
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 127; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD10; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417880"

<400> 753
Met Ala Val Ala Arg Leu Ala Ala Val Ala Ala Trp Val Pro Cys Arg
1 5 10 15

Ser Trp Gly Trp Ala Ala Val Pro Phe Gly Pro His Arg Gly Leu Ser
20 25 30

Val Leu Leu Ala Arg Ile Pro Gln Arg Ala Pro Arg Trp Leu Pro Asp
35 40 45

Ser Cys Trp Ile
50

<210> 754
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 127; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD10; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase

domain containing 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418162"

<400> 754
Met Ala Val Ala Arg Leu Ala Ala Val Ala Ala Trp Val Pro Cys Arg
1   5   10   15

Ser Trp Gly Trp Ala Ala Val Pro Phe Gly Pro His Arg Gly Leu Ser
            20   25   30

Val Leu Leu Ala Arg Ile Pro Gln Arg Ala Pro Arg Trp Leu Pro Gly
        35   40   45

Leu Ile Thr Gln Glu Leu Glu Val Gln Met Val Thr Gln Arg Lys Ala
    50   55   60

His Trp Gly Asn Gly Glu Lys Met Phe Phe Leu
65   70   75

<210> 755
<211> 205
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 127; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD10; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 10; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUJ1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418973"

<400> 755
Met Ala Val Ala Arg Leu Ala Ala Val Ala Ala Trp Val Pro Cys Arg
1   5   10   15

```
Ser Trp Gly Trp Ala Ala Val Pro Phe Gly Pro His Arg Gly Leu Ser
            20                  25                  30

Val Leu Leu Ala Arg Ile Pro Gln Arg Ala Pro Arg Trp Leu Pro Ala
        35                  40                  45

Cys Arg Gln Lys Thr Ser Leu Ser Phe Leu Asn Arg Pro Asp Leu Pro
    50                  55                  60

Asn Leu Ala Tyr Lys Lys Leu Lys Gly Lys Ser Pro Gly Ile Ile Phe
65                  70                  75                  80

Ile Pro Gly Tyr Leu Ser Tyr Met Asn Gly Thr Lys Ala Leu Ala Ile
                85                  90                  95

Glu Glu Phe Cys Lys Ser Leu Gly His Ala Cys Ile Arg Phe Asp Tyr
            100                 105                 110

Ser Gly Val Gly Ser Ser Asp Gly Asn Ser Glu Glu Ser Thr Leu Gly
        115                 120                 125

Lys Trp Arg Lys Asp Val Leu Ser Ile Ile Asp Asp Leu Ala Asp Gly
    130                 135                 140

Pro Gln Ile Leu Val Gly Ser Ser Leu Gly Gly Trp Leu Met Leu His
145                 150                 155                 160

Ala Ala Ile Ala Arg Pro Glu Lys Val Val Ala Leu Ile Gly Val Ala
                165                 170                 175

Thr Ala Ala Asp Thr Leu Val Thr Lys Phe Asn Gln Leu Pro Val Glu
            180                 185                 190

Asp Ser Gly Arg Lys Asn Tyr Ile Ser Leu His Ser Ala
        195                 200                 205


<210> 756
<211> 315
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 128; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD11; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 11; "

<220>
<221> source
<223> /note="Uniprot ID: Q8NFV4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000222800"

<400> 756

```
Met Arg Ala Gly Gln Gln Leu Ala Ser Met Leu Arg Trp Thr Arg Ala
1               5                  10                  15

Trp Arg Leu Pro Arg Glu Gly Leu Gly Pro His Gly Pro Ser Phe Ala
            20                  25                  30

Arg Val Pro Val Ala Pro Ser Ser Ser Ser Gly Gly Arg Gly Gly Ala
        35                  40                  45

Glu Pro Arg Pro Leu Pro Leu Ser Tyr Arg Leu Leu Asp Gly Glu Ala
    50                  55                  60

Ala Leu Pro Ala Val Val Phe Leu His Gly Leu Phe Gly Ser Lys Thr
65                  70                  75                  80

Asn Phe Asn Ser Ile Ala Lys Ile Leu Ala Gln Gln Thr Gly Arg Arg
                85                  90                  95

Val Leu Thr Val Asp Ala Arg Asn His Gly Asp Ser Pro His Ser Pro
            100                 105                 110

Asp Met Ser Tyr Glu Ile Met Ser Gln Asp Leu Gln Asp Leu Leu Pro
        115                 120                 125

Gln Leu Gly Leu Val Pro Cys Val Val Val Gly His Ser Met Gly Gly
    130                 135                 140
```

```
Lys Thr Ala Met Leu Leu Ala Leu Gln Arg Pro Glu Leu Val Glu Arg
145                 150                 155                 160

Leu Ile Ala Val Asp Ile Ser Pro Val Glu Ser Thr Gly Val Ser His
                165                 170                 175

Phe Ala Thr Tyr Val Ala Ala Met Arg Ala Ile Asn Ile Ala Asp Glu
            180                 185                 190

Leu Pro Arg Ser Arg Ala Arg Lys Leu Ala Asp Glu Gln Leu Ser Ser
        195                 200                 205

Val Ile Gln Asp Met Ala Val Arg Gln His Leu Leu Thr Asn Leu Val
    210                 215                 220

Glu Val Asp Gly Arg Phe Val Trp Arg Val Asn Leu Asp Ala Leu Thr
225                 230                 235                 240

Gln His Leu Asp Lys Ile Leu Ala Phe Pro Gln Arg Gln Glu Ser Tyr
                245                 250                 255

Leu Gly Pro Thr Leu Phe Leu Leu Gly Gly Asn Ser Gln Phe Val His
            260                 265                 270

Pro Ser His His Pro Glu Ile Met Arg Leu Phe Pro Arg Ala Gln Met
        275                 280                 285

Gln Thr Val Pro Asn Ala Gly His Trp Ile His Ala Asp Arg Pro Gln
    290                 295                 300

Asp Phe Ile Ala Ala Ile Arg Gly Phe Leu Val
305                 310                 315


<210> 757
<211> 258
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 128; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD11; "
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<220>
<221> source
<223> /note="Gene Name:
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domain containing 11; "

<220>
<221> source
<223> /note="Uniprot ID: Q8NFV4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378579"

<400> 757

```
Met Arg Ala Gly Gln Gln Leu Ala Ser Met Leu Arg Trp Thr Arg Ala
1               5                  10                  15

Trp Arg Leu Pro Arg Glu Gly Leu Gly Pro His Gly Pro Ser Phe Ala
            20                  25                  30

Arg Val Pro Val Ala Pro Ser Ser Ser Ser Gly Gly Arg Gly Gly Ala
        35                  40                  45

Glu Pro Arg Pro Leu Pro Leu Ser Tyr Arg Leu Leu Asp Gly Glu Ala
    50                  55                  60

Ala Leu Pro Ala Val Val Phe Leu His Gly Leu Phe Gly Ser Lys Thr
65                  70                  75                  80

Asn Phe Asn Ser Ile Ala Lys Ile Leu Ala Gln Gln Thr Gly Arg Arg
                85                  90                  95

Val Leu Thr Val Asp Ala Arg Asn His Gly Asp Ser Pro His Ser Pro
            100                 105                 110

Asp Met Ser Tyr Glu Ile Met Ser Gln Asp Leu Gln Asp Leu Leu Pro
        115                 120                 125

Gln Leu Gly Leu Val Pro Cys Val Val Val Gly His Ser Met Gly Gly
    130                 135                 140

Lys Thr Ala Met Leu Leu Ala Leu Gln Arg Asp Met Ala Val Arg Gln
145                 150                 155                 160

His Leu Leu Thr Asn Leu Val Glu Val Asp Gly Arg Phe Val Trp Arg
                165                 170                 175
```

```
Val Asn Leu Asp Ala Leu Thr Gln His Leu Asp Lys Ile Leu Ala Phe
            180                 185                 190

Pro Gln Arg Gln Glu Ser Tyr Leu Gly Pro Thr Leu Phe Leu Leu Gly
        195                 200                 205

Gly Asn Ser Gln Phe Val His Pro Ser His His Pro Glu Ile Met Arg
    210                 215                 220

Leu Phe Pro Arg Ala Gln Met Gln Thr Val Pro Asn Ala Gly His Trp
225                 230                 235                 240

Ile His Ala Asp Arg Pro Gln Asp Phe Ile Ala Ala Ile Arg Gly Phe
                245                 250                 255

Leu Val
```

<210> 758
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 128; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD11; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387908"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 758
Xaa Arg Glu Gly Leu Gly Pro His Gly Pro Ser Phe Ala Arg Val Pro

```
1               5                   10                  15

Val Ala Pro Ser Ser Ser Ser Gly Gly Arg Gly Gly Ala Glu Pro Arg
            20                  25                  30

Pro Leu Pro Leu Ser Tyr Arg Leu Leu Asp Gly Glu Ala Ala Leu Pro
        35                  40                  45

Ala Val Val Phe Leu His Gly Leu Phe Gly Ser Lys Thr Asn Phe Asn
    50                  55                  60

Ser Ile Ala Lys Ile Leu Ala Gln Gln Thr Gly Arg Arg Val Leu Thr
65                  70                  75                  80

Val Asp Ala Arg Asn His Gly Asp Ser Pro His Ser Pro Asp Met Ser
                85                  90                  95

Tyr Glu Ile Met Ser Gln Asp Leu Gln Asp Leu Leu Pro Gln Leu Gly
            100                 105                 110

Leu Val Pro Cys Val Val Val Gly His Ser Met Gly Gly Lys Thr Ala
        115                 120                 125

Met Leu Leu Ala Leu Gln Arg Val Ile His Pro Arg Cys Pro Gly Trp
    130                 135                 140

Tyr Cys Arg Pro Gly Pro Val Lys Gly Arg Val Ala Pro Pro Asp Arg
145                 150                 155                 160

Thr Arg Asn Leu Pro Gln Leu Leu His Pro His Arg Thr Trp Pro Cys
                165                 170                 175

Gly Ser Thr Cys Ser Leu Thr Trp
            180


<210> 759
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 128; "

<220>
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<221> source
<223> /note="Gene Symbol: ABHD11; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 11; "

<220>
<221> source
<223> /note="Uniprot ID: Q8NFV4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392945"

<400> 759
Met Arg Ala Gly Gln Gln Leu Ala Ser Met Leu Arg Trp Thr Arg Ala
1   5   10   15

Trp Arg Leu Pro Arg Glu Gly Leu Gly Pro His Gly Pro Ser Phe Ala
            20   25   30

Arg Val Pro Val Ala Pro Ser Ser Ser Ser Gly Gly Arg Gly Gly Ala
        35   40   45

Glu Pro Arg Pro Leu Pro Leu Ser Tyr Arg Leu Leu Asp Gly Glu Ala
    50   55   60

Ala Leu Pro Ala Val Val Phe Leu His Gly Leu Phe Gly Ser Lys Thr
65   70   75   80

Asn Phe Asn Ser Ile Ala Lys Ile Leu Ala Gln Gln Thr Gly Arg Ala
                85   90   95

Asp Gly Gly Cys Ser
            100

<210> 760
<211> 159
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 128; "

<220>
<221> source

<223> /note="Gene Symbol: ABHD11; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397666"

<400> 760
Met Arg Ala Gly Gln Gln Leu Ala Ser Met Leu Arg Trp Thr Arg Ala
1 5 10 15

Trp Arg Leu Pro Arg Glu Gly Leu Gly Pro His Gly Pro Ser Phe Ala
20 25 30

Arg Val Pro Val Ala Pro Ser Ser Ser Ser Gly Gly Arg Gly Gly Ala
35 40 45

Glu Pro Arg Pro Leu Pro Leu Ser Tyr Arg Leu Leu Asp Gly Glu Ala
50 55 60

Ala Leu Pro Ala Val Val Phe Leu His Gly Leu Phe Gly Ser Lys Thr
65 70 75 80

Asn Phe Asn Ser Ile Ala Lys Ile Leu Ala Gln Gln Thr Gly Arg Arg
85 90 95

Val Leu Thr Val Asp Ala Arg Asn His Gly Asp Ser Pro His Ser Pro
100 105 110

Asp Met Ser Tyr Glu Ile Met Ser Gln Asp Leu Gln Asp Leu Leu Pro
115 120 125

Gln Leu Gly Leu Val Pro Cys Val Val Val Gly His Ser Met Gly Gly
130 135 140

Lys Thr Ala Met Leu Leu Ala Leu Gln Arg Ser Gln Pro Pro Pro
145 150 155

<210> 761
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 128; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD11; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410536"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 761
Xaa Pro Leu Pro Leu Ser Tyr Arg Leu Leu Asp Gly Glu Ala Ala Leu
1 5 10 15

Pro Ala Val Val Phe Leu His Gly Leu Phe Gly Ser Lys Thr Asn Phe
20 25 30

Asn Ser Ile Ala Lys Ile Leu Ala Gln Gln Thr Gly Arg Arg Val Leu
35 40 45

Thr Val Asp Ala Arg Asn His Gly Asp Ser Pro His Ser Pro Asp Met
50 55 60

Ser Tyr Glu Ile Met Ser Gln Asp Leu Gln Asp Leu Leu Pro Gln Leu
65 70 75 80

Gly Leu Val Pro Cys Val Val Val Gly His Ser Met Gly Gly Lys Thr
85 90 95

Ala Met Leu Leu Ala Leu Gln Arg Ile Ser Ala Gln Trp Lys Ala Gln
100 105 110

Val Ser Pro Thr Leu Gln Pro Met Trp Gln Pro
115 120

<210> 762
<211> 308
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 128; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD11; "

<220>
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<400> 762
Met Arg Ala Gly Gln Gln Leu Ala Ser Met Leu Arg Trp Thr Arg Ala
1   5   10   15

Trp Arg Leu Pro Arg Glu Gly Leu Gly Pro His Gly Pro Ser Phe Ala
            20   25   30

Arg Val Pro Val Ala Pro Ser Ser Ser Ser Gly Gly Arg Gly Gly Ala
        35   40   45

Glu Pro Arg Leu Leu Asp Gly Glu Ala Ala Leu Pro Ala Val Val Phe
    50   55   60

Leu His Gly Leu Phe Gly Ser Lys Thr Asn Phe Asn Ser Ile Ala Lys
65   70   75   80

Ile Leu Ala Gln Gln Thr Gly Arg Arg Val Leu Thr Val Asp Ala Arg
                85   90   95

Asn His Gly Asp Ser Pro His Ser Pro Asp Met Ser Tyr Glu Ile Met
            100   105   110

```
Ser Gln Asp Leu Gln Asp Leu Leu Pro Gln Leu Gly Leu Val Pro Cys
        115                 120                 125

Val Val Val Gly His Ser Met Gly Gly Lys Thr Ala Met Leu Leu Ala
    130                 135                 140

Leu Gln Arg Pro Glu Leu Val Glu Arg Leu Ile Ala Val Asp Ile Ser
145                 150                 155                 160

Pro Val Glu Ser Thr Gly Val Ser His Phe Ala Thr Tyr Val Ala Ala
                165                 170                 175

Met Arg Ala Ile Asn Ile Ala Asp Glu Leu Pro Arg Ser Arg Ala Arg
            180                 185                 190

Lys Leu Ala Asp Glu Gln Leu Ser Ser Val Ile Gln Asp Met Ala Val
        195                 200                 205

Arg Gln His Leu Leu Thr Asn Leu Val Glu Val Asp Gly Arg Phe Val
    210                 215                 220

Trp Arg Val Asn Leu Asp Ala Leu Thr Gln His Leu Asp Lys Ile Leu
225                 230                 235                 240

Ala Phe Pro Gln Arg Gln Glu Ser Tyr Leu Gly Pro Thr Leu Phe Leu
                245                 250                 255

Leu Gly Gly Asn Ser Gln Phe Val His Pro Ser His His Pro Glu Ile
            260                 265                 270

Met Arg Leu Phe Pro Arg Ala Gln Met Gln Thr Val Pro Asn Ala Gly
        275                 280                 285

His Trp Ile His Ala Asp Arg Pro Gln Asp Phe Ile Ala Ala Ile Arg
    290                 295                 300

Gly Phe Leu Val
305
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<210> 763
<211> 87
<212> PRT
<213> Homo sapiens

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<400> 763
Leu Arg Trp Thr Arg Ala Trp Arg Leu Pro Arg Glu Gly Leu Gly Pro
1 5 10 15

His Gly Pro Ser Phe Ala Arg Val Pro Val Ala Pro Ser Ser Ser Ser
20 25 30

Gly Gly Arg Gly Gly Ala Glu Pro Arg Pro Leu Pro Leu Ser Tyr Arg
35 40 45

Leu Leu Asp Gly Glu Ala Ala Leu Pro Ala Val Val Phe Leu His Gly
50 55 60

Leu Phe Gly Ser Lys Thr Asn Phe Asn Ser Ile Ala Lys Ile Leu Ala
65 70 75 80

Gln Gln Thr Gly Arg Arg Gly
85

<210> 764
<211> 398
<212> PRT
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<220>
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<220>
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<400> 764

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Met Arg Lys Arg Thr Glu Pro Val Ala Leu Glu His Glu Arg Cys Ala
1               5                  10                  15

Ala Ala Gly Ser Ser Ser Ser Gly Ser Ala Ala Ala Ala Leu Asp Ala
            20                  25                  30

Asp Cys Arg Leu Lys Gln Asn Leu Arg Leu Thr Gly Pro Ala Ala Ala
        35                  40                  45

Glu Pro Arg Cys Ala Ala Asp Ala Gly Met Lys Arg Ala Leu Gly Arg
    50                  55                  60

Arg Lys Gly Val Trp Leu Arg Leu Arg Lys Ile Leu Phe Cys Val Leu
65                  70                  75                  80

Gly Leu Tyr Ile Ala Ile Pro Phe Leu Ile Lys Leu Cys Pro Gly Ile
                85                  90                  95

Gln Ala Lys Leu Ile Phe Leu Asn Phe Val Arg Val Pro Tyr Phe Ile
            100                 105                 110

Asp Leu Lys Lys Pro Gln Asp Gln Gly Leu Asn His Thr Cys Asn Tyr
        115                 120                 125

Tyr Leu Gln Pro Glu Glu Asp Val Thr Ile Gly Val Trp His Thr Val
    130                 135                 140

Pro Ala Val Trp Trp Lys Asn Ala Gln Gly Lys Asp Gln Met Trp Tyr
145                 150                 155                 160

Glu Asp Ala Leu Ala Ser Ser His Pro Ile Ile Leu Tyr Leu His Gly
                165                 170                 175
```

```
Asn Ala Gly Thr Arg Gly Gly Asp His Arg Val Glu Leu Tyr Lys Val
            180                 185                 190

Leu Ser Ser Leu Gly Tyr His Val Val Thr Phe Asp Tyr Arg Gly Trp
        195                 200                 205

Gly Asp Ser Val Gly Thr Pro Ser Glu Arg Gly Met Thr Tyr Asp Ala
    210                 215                 220

Leu His Val Phe Asp Trp Ile Lys Ala Arg Ser Gly Asp Asn Pro Val
225                 230                 235                 240

Tyr Ile Trp Gly His Ser Leu Gly Thr Gly Val Ala Thr Asn Leu Val
                245                 250                 255

Arg Arg Leu Cys Glu Arg Glu Thr Pro Pro Asp Ala Leu Ile Leu Glu
            260                 265                 270

Ser Pro Phe Thr Asn Ile Arg Glu Glu Ala Lys Ser His Pro Phe Ser
        275                 280                 285

Val Ile Tyr Arg Tyr Phe Pro Gly Phe Asp Trp Phe Phe Leu Asp Pro
    290                 295                 300

Ile Thr Ser Ser Gly Ile Lys Phe Ala Asn Asp Glu Asn Val Lys His
305                 310                 315                 320

Ile Ser Cys Pro Leu Leu Ile Leu His Ala Glu Asp Asp Pro Val Val
                325                 330                 335

Pro Phe Gln Leu Gly Arg Lys Leu Tyr Ser Ile Ala Ala Pro Ala Arg
            340                 345                 350

Ser Phe Arg Asp Phe Lys Val Gln Phe Val Pro Phe His Ser Asp Leu
        355                 360                 365

Gly Tyr Arg His Lys Tyr Ile Tyr Lys Ser Pro Glu Leu Pro Arg Ile
    370                 375                 380

Leu Arg Glu Phe Leu Gly Lys Ser Glu Pro Glu His Gln His
385                 390                 395
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<210> 765
<211> 404
<212> PRT
<213> Homo sapiens

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<220>
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<223> /note="Gene Symbol: ABHD12; "

<220>
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<223> /note="Gene Name:
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domain containing 12; "

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<223> /note="Uniprot ID: Q8N2K0; "

<220>
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<223> /note="ENSP ID: ENSP00000365725"

<400> 765
Met Arg Lys Arg Thr Glu Pro Val Ala Leu Glu His Glu Arg Cys Ala
1   5   10   15

Ala Ala Gly Ser Ser Ser Ser Gly Ser Ala Ala Ala Ala Leu Asp Ala
            20   25   30

Asp Cys Arg Leu Lys Gln Asn Leu Arg Leu Thr Gly Pro Ala Ala Ala
        35   40   45

Glu Pro Arg Cys Ala Ala Asp Ala Gly Met Lys Arg Ala Leu Gly Arg
    50   55   60

Arg Lys Gly Val Trp Leu Arg Leu Arg Lys Ile Leu Phe Cys Val Leu
65   70   75   80

Gly Leu Tyr Ile Ala Ile Pro Phe Leu Ile Lys Leu Cys Pro Gly Ile
                85   90   95

Gln Ala Lys Leu Ile Phe Leu Asn Phe Val Arg Val Pro Tyr Phe Ile
            100   105   110

Asp Leu Lys Lys Pro Gln Asp Gln Gly Leu Asn His Thr Cys Asn Tyr

```
        115                 120                 125

Tyr Leu Gln Pro Glu Glu Asp Val Thr Ile Gly Val Trp His Thr Val
    130                 135                 140

Pro Ala Val Trp Trp Lys Asn Ala Gln Gly Lys Asp Gln Met Trp Tyr
145                 150                 155                 160

Glu Asp Ala Leu Ala Ser Ser His Pro Ile Ile Leu Tyr Leu His Gly
                165                 170                 175

Asn Ala Gly Thr Arg Gly Gly Asp His Arg Val Glu Leu Tyr Lys Val
            180                 185                 190

Leu Ser Ser Leu Gly Tyr His Val Val Thr Phe Asp Tyr Arg Gly Trp
        195                 200                 205

Gly Asp Ser Val Gly Thr Pro Ser Glu Arg Gly Met Thr Tyr Asp Ala
    210                 215                 220

Leu His Val Phe Asp Trp Ile Lys Ala Arg Ser Gly Asp Asn Pro Val
225                 230                 235                 240

Tyr Ile Trp Gly His Ser Leu Gly Thr Gly Val Ala Thr Asn Leu Val
                245                 250                 255

Arg Arg Leu Cys Glu Arg Glu Thr Pro Pro Asp Ala Leu Ile Leu Glu
            260                 265                 270

Ser Pro Phe Thr Asn Ile Arg Glu Glu Ala Lys Ser His Pro Phe Ser
        275                 280                 285

Val Ile Tyr Arg Tyr Phe Pro Gly Phe Asp Trp Phe Phe Leu Asp Pro
    290                 295                 300

Ile Thr Ser Ser Gly Ile Lys Phe Ala Asn Asp Glu Asn Val Lys His
305                 310                 315                 320

Ile Ser Cys Pro Leu Leu Ile Leu His Ala Glu Asp Asp Pro Val Val
                325                 330                 335

Pro Phe Gln Leu Gly Arg Lys Leu Tyr Ser Ile Ala Ala Pro Ala Arg
            340                 345                 350
```

```
Ser Phe Arg Asp Phe Lys Val Gln Phe Val Pro Phe His Ser Asp Leu
        355                 360                 365

Gly Tyr Arg His Lys Tyr Ile Tyr Lys Ser Pro Glu Leu Pro Arg Ile
    370                 375                 380

Leu Arg Pro Gln Gln Gly Pro Gly Ser Ser Pro Asp Pro Ser Met Trp
385                 390                 395                 400

Ser Glu Leu Val
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<210> 766
<211> 187
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<400> 766

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Met Ser Gly Gly Gly His Gly Gly Val Cys Phe Leu Cys Cys Ile Leu
1               5                  10                  15

Leu Gln Gly Arg Lys Gly Val Trp Leu Arg Leu Arg Lys Ile Leu Phe
            20                  25                  30

Cys Val Leu Gly Leu Tyr Ile Ala Ile Pro Phe Leu Ile Lys Leu Cys
        35                  40                  45

Pro Gly Ile Gln Ala Lys Leu Ile Phe Leu Asn Phe Val Arg Val Pro
    50                  55                  60
```

```
Tyr Phe Ile Asp Leu Lys Lys Pro Gln Asp Gln Gly Leu Asn His Thr
65                  70                  75                  80

Cys Asn Tyr Tyr Leu Gln Pro Glu Glu Asp Val Thr Ile Gly Val Trp
                85                  90                  95

His Thr Val Pro Ala Val Trp Trp Lys Asn Ala Gln Gly Lys Asp Gln
            100                 105                 110

Met Trp Tyr Glu Asp Ala Leu Ala Ser Ser His Pro Ile Ile Leu Tyr
        115                 120                 125

Leu His Gly Asn Ala Gly Thr Arg Gly Gly Asp His Arg Val Glu Leu
    130                 135                 140

Tyr Lys Val Leu Ser Ser Leu Gly Tyr His Val Val Thr Phe Asp Tyr
145                 150                 155                 160

Arg Gly Trp Gly Asp Ser Val Gly Thr Pro Ser Glu Arg Gly Met Thr
                165                 170                 175

Tyr Asp Ala Leu His Val Phe Asp Trp Ile Lys
            180                 185


<210> 767
<211> 194
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ABHD12; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000459121"

<400> 767
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Ala Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His Ser Leu Gly
1 5 10 15

Thr Gly Val Ala Thr Asn Leu Val Arg Arg Leu Cys Glu Arg Glu Thr
20 25 30

Pro Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile Arg Glu
35 40 45

Glu Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe Pro Gly
50 55 60

Phe Asp Trp Phe Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile Lys Phe
65 70 75 80

Ala Asn Asp Glu Asn Val Lys His Ile Ser Cys Pro Leu Leu Ile Leu
85 90 95

His Ala Glu Asp Asp Pro Val Val Pro Phe Gln Leu Gly Arg Lys Val
100 105 110

Gly Pro Gly Leu Cys Leu Trp Cys Ser Trp His Leu Ala His Ser Ala
115 120 125

Ser Val Gly Gly Pro Gly Trp Glu Trp Ala Gly Gly Lys Ala Ala Pro
130 135 140

Ala Cys Cys Ile Thr Gly Cys Ala Pro Ala Thr Ser Gly Ser Gly Gly
145 150 155 160

His Leu Ile Leu Pro Ala Ser Pro Pro Gly Cys Phe Gly Arg Thr Trp
165 170 175

Glu Val Trp Cys Lys Gly Trp Gly Arg Gly Pro Leu Met Leu Ser Pro
180 185 190

Arg Ile

<210> 768
<211> 13
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 768
Xaa Glu Phe Leu Gly Lys Ser Glu Pro Glu His Gln His
1 5 10

<210> 769
<211> 159
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
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domain containing 12; "

<220>
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<223> /note="ENSP ID: ENSP00000459495"

<400> 769
Met Trp Tyr Glu Asp Ala Leu Ala Ser Ser His Pro Ile Ile Leu Tyr
1 5 10 15

```
Leu His Gly Asn Ala Gly Thr Arg Gly Gly Asp His Arg Val Glu Leu
            20                  25                  30

Tyr Lys Val Leu Ser Ser Leu Gly Tyr His Val Val Thr Phe Asp Tyr
        35                  40                  45

Arg Gly Trp Gly Asp Ser Val Gly Thr Pro Ser Glu Arg Gly Met Thr
    50                  55                  60

Tyr Asp Ala Leu His Val Phe Asp Trp Ile Lys Ala Arg Ser Gly Asp
65                  70                  75                  80

Asn Pro Val Tyr Ile Trp Gly His Ser Leu Gly Thr Gly Val Ala Thr
                85                  90                  95

Asn Leu Val Arg Arg Leu Cys Glu Arg Glu Thr Pro Pro Asp Ala Leu
            100                 105                 110

Ile Leu Glu Ser Pro Phe Thr Asn Ile Arg Glu Glu Ala Lys Ser His
        115                 120                 125

Pro Phe Ser Val Ile Tyr Arg Tyr Phe Pro Gly Phe Asp Trp Phe Phe
    130                 135                 140

Leu Asp Pro Ile Thr Ser Ser Gly Ile Lys Phe Ala Asn Asp Glu
145                 150                 155


<210> 770
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 129; "

<220>
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<220>
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<223> /note="Gene Name:
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      domain containing 12; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000460249"

<400> 770
Met Arg Lys Arg Thr Glu Pro Val Ala Leu Glu His Glu Arg Cys Ala
1   5   10   15

Ala Ala Gly Ser Ser Ser Ser Gly Ser Ala Ala Ala Ala Leu Asp Ala
            20   25   30

Asp Cys Arg Leu Lys Gln Asn Leu Arg Leu Thr Gly Pro Ala Ala Ala
        35   40   45

Glu Pro Arg Cys Ala Ala Asp Ala Gly Met Lys Arg Ala Leu Gly Arg
    50   55   60

Arg Lys Gly Val Trp Leu Arg Leu Arg Lys Ile Leu Phe Cys Val Leu
65   70   75   80

Gly Leu Tyr Ile Ala Ile Pro Phe Leu Ile Lys Leu Cys Pro Gly Ile
                85   90   95

Gln Ala Lys Leu Ile Phe Leu Asn Phe Gly Pro Cys Ala Pro Ser Gln
            100   105   110

Leu Glu Asp Phe Leu Cys
        115

<210> 771
<211> 105
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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      domain containing 12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460950"

<400> 771
Met Trp Tyr Glu Asp Ala Leu Ala Ser Ser His Pro Ile Ile Leu Tyr
1   5   10   15

Leu His Gly Asn Ala Gly Thr Arg Gly Gly Asp His Arg Val Glu Leu
            20   25   30

Tyr Lys Val Leu Ser Ser Leu Gly Tyr His Val Val Thr Phe Asp Tyr
        35   40   45

Arg Gly Trp Gly Asp Ser Val Gly Thr Pro Ser Glu Arg Gly Met Thr
    50   55   60

Tyr Asp Ala Leu His Val Phe Asp Trp Ile Lys Ala Arg Ser Gly Asp
65   70   75   80

Asn Pro Val Tyr Ile Trp Gly His Ser Leu Gly Thr Gly Val Ala Thr
                85   90   95

Asn Leu Val Arg Arg Leu Cys Glu Arg
            100   105

<210> 772
<211> 362
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 130; "

<220>
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<223> /note="Gene Symbol: ABHD12B; "

<220>
<221> source
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      domain containing 12B; "

<220>
<221> source
<223> /note="Uniprot ID: Q7Z5M8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000336693"

<400> 772
Met Asp Ala Gln Asp Cys Gln Ala Ala Ala Ser Pro Glu Pro Pro Gly
1   5   10   15

Pro Pro Ala Arg Ser Cys Val Ala Ala Trp Trp Asp Met Val Asp Arg
            20   25   30

Asn Leu Arg Tyr Phe Pro His Ser Cys Ser Met Leu Gly Arg Lys Ile
        35   40   45

Ala Ala Leu Tyr Asp Ser Phe Thr Ser Lys Ser Leu Lys Glu His Val
    50   55   60

Phe Leu Pro Leu Ile Asp Met Leu Ile Tyr Phe Asn Phe Phe Lys Ala
65   70   75   80

Pro Phe Leu Val Asp Leu Lys Lys Pro Glu Leu Lys Ile Pro His Thr
                85   90   95

Val Asn Phe Tyr Leu Arg Val Glu Pro Gly Val Met Leu Gly Ile Trp
            100   105   110

His Thr Val Pro Ser Cys Arg Gly Glu Asp Ala Lys Gly Lys Asp Cys
        115   120   125

Cys Trp Tyr Glu Ala Ala Leu Arg Asp Gly Asn Pro Ile Ile Val Tyr
    130   135   140

Leu His Gly Ser Ala Glu His Arg Ala Ala Ser His Arg Leu Lys Leu
145   150   155   160

Val Lys Val Leu Ser Asp Gly Gly Phe His Val Leu Ser Val Asp Tyr
                165   170   175

Arg Gly Phe Gly Asp Ser Thr Gly Lys Pro Thr Glu Glu Gly Leu Thr
            180   185   190

Thr Asp Ala Ile Cys Val Tyr Glu Trp Thr Lys Ala Arg Ser Gly Ile
        195   200   205

Thr Pro Val Cys Leu Trp Gly His Ser Leu Gly Thr Gly Val Ala Thr
    210   215   220

```
Asn Ala Ala Lys Val Leu Glu Glu Lys Gly Cys Pro Val Asp Ala Ile
225                 230                 235                 240

Val Leu Glu Ala Pro Phe Thr Asn Met Trp Val Ala Ser Ile Asn Tyr
                245                 250                 255

Pro Leu Leu Lys Ile Tyr Arg Asn Ile Pro Gly Phe Leu Arg Thr Leu
            260                 265                 270

Met Asp Ala Leu Arg Lys Asp Lys Ile Ile Phe Pro Asn Asp Glu Asn
        275                 280                 285

Val Lys Phe Leu Ser Ser Pro Leu Leu Ile Leu His Gly Glu Asp Asp
    290                 295                 300

Arg Thr Val Pro Leu Glu Tyr Gly Lys Lys Leu Tyr Glu Ile Ala Arg
305                 310                 315                 320

Asn Ala Tyr Arg Asn Lys Glu Arg Val Lys Met Val Ile Phe Pro Pro
                325                 330                 335

Gly Phe Gln His Asn Leu Leu Cys Lys Ser Pro Thr Leu Leu Ile Thr
            340                 345                 350

Val Arg Asp Phe Leu Ser Lys Gln Trp Ser
        355                 360


<210> 773
<211> 285
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
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<220>
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      domain containing 12B; "

<220>
<221> source
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<223> /note="Uniprot ID: Q7Z5M8; "

<220>
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<400> 773
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Met Asp Ala Gln Asp Cys Gln Ala Ala Ala Ser Pro Glu Pro Pro Gly
1               5                  10                  15

Pro Pro Ala Arg Ser Cys Val Ala Ala Trp Trp Asp Met Val Asp Arg
            20                  25                  30

Asn Leu Arg His Thr Val Pro Ser Cys Arg Gly Glu Asp Ala Lys Gly
        35                  40                  45

Lys Asp Cys Cys Trp Tyr Glu Ala Ala Leu Arg Asp Gly Asn Pro Ile
    50                  55                  60

Ile Val Tyr Leu His Gly Ser Ala Glu His Arg Ala Ala Ser His Arg
65                  70                  75                  80

Leu Lys Leu Val Lys Val Leu Ser Asp Gly Gly Phe His Val Leu Ser
                85                  90                  95

Val Asp Tyr Arg Gly Phe Gly Asp Ser Thr Gly Lys Pro Thr Glu Glu
            100                 105                 110

Gly Leu Thr Thr Asp Ala Ile Cys Val Tyr Glu Trp Thr Lys Ala Arg
        115                 120                 125

Ser Gly Ile Thr Pro Val Cys Leu Trp Gly His Ser Leu Gly Thr Gly
    130                 135                 140

Val Ala Thr Asn Ala Ala Lys Val Leu Glu Glu Lys Gly Cys Pro Val
145                 150                 155                 160

Asp Ala Ile Val Leu Glu Ala Pro Phe Thr Asn Met Trp Val Ala Ser
                165                 170                 175

Ile Asn Tyr Pro Leu Leu Lys Ile Tyr Arg Asn Ile Pro Gly Phe Leu
            180                 185                 190

Arg Thr Leu Met Asp Ala Leu Arg Lys Asp Lys Ile Ile Phe Pro Asn
        195                 200                 205
```

```
Asp Glu Asn Val Lys Phe Leu Ser Ser Pro Leu Leu Ile Leu His Gly
    210                 215                 220

Glu Asp Asp Arg Thr Val Pro Leu Glu Tyr Gly Lys Lys Leu Tyr Glu
225                 230                 235                 240

Ile Ala Arg Asn Ala Tyr Arg Asn Lys Glu Arg Val Lys Met Val Ile
                245                 250                 255

Phe Pro Pro Gly Phe Gln His Asn Leu Leu Cys Lys Ser Pro Thr Leu
            260                 265                 270

Leu Ile Thr Val Arg Asp Phe Leu Ser Lys Gln Trp Ser
        275                 280                 285


<210> 774
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Symbol: ABHD12B; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 12B; "

<220>
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<223> /note="Uniprot ID:  Q7Z5M8; "

<220>
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<223> /note="ENSP ID: ENSP00000371460"

<400> 774
Met Asp Ala Gln Asp Cys Gln Ala Ala Ala Ser Pro Glu Pro Pro Gly
1               5                   10                  15

Pro Pro Ala Arg Ser Cys Val Ala Ala Trp Trp Asp Met Val Asp Arg
            20                  25                  30
```

```
Asn Leu Arg Gln Ser Pro Ile Ser Cys Gly Phe Lys Glu Thr Arg Val
        35                  40                  45


Lys Asp Ser Ser His Ser Glu Leu Leu Pro Glu Ser
    50                  55                  60


<210> 775
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 130; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD12B; "

<220>
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<223> /note="Gene Name:
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      domain containing 12B; "

<220>
<221> source
<223> /note="Uniprot ID:  Q7Z5M8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450643"

<400> 775
Met Asp Ala Gln Asp Cys Gln Ala Ala Ala Ser Pro Glu Pro Pro Gly
1               5                   10                  15


Pro Pro Ala Arg Ser Cys Val Ala Ala Trp Trp Asp Met Val Asp Arg
            20                  25                  30


Asn Leu Arg Gln Ser Pro Ile Ser Cys Gly Phe Lys Glu Thr Arg Val
        35                  40                  45


Lys Asp Ser Ser His Ser Glu Leu Leu Pro Glu Ser
    50                  55                  60


<210> 776
<211> 337
<212> PRT
<213> Homo sapiens
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<220>
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<223> /note="Payload ID: 131; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD13; "

<220>
<221> source
<223> /note="Gene Name:
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domain containing 13; "

<220>
<221> source
<223> /note="Uniprot ID: Q7L211; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000365063"

<400> 776

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Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
1               5                  10                  15


Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
            20                  25                  30


Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu
        35                  40                  45


Ile Phe Ile Ser Ile Ala Gly Ile Leu Tyr Lys Phe Gln Asp Val Leu
    50                  55                  60


Leu Tyr Phe Pro Glu Gln Pro Ser Ser Ser Arg Leu Tyr Val Pro Met
65                  70                  75                  80


Pro Thr Gly Ile Pro His Glu Asn Ile Phe Ile Arg Thr Lys Asp Gly
                85                  90                  95


Ile Arg Leu Asn Leu Ile Leu Ile Arg Tyr Thr Gly Asp Asn Ser Pro
            100                 105                 110


Tyr Ser Pro Thr Ile Ile Tyr Phe His Gly Asn Ala Gly Asn Ile Gly
        115                 120                 125


His Arg Leu Pro Asn Ala Leu Leu Met Leu Val Asn Leu Lys Val Asn
```

```
    130                 135                 140

Leu Leu Leu Val Asp Tyr Arg Gly Tyr Gly Lys Ser Glu Gly Glu Ala
145                 150                 155                 160

Ser Glu Glu Gly Leu Tyr Leu Asp Ser Glu Ala Val Leu Asp Tyr Val
                165                 170                 175

Met Thr Arg Pro Asp Leu Asp Lys Thr Lys Ile Phe Leu Phe Gly Arg
            180                 185                 190

Ser Leu Gly Gly Ala Val Ala Ile His Leu Ala Ser Glu Asn Ser His
        195                 200                 205

Arg Ile Ser Ala Ile Met Val Glu Asn Thr Phe Leu Ser Ile Pro His
    210                 215                 220

Met Ala Ser Thr Leu Phe Ser Phe Phe Pro Met Arg Tyr Leu Pro Leu
225                 230                 235                 240

Trp Cys Tyr Lys Asn Lys Phe Leu Ser Tyr Arg Lys Ile Ser Gln Cys
                245                 250                 255

Arg Met Pro Ser Leu Phe Ile Ser Gly Leu Ser Asp Gln Leu Ile Pro
            260                 265                 270

Pro Val Met Met Lys Gln Leu Tyr Glu Leu Ser Pro Ser Arg Thr Lys
        275                 280                 285

Arg Leu Ala Ile Phe Pro Asp Gly Thr His Asn Asp Thr Trp Gln Cys
    290                 295                 300

Gln Gly Tyr Phe Thr Ala Leu Glu Gln Phe Ile Lys Glu Val Val Lys
305                 310                 315                 320

Ser His Ser Pro Glu Glu Met Ala Lys Thr Ser Ser Asn Val Thr Ile
                325                 330                 335

Ile
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<210> 777
<211> 271

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 132; "

<220>
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<223> /note="Gene Symbol: ABHD14A; "

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<223> /note="Gene Name:
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domain containing 14A; "

<220>
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<223> /note="Uniprot ID: Q9BUJ0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000273596"

<400> 777
Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu Gly Gly Ala Arg
1   5   10   15

Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr Ser Met Ser Arg
            20   25   30

Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu
        35   40   45

Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly
    50   55   60

Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro
65   70   75   80

Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala His Arg Val Glu
                85   90   95

Val Val Leu Leu His Gly Lys Ala Phe Asn Ser His Thr Trp Glu Gln
            100   105   110

Leu Gly Thr Leu Gln Leu Leu Ser Gln Arg Gly Tyr Arg Ala Val Ala
        115   120   125

```
Leu Asp Leu Pro Gly Phe Gly Asn Ser Ala Pro Ser Lys Glu Ala Ser
    130                 135                 140

Thr Glu Ala Gly Arg Ala Ala Leu Leu Glu Arg Ala Leu Arg Asp Leu
145                 150                 155                 160

Glu Val Gln Asn Ala Val Leu Val Ser Pro Ser Leu Ser Gly His Tyr
                165                 170                 175

Ala Leu Pro Phe Leu Met Arg Gly His His Gln Leu His Gly Phe Val
            180                 185                 190

Pro Ile Ala Pro Thr Ser Thr Gln Asn Tyr Thr Gln Glu Gln Phe Trp
        195                 200                 205

Ala Val Lys Thr Pro Thr Leu Ile Leu Tyr Gly Glu Leu Asp His Ile
    210                 215                 220

Leu Ala Arg Glu Ser Leu Arg Gln Leu Arg His Leu Pro Asn His Ser
225                 230                 235                 240

Val Val Lys Leu Arg Asn Ala Gly His Ala Cys Tyr Leu His Lys Pro
                245                 250                 255

Gln Asp Phe His Leu Val Leu Leu Ala Phe Leu Asp His Leu Pro
            260                 265                 270


<210> 778
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 132; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14A; "

<220>
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<223> /note="Gene Name:
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      domain containing 14A; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000390557"

<400> 778
Met Leu Leu Leu Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser
1 5 10 15

Cys Leu Trp Gly Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro
20 25 30

Gly Asn Ser Pro Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala
35 40 45

His Arg Val Glu Val Val Leu Leu His Gly Lys Ala Phe Asn Ser His
50 55 60

Thr Trp Glu Gln Leu Gly Thr Leu Gln Leu Leu Ser Gln Arg Gly Tyr
65 70 75 80

Arg Ala Val Ala Leu Asp Leu Pro Val Pro Gly Ser Ser Asn Ser Pro
85 90 95

Ala Ser Ala Ser Pro Val Ala Glu Ile Thr Glu Asn Ser Phe Trp Ala
100 105 110

Val Leu Val Arg Asp Leu Glu Val Gln Asn Ala Val Leu Val Ser Pro
115 120 125

Ser Leu Ser Gly His Tyr Ala Leu Pro Phe Leu Met Arg Gly His His
130 135 140

Gln Leu His Gly Phe Val Pro Ile Ala Pro Thr Ser Thr Gln Asn Tyr
145 150 155 160

Thr Gln Glu Gln Phe Trp Ala Val Lys Thr Pro Thr Leu Ile Leu Tyr
165 170 175

Gly Glu Leu Asp His Ile Leu Ala Arg Glu Ser Leu Arg Gln Leu Arg
180 185 190

His Leu Pro Asn His Ser Val Val Lys Leu Arg Asn Ala Gly His Ala
195 200 205

Cys Tyr Leu His Lys Pro Gln Asp Phe His Leu Val Leu Leu Ala Phe

```
    210                 215                 220

Leu Asp His Leu Pro
225


<210> 779
<211> 224
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 132; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14A; "

<220>
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<223> /note="Gene Name:
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      domain containing 14A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418242"

<400> 779
Met Gln Gln Gln Tyr Arg Glu Ala Ser Leu Pro Thr Ala Gly Gln Gly
1               5                   10                  15


Leu Ser Glu Glu Glu Gly Leu Ala Leu His Leu Asp Gly Ala Leu Ala
            20                  25                  30


Leu Leu His Ala Cys Cys His Ala Cys Cys Cys Cys Ala Gly Glu Gly
        35                  40                  45


Pro Val Val Gln Asn His Asp Asp Glu Gly Pro Gln Asn Thr Leu Pro
    50                  55                  60


Arg Val Ala Val Pro Glu Glu Gln Gln Gly Ser Leu Gln Glu Val Ser
65                  70                  75                  80


Arg Thr Leu Arg Thr Cys Leu Gly Thr Val Val Gln Thr Ser Met Ser
                85                  90                  95


Arg Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu
            100                 105                 110
```

```
Leu Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp
        115                 120                 125

Gly Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser
    130                 135                 140

Pro Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala His Arg Val
145                 150                 155                 160

Glu Val Val Leu Leu His Gly Lys Ala Phe Asn Ser His Thr Trp Glu
                165                 170                 175

Gln Leu Gly Thr Leu Gln Leu Leu Ser Gln Arg Gly Tyr Arg Ala Val
            180                 185                 190

Ala Leu Asp Leu Pro Gly Phe Gly Asn Ser Ala Pro Ser Lys Glu Ala
        195                 200                 205

Ser Thr Glu Ala Gly Arg Ala Ala Leu Leu Glu Arg Ala Leu Arg Asp
    210                 215                 220


<210> 780
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 132; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14A; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 14A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418824"

<400> 780
Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu Gly Gly Ala Arg
1               5                   10                  15
```

```
Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr Ser Met Ser Arg
            20                  25                  30

Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu
        35                  40                  45

Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly
    50                  55                  60

Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro
65                  70                  75                  80

Ile Phe Tyr Arg Glu Val Leu Pro Leu Asn Gln Ala His Arg Leu Gln
                85                  90                  95

Pro Leu Ser Cys Met Glu Ser Trp Thr Thr Ser Trp Leu Glu Ser His
            100                 105                 110

Cys Gly Ser Ser Ala Thr Cys Pro Thr Thr Leu Trp
        115                 120


<210> 781
<211> 152
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ABHD14A; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 14A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420475"

<400> 781
Met Val Ala Thr Pro Lys Glu Gly Thr Gln Gly Ser Glu Lys Gly Arg
1               5                   10                  15
```

```
Leu Gly Thr Val Val Gln Thr Ser Met Ser Arg Ser Gln Val Ala Leu
            20                  25                  30

Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu Tyr Val Gly Leu Pro
        35                  40                  45

Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly Asp Pro Asn Val Thr
    50                  55                  60

Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro Ile Phe Tyr Arg Glu
65                  70                  75                  80

Val Leu Pro Leu Asn Gln Ala His Arg Val Glu Val Val Leu Leu His
                85                  90                  95

Gly Lys Ala Phe Asn Ser His Thr Trp Glu Gln Leu Gly Thr Leu Gln
            100                 105                 110

Leu Leu Ser Gln Arg Gly Tyr Arg Ala Val Ala Leu Asp Leu Pro Gly
        115                 120                 125

Phe Gly Asn Ser Ala Pro Ser Lys Glu Ala Ser Thr Glu Ala Gly Arg
    130                 135                 140

Ala Ala Leu Leu Glu Arg Ala Leu
145                 150


<210> 782
<211> 208
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 133; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14B; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 14B; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000318248"

<400> 782

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Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
1               5                  10                  15

Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
            20                  25                  30

Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
        35                  40                  45

Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
    50                  55                  60

Val Ala Ile Asp Leu Pro Gly Leu Lys Gly Glu Pro Pro Ala Gln Glu
65                  70                  75                  80

Pro Leu Leu Ser Gln Ser Arg Ala Ser Phe Leu Ala Ala Val Val Asp
                85                  90                  95

Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly
            100                 105                 110

Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly
        115                 120                 125

Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala Ala Asn
    130                 135                 140

Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp Gln Asp
145                 150                 155                 160

Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro Asn His
                165                 170                 175

Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu Asp Lys
            180                 185                 190

Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly Leu Gln
        195                 200                 205
```

<210> 783
<211> 210

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 133; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14B; "

<220>
<221> source
<223> /note="Gene Name:
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domain containing 14B; "

<220>
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<223> /note="Uniprot ID: Q96IU4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000354841"

<400> 783

```
Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
1               5                   10                  15


Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
            20                  25                  30


Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
        35                  40                  45


Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
    50                  55                  60


Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
65                  70                  75                  80


Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
                85                  90                  95


Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
            100                 105                 110


Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
        115                 120                 125
```

```
Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
    130                 135                 140

Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
145                 150                 155                 160

Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
                165                 170                 175

Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
            180                 185                 190

Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
        195                 200                 205

Leu Gln
    210
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<210> 784
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 133; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14B; "

<220>
<221> source
<223> /note="Gene Name:
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domain containing 14B; "

<220>
<221> source
<223> /note="Uniprot ID: Q96IU4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378455"

<400> 784

```
Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
1               5                   10                  15
```

```
Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
            20                  25                  30

Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
        35                  40                  45

Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
    50                  55                  60

Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
65                  70                  75                  80

Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
                85                  90                  95

Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
            100                 105                 110

Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
        115                 120                 125

Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
    130                 135                 140

Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
145                 150                 155                 160

Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
                165                 170                 175

Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
            180                 185                 190

Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
        195                 200                 205

Leu Gln
    210
```

<210> 785
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 133; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14B; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 14B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417564"

<400> 785
Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
1 5 10 15

Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
20 25 30

Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
35 40 45

Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
50 55 60

Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
65 70 75 80

Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
85 90 95

Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
100 105 110

Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
115 120 125

Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
130 135 140

Ala Asn Tyr Ala Ser Val Lys Val Pro Leu Cys Gly Lys Leu Arg Cys
145 150 155 160

```
Pro Cys Gln Glu Gln Gly Arg Val His Pro Trp Ala Phe Leu Ile Trp
                165                 170                 175


Gly Leu Asp Asn Gln Gly Val Ser Ser Gly Arg Ser
            180                 185


<210> 786
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 133; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14B; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 14B; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96IU4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420065"

<400> 786
Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
1               5                   10                  15


Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
            20                  25                  30


Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
        35                  40                  45


Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
    50                  55                  60


Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
65                  70                  75                  80
```

```
Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
                85                  90                  95

Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
            100                 105                 110

Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
        115                 120                 125

Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
    130                 135                 140

Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
145                 150                 155                 160

Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
                165                 170                 175

Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
            180                 185                 190

Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
        195                 200                 205

Leu Gln
    210


<210> 787
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 133; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD14B; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 14B; "

<220>
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<221> source
<223> /note="Uniprot ID: Q96IU4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433388"

<400> 787
Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
1   5   10   15

Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
            20   25   30

Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
        35   40   45

Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
    50   55   60

Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
65   70   75   80

Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
                85   90   95

Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
            100   105   110

Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
        115   120   125

Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
    130   135   140

Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
145   150   155   160

Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
                165   170   175

Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
            180   185   190

Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly

```
        195                 200                 205

Leu Gln
    210


<210> 788
<211> 468
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 134; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD15; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 15; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6UXT9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000302657"

<400> 788
Met Pro Pro Trp Gly Ala Ala Leu Ala Leu Ile Leu Ala Val Leu Ala
1               5                  10                  15


Leu Leu Gly Leu Leu Gly Pro Arg Leu Arg Gly Pro Trp Gly Arg Ala
            20                  25                  30


Val Gly Glu Arg Thr Leu Pro Gly Ala Gln Asp Arg Asp Asp Gly Glu
        35                  40                  45


Glu Ala Asp Gly Gly Gly Pro Ala Asp Gln Phe Ser Asp Gly Arg Glu
    50                  55                  60


Pro Leu Pro Gly Gly Cys Ser Leu Val Cys Lys Pro Ser Ala Leu Ala
65                  70                  75                  80


Gln Cys Leu Leu Arg Ala Leu Arg Arg Ser Glu Ala Leu Glu Ala Gly
                85                  90                  95
```

```
Pro Arg Ser Trp Phe Ser Gly Pro His Leu Gln Thr Leu Cys His Phe
            100                 105                 110

Val Leu Pro Val Ala Pro Gly Pro Glu Leu Ala Arg Glu Tyr Leu Gln
        115                 120                 125

Leu Ala Asp Asp Gly Leu Val Ala Leu Asp Trp Val Val Gly Pro Cys
    130                 135                 140

Val Arg Gly Arg Arg Ile Thr Ser Ala Gly Gly Leu Pro Ala Val Leu
145                 150                 155                 160

Leu Val Ile Pro Asn Ala Trp Gly Arg Leu Thr Arg Asn Val Leu Gly
                165                 170                 175

Leu Cys Leu Leu Ala Leu Glu Arg Gly Tyr Tyr Pro Val Ile Phe His
            180                 185                 190

Arg Arg Gly His His Gly Cys Pro Leu Val Ser Pro Arg Leu Gln Pro
        195                 200                 205

Phe Gly Asp Pro Ser Asp Leu Lys Glu Ala Val Thr Tyr Ile Arg Phe
    210                 215                 220

Arg His Pro Ala Ala Pro Leu Phe Ala Val Ser Glu Gly Ser Gly Ser
225                 230                 235                 240

Ala Leu Leu Leu Ser Tyr Leu Gly Glu Cys Gly Ser Ser Ser Tyr Val
                245                 250                 255

Thr Gly Ala Ala Cys Ile Ser Pro Val Leu Arg Cys Arg Glu Trp Phe
            260                 265                 270

Glu Ala Gly Leu Pro Trp Pro Tyr Glu Arg Gly Phe Leu Leu His Gln
        275                 280                 285

Lys Ile Ala Leu Ser Arg Tyr Ala Thr Ala Leu Glu Asp Thr Val Asp
    290                 295                 300

Thr Ser Arg Leu Phe Arg Ser Arg Ser Leu Arg Glu Phe Glu Glu Ala
305                 310                 315                 320
```

```
Leu Phe Cys His Thr Lys Ser Phe Pro Ile Ser Trp Asp Thr Tyr Trp
                325                 330                 335

Asp Arg Asn Asp Pro Leu Arg Asp Val Asp Glu Ala Ala Val Pro Val
            340                 345                 350

Leu Cys Ile Cys Ser Ala Asp Asp Pro Val Cys Gly Pro Pro Asp His
        355                 360                 365

Thr Leu Thr Thr Glu Leu Phe His Ser Asn Pro Tyr Phe Phe Leu Leu
    370                 375                 380

Leu Ser Arg His Gly Gly His Cys Gly Phe Leu Arg Gln Glu Pro Leu
385                 390                 395                 400

Pro Ala Trp Ser His Glu Val Ile Leu Glu Ser Phe Arg Ala Leu Thr
                405                 410                 415

Glu Phe Phe Arg Thr Glu Glu Arg Ile Lys Gly Leu Ser Arg His Arg
            420                 425                 430

Ala Ser Phe Leu Gly Gly Arg Arg Arg Gly Gly Ala Leu Gln Arg Arg
        435                 440                 445

Glu Val Ser Ser Ser Ser Asn Leu Glu Glu Ile Phe Asn Trp Lys Arg
    450                 455                 460

Ser Tyr Thr Arg
465
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<210> 789
<211> 558
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 135; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD16A; "

<220>
<221> source
<223> /note="Gene Name:

abhydrolase
domain containing 16A; "

<220>
<221> source
<223> /note="Uniprot ID: O95870; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000379282"

<400> 789

```
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
1               5                  10                  15

Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
            20                  25                  30

Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr
        35                  40                  45

Gln Pro Arg Ala Leu Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala
    50                  55                  60

Ser Val Phe Trp Ser Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe
65                  70                  75                  80

Tyr Leu Tyr Arg Lys Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe
                85                  90                  95

Ser His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys
            100                 105                 110

Leu Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile
        115                 120                 125

Thr Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg
    130                 135                 140

Gln Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe
145                 150                 155                 160

His Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser
                165                 170                 175

Arg Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr
```

```
            180                 185                 190

Ala Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr
        195                 200                 205

Ser Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly
    210                 215                 220

Ser Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly
225                 230                 235                 240

Gln Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu
                245                 250                 255

Ala Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly
            260                 265                 270

Thr Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn
        275                 280                 285

Ala Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly
    290                 295                 300

Tyr Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly
305                 310                 315                 320

Val Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln
                325                 330                 335

Phe Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr
            340                 345                 350

Ala Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr
        355                 360                 365

Pro Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val
    370                 375                 380

Pro Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr
385                 390                 395                 400

Arg Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys
                405                 410                 415
```

```
Arg Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile
            420                 425                 430

Ile Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp
        435                 440                 445

Leu Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu
    450                 455                 460

Glu Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu
465                 470                 475                 480

Glu Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys
                485                 490                 495

Leu Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro
            500                 505                 510

Trp Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala
        515                 520                 525

Leu Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys
    530                 535                 540

Thr Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
545                 550                 555


<210> 790
<211> 263
<212> PRT
<213> Homo sapiens

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
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Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20   25   30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35   40   45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50   55   60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65   70   75   80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85   90   95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100   105   110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115   120   125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130   135   140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145   150   155   160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165   170   175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180   185   190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195   200   205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
210 215 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225 230 235 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
245 250 255

Gly Phe Tyr Glu Val Gly Cys
260

<210> 791
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<213> Homo sapiens

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Met Ser Gln Leu Ala Arg Arg Arg Ser Arg Tyr Gly Leu Thr Ser Arg
1 5 10 15

Ala His Asn Thr Ser Glu Ala Gly Arg Ala Gly Pro Ala Gly Gly Pro
20 25 30

Ala Ala Gly Arg Ala Ala Ala Arg Ala Gly Ala Met Ala Lys Leu Leu
35 40 45

Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile Tyr Arg Glu Arg Asp
50 55 60

Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr Pro Thr Ala Val Thr

65 70 75 80

Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr Gln Pro Arg Ala Leu
85 90 95

Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala Ser Val Phe Trp Ser
100 105 110

Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe Tyr Leu Tyr Arg Lys
115 120 125

Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser His Tyr Ala Gly
130 135 140

Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu Arg Gly Ile Gly
145 150 155 160

Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr Ile Leu Glu Ala
165 170 175

Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln Leu Ala Asn Tyr
180 185 190

Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His Trp Glu Glu Pro
195 200 205

Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg Arg Gly Val Ala
210 215 220

Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala Asp Thr Leu Leu
225 230 235 240

Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser Tyr Leu Val Ala
245 250 255

His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser Val Tyr Leu Leu
260 265 270

Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln Ala Arg Leu Val
275 280 285

Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala Cys Asp Gly Asn
290 295 300

```
Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr Ala Glu Pro Gln
305                 310                 315                 320

Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala Gly Phe Tyr Glu
                325                 330                 335

Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr Ser Val Leu Gly
            340                 345                 350

Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val Pro Phe Pro Gln
        355                 360                 365

Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe Ala Ile His Arg
    370                 375                 380

Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala Trp Ser Ile Gly
385                 390                 395                 400

Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro Asp Val Ser Ala
                405                 410                 415

Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro Leu Ala Leu Lys
            420                 425                 430

Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg Thr Val Arg Gln
        435                 440                 445

His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg Tyr Gln Gly Pro
    450                 455                 460

Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile Thr Thr Thr Val
465                 470                 475                 480

Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu Leu Leu Lys Leu
                485                 490                 495

Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu Gly Leu Arg Val
            500                 505                 510

Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu Glu Ala Ser Ile
        515                 520                 525
```

```
Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu Ser Val Leu Arg
    530                 535                 540

Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp Ser Val Gly Glu
545                 550                 555                 560

Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu Phe Leu Ala Arg
                565                 570                 575

Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr Pro Leu Pro Ala
            580                 585                 590

Gln Asn Phe Gln Met Pro Trp His Leu
        595                 600


<210> 792
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<400> 792
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45
```

```
Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60

His Tyr Ala Gly Thr Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys
            260
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<210> 793

<211> 263
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<400> 793

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140
```

```
Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys
            260
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<400> 794
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
1   5   10   15

Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
            20   25   30

Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr
        35   40   45

Gln Pro Arg Ala Leu Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala
    50   55   60

Ser Val Phe Trp Ser Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe
65   70   75   80

Tyr Leu Tyr Arg Lys Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe
                85   90   95

Ser His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys
            100   105   110

Leu Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile
        115   120   125

Thr Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg
    130   135   140

Gln Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe
145   150   155   160

His Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser
                165   170   175

Arg Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr
            180   185   190

Ala Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr
        195   200   205

```
Ser Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly
    210                 215                 220

Ser Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly
225                 230                 235                 240

Gln Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu
                245                 250                 255

Ala Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly
            260                 265                 270

Thr Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn
        275                 280                 285

Ala Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly
    290                 295                 300

Tyr Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly
305                 310                 315                 320

Val Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln
                325                 330                 335

Phe Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr
            340                 345                 350

Ala Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr
        355                 360                 365

Pro Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val
    370                 375                 380

Pro Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr
385                 390                 395                 400

Arg Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys
                405                 410                 415

Arg Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile
            420                 425                 430

Ile Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp
```

```
        435                 440                 445

Leu Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu
    450                 455                 460

Glu Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu
465                 470                 475                 480

Glu Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys
                485                 490                 495

Leu Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro
            500                 505                 510

Trp Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala
        515                 520                 525

Leu Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys
    530                 535                 540

Thr Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
545                 550                 555


<210> 795
<211> 263
<212> PRT
<213> Homo sapiens

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15
```

```
Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240
```

```
Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255


Gly Phe Tyr Glu Val Gly Cys
            260


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<400> 796
Met Ser Gln Leu Ala Arg Arg Arg Ser Arg Tyr Gly Leu Thr Ser Arg
1               5                   10                  15


Ala His Asn Thr Ser Glu Ala Gly Arg Ala Gly Pro Ala Gly Gly Pro
            20                  25                  30


Ala Ala Gly Arg Ala Ala Ala Arg Ala Gly Ala Met Ala Lys Leu Leu
        35                  40                  45


Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile Tyr Arg Glu Arg Asp
    50                  55                  60


Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr Pro Thr Ala Val Thr
65                  70                  75                  80


Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr Gln Pro Arg Ala Leu
                85                  90                  95
```

```
Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala Ser Val Phe Trp Ser
            100                 105                 110

Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe Tyr Leu Tyr Arg Lys
        115                 120                 125

Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser His Tyr Ala Gly
    130                 135                 140

Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu Arg Gly Ile Gly
145                 150                 155                 160

Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr Ile Leu Glu Ala
                165                 170                 175

Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln Leu Ala Asn Tyr
            180                 185                 190

Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His Trp Glu Glu Pro
        195                 200                 205

Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg Arg Gly Val Ala
    210                 215                 220

Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala Asp Thr Leu Leu
225                 230                 235                 240

Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser Tyr Leu Val Ala
                245                 250                 255

His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser Val Tyr Leu Leu
            260                 265                 270

Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln Ala Arg Leu Val
        275                 280                 285

Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala Cys Asp Gly Asn
    290                 295                 300

Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr Ala Glu Pro Gln
305                 310                 315                 320

Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala Gly Phe Tyr Glu
```

```
                325                 330                 335

Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr Ser Val Leu Gly
            340                 345                 350

Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val Pro Phe Pro Gln
        355                 360                 365

Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe Ala Ile His Arg
    370                 375                 380

Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala Trp Ser Ile Gly
385                 390                 395                 400

Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro Asp Val Ser Ala
                405                 410                 415

Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro Leu Ala Leu Lys
            420                 425                 430

Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg Thr Val Arg Gln
        435                 440                 445

His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg Tyr Gln Gly Pro
    450                 455                 460

Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile Thr Thr Thr Val
465                 470                 475                 480

Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu Leu Leu Lys Leu
                485                 490                 495

Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu Gly Leu Arg Val
            500                 505                 510

Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu Glu Ala Ser Ile
        515                 520                 525

Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu Ser Val Leu Arg
    530                 535                 540

Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp Ser Val Gly Glu
545                 550                 555                 560
```

```
Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu Phe Leu Ala Arg
                565                 570                 575

Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr Pro Leu Pro Ala
            580                 585                 590

Gln Asn Phe Gln Met Pro Trp His Leu
        595                 600


<210> 797
<211> 601
<212> PRT
<213> Homo sapiens

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<400> 797
Met Ser Gln Leu Ala Arg Arg Arg Ser Arg Tyr Gly Leu Thr Ser Arg
1               5                   10                  15

Ala His Asn Thr Ser Glu Ala Gly Arg Ala Gly Pro Ala Gly Gly Pro
            20                  25                  30

Ala Ala Gly Arg Ala Ala Ala Arg Ala Gly Ala Met Ala Lys Leu Leu
        35                  40                  45

Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile Tyr Arg Glu Arg Asp
    50                  55                  60

Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr Pro Thr Ala Val Thr
65                  70                  75                  80
```

```
Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr Gln Pro Arg Ala Leu
                85                  90                  95

Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala Ser Val Phe Trp Ser
            100                 105                 110

Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe Tyr Leu Tyr Arg Lys
        115                 120                 125

Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser His Tyr Ala Gly
    130                 135                 140

Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu Arg Gly Ile Gly
145                 150                 155                 160

Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr Ile Leu Glu Ala
                165                 170                 175

Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln Leu Ala Asn Tyr
            180                 185                 190

Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His Trp Glu Glu Pro
        195                 200                 205

Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg Arg Gly Val Ala
    210                 215                 220

Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala Asp Thr Leu Leu
225                 230                 235                 240

Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser Tyr Leu Val Ala
                245                 250                 255

His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser Val Tyr Leu Leu
            260                 265                 270

Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln Ala Arg Leu Val
        275                 280                 285

Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala Cys Asp Gly Asn
    290                 295                 300
```

```
Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr Ala Glu Pro Gln
305                 310                 315                 320

Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala Gly Phe Tyr Glu
                325                 330                 335

Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr Ser Val Leu Gly
            340                 345                 350

Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val Pro Phe Pro Gln
        355                 360                 365

Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe Ala Ile His Arg
    370                 375                 380

Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala Trp Ser Ile Gly
385                 390                 395                 400

Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro Asp Val Ser Ala
                405                 410                 415

Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro Leu Ala Leu Lys
            420                 425                 430

Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg Thr Val Arg Gln
        435                 440                 445

His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg Tyr Gln Gly Pro
    450                 455                 460

Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile Thr Thr Thr Val
465                 470                 475                 480

Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu Leu Leu Lys Leu
                485                 490                 495

Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu Gly Leu Arg Val
            500                 505                 510

Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu Glu Ala Ser Ile
        515                 520                 525

Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu Ser Val Leu Arg
```

```
    530                 535                 540

Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp Ser Val Gly Glu
545                 550                 555                 560

Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu Phe Leu Ala Arg
                565                 570                 575

Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr Pro Leu Pro Ala
            580                 585                 590

Gln Asn Phe Gln Met Pro Trp His Leu
        595                 600


<210> 798
<211> 263
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 135; "

<220>
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<220>
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      domain containing 16A; "

<220>
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<400> 798
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60
```

```
His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys
            260
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<210> 799
<211> 601
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 135; "

<220>
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<220>
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domain containing 16A; "

<220>
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<223> /note="ENSP ID: ENSP00000407727"

<400> 799
Met Ser Gln Leu Ala Arg Arg Arg Ser Arg Tyr Gly Leu Thr Ser Arg
1 5 10 15

Ala His Asn Thr Ser Glu Ala Gly Arg Ala Gly Pro Ala Gly Gly Pro
20 25 30

Ala Ala Gly Arg Ala Ala Ala Arg Ala Gly Ala Met Ala Lys Leu Leu
35 40 45

Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile Tyr Arg Glu Arg Asp
50 55 60

Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr Pro Thr Ala Val Thr
65 70 75 80

Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr Gln Pro Arg Ala Leu
85 90 95

Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala Ser Val Phe Trp Ser
100 105 110

Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe Tyr Leu Tyr Arg Lys
115 120 125

Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser His Tyr Ala Gly
130 135 140

```
Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu Arg Gly Ile Gly
145                 150                 155                 160

Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr Ile Leu Glu Ala
                165                 170                 175

Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln Leu Ala Asn Tyr
            180                 185                 190

Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His Trp Glu Glu Pro
        195                 200                 205

Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg Arg Gly Val Ala
    210                 215                 220

Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala Asp Thr Leu Leu
225                 230                 235                 240

Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser Tyr Leu Val Ala
                245                 250                 255

His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser Val Tyr Leu Leu
            260                 265                 270

Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln Ala Arg Leu Val
        275                 280                 285

Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala Cys Asp Gly Asn
    290                 295                 300

Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr Ala Glu Pro Gln
305                 310                 315                 320

Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala Gly Phe Tyr Glu
                325                 330                 335

Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr Ser Val Leu Gly
            340                 345                 350

Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val Pro Phe Pro Gln
        355                 360                 365

Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe Ala Ile His Arg
```

```
    370                 375                 380

Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala Trp Ser Ile Gly
385                 390                 395                 400

Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro Asp Val Ser Ala
                405                 410                 415

Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro Leu Ala Leu Lys
            420                 425                 430

Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg Thr Val Arg Gln
        435                 440                 445

His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg Tyr Gln Gly Pro
    450                 455                 460

Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile Thr Thr Thr Val
465                 470                 475                 480

Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu Leu Leu Lys Leu
                485                 490                 495

Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu Gly Leu Arg Val
            500                 505                 510

Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu Glu Ala Ser Ile
        515                 520                 525

Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu Ser Val Leu Arg
    530                 535                 540

Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp Ser Val Gly Glu
545                 550                 555                 560

Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu Phe Leu Ala Arg
                565                 570                 575

Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr Pro Leu Pro Ala
            580                 585                 590

Gln Asn Phe Gln Met Pro Trp His Leu
        595                 600
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<210> 800
<211> 525
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Uniprot ID: O95870; "

<220>
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<400> 800
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1   5   10   15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20   25   30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35   40   45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50   55   60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65   70   75   80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85   90   95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100   105   110

```
Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
            260                 265                 270

Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
        275                 280                 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
    290                 295                 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305                 310                 315                 320

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
                325                 330                 335
```

```
Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
            340                 345                 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
        355                 360                 365

Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
    370                 375                 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385                 390                 395                 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
                405                 410                 415

Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
            420                 425                 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
        435                 440                 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
    450                 455                 460

Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465                 470                 475                 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
                485                 490                 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
            500                 505                 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
        515                 520                 525


<210> 801
<211> 263
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 135; "
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<220>
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<223> /note="Gene Symbol: ABHD16A; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000415240"

<400> 801
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1 5 10 15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
20 25 30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
35 40 45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
50 55 60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65 70 75 80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
85 90 95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
100 105 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
115 120 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
130 135 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145 150 155 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
165 170 175

```
Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys
            260


<210> 802
<211> 601
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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      domain containing 16A; "

<220>
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<400> 802
Met Ser Gln Leu Ala Arg Arg Arg Ser Arg Tyr Gly Leu Thr Ser Arg
1               5                   10                  15

Ala His Asn Thr Ser Glu Ala Gly Arg Ala Gly Pro Ala Gly Gly Pro
            20                  25                  30
```

```
Ala Ala Gly Arg Ala Ala Ala Arg Ala Gly Ala Met Ala Lys Leu Leu
        35                  40                  45

Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile Tyr Arg Glu Arg Asp
    50                  55                  60

Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr Pro Thr Ala Val Thr
65                  70                  75                  80

Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr Gln Pro Arg Ala Leu
                85                  90                  95

Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala Ser Val Phe Trp Ser
            100                 105                 110

Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe Tyr Leu Tyr Arg Lys
        115                 120                 125

Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser His Tyr Ala Gly
    130                 135                 140

Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu Arg Gly Ile Gly
145                 150                 155                 160

Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr Ile Leu Glu Ala
                165                 170                 175

Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln Leu Ala Asn Tyr
            180                 185                 190

Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His Trp Glu Glu Pro
        195                 200                 205

Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg Arg Gly Val Ala
    210                 215                 220

Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala Asp Thr Leu Leu
225                 230                 235                 240

Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser Tyr Leu Val Ala
                245                 250                 255
```

```
His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser Val Tyr Leu Leu
            260                 265                 270

Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln Ala Arg Leu Val
        275                 280                 285

Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala Cys Asp Gly Asn
    290                 295                 300

Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr Ala Glu Pro Gln
305                 310                 315                 320

Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala Gly Phe Tyr Glu
                325                 330                 335

Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr Ser Val Leu Gly
            340                 345                 350

Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val Pro Phe Pro Gln
        355                 360                 365

Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe Ala Ile His Arg
    370                 375                 380

Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala Trp Ser Ile Gly
385                 390                 395                 400

Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro Asp Val Ser Ala
                405                 410                 415

Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro Leu Ala Leu Lys
            420                 425                 430

Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg Thr Val Arg Gln
        435                 440                 445

His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg Tyr Gln Gly Pro
    450                 455                 460

Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile Thr Thr Thr Val
465                 470                 475                 480

Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu Leu Leu Lys Leu
```

```
                485                 490                 495

Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu Gly Leu Arg Val
            500                 505                 510

Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu Glu Ala Ser Ile
        515                 520                 525

Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu Ser Val Leu Arg
    530                 535                 540

Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp Ser Val Gly Glu
545                 550                 555                 560

Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu Phe Leu Ala Arg
                565                 570                 575

Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr Pro Leu Pro Ala
            580                 585                 590

Gln Asn Phe Gln Met Pro Trp His Leu
        595                 600


<210> 803
<211> 65
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000417566"

<400> 803
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15
```

```
Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45

Leu Ala Gly Gly Gly Tyr Val Leu Ser Ala Pro Cys Pro Gly Glu Thr
    50                  55                  60

Cys
65


<210> 804
<211> 65
<212> PRT
<213> Homo sapiens

<220>
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      domain containing 16A; "

<220>
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<223> /note="ENSP ID: ENSP00000418170"

<400> 804
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
1               5                   10                  15

Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
            20                  25                  30

Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr
        35                  40                  45

Gln Pro Arg Ala Leu Glu Lys His Ala Asp Ser Ile Leu Ala Leu Val
    50                  55                  60
```

Thr
65

<210> 805
<211> 46
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 135; "

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domain containing 16A; "

<220>
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<223> /note="ENSP ID: ENSP00000418331"

<400> 805
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
1 5 10 15

Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
20 25 30

Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Val Thr
35 40 45

<210> 806
<211> 65
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:

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domain containing 16A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419742"

<400> 806
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
1 5 10 15

Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
20 25 30

Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr
35 40 45

Gln Pro Arg Ala Leu Glu Lys His Ala Asp Ser Ile Leu Ala Leu Val
50 55 60

Thr
65

<210> 807
<211> 65
<212> PRT
<213> Homo sapiens

<220>
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domain containing 16A; "

<220>
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<223> /note="ENSP ID: ENSP00000420585"

<400> 807
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1 5 10 15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln

20 25 30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
35 40 45

Leu Ala Gly Gly Gly Tyr Val Leu Ser Ala Pro Cys Pro Gly Glu Thr
50 55 60

Cys
65

<210> 808
<211> 46
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 135; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD16A; "

<220>
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<223> /note="Gene Name:
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domain containing 16A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420628"

<400> 808
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
1 5 10 15

Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
20 25 30

Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Val Thr
35 40 45

<210> 809
<211> 525
<212> PRT
<213> Homo sapiens

<220>

<221> source
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000447498"

<400> 809

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15


Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30


Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45


Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60


His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80


Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95


Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110


Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125


Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140
```

```
Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
            260                 265                 270

Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
        275                 280                 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
    290                 295                 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305                 310                 315                 320

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
                325                 330                 335

Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
            340                 345                 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
        355                 360                 365
```

```
Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
    370                 375                 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385                 390                 395                 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
                405                 410                 415

Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
            420                 425                 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
        435                 440                 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
    450                 455                 460

Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465                 470                 475                 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
                485                 490                 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
            500                 505                 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
        515                 520                 525


<210> 810
<211> 525
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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domain containing 16A; "

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1   5   10   15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20   25   30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35   40   45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50   55   60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65   70   75   80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85   90   95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100   105   110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115   120   125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130   135   140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145   150   155   160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165   170   175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180   185   190

```
Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
            260                 265                 270

Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
        275                 280                 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
    290                 295                 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305                 310                 315                 320

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
                325                 330                 335

Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
            340                 345                 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
        355                 360                 365

Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
    370                 375                 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385                 390                 395                 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
                405                 410                 415
```

```
Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
            420                 425                 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
        435                 440                 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
    450                 455                 460

Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465                 470                 475                 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
                485                 490                 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
            500                 505                 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
        515                 520                 525
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<210> 811
<211> 525
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<213> Homo sapiens

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<400> 811

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                  10                  15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
```

225 230 235 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
245 250 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
260 265 270

Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
275 280 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
290 295 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305 310 315 320

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
325 330 335

Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
340 345 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
355 360 365

Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
370 375 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385 390 395 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
405 410 415

Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
420 425 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
435 440 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
450 455 460

```
Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465                 470                 475                 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
                485                 490                 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
            500                 505                 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
        515                 520                 525


<210> 812
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<213> Homo sapiens

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<220>
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<400> 812
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45
```

```
Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
            260                 265                 270
```

```
Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
        275                 280                 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
    290                 295                 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305                 310                 315                 320

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
                325                 330                 335

Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
            340                 345                 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
        355                 360                 365

Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
    370                 375                 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385                 390                 395                 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
                405                 410                 415

Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
            420                 425                 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
        435                 440                 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
    450                 455                 460

Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465                 470                 475                 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
                485                 490                 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
```

```
            500                 505                 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
        515                 520                 525


<210> 813
<211> 525
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Uniprot ID:  O95870; "

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<400> 813
Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                   10                  15


Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30


Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45


Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60


His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80


Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95
```

```
Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
            260                 265                 270

Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
        275                 280                 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
    290                 295                 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305                 310                 315                 320
```

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
325 330 335

Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
340 345 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
355 360 365

Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
370 375 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385 390 395 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
405 410 415

Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
420 425 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
435 440 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
450 455 460

Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465 470 475 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
485 490 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
500 505 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
515 520 525

<210> 814
<211> 525
<212> PRT
<213> Homo sapiens

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<400> 814

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Met Pro Pro Pro Ala Leu Phe Leu Ser Ser Leu Tyr Pro Arg Leu Glu
1               5                  10                  15

Phe Gln Asn Asp Phe Tyr Arg Ser Cys Ile Arg Arg Ser Ser Pro Gln
            20                  25                  30

Pro Pro Pro Asn Leu Ala Trp Arg Pro Glu Ser Leu Tyr Ser Gly Glu
        35                  40                  45

Leu Ala Gly Gly Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe Ser
    50                  55                  60

His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys Leu
65                  70                  75                  80

Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile Thr
                85                  90                  95

Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg Gln
            100                 105                 110

Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe His
        115                 120                 125

Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser Arg
```

```
    130                 135                 140

Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr Ala
145                 150                 155                 160

Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr Ser
                165                 170                 175

Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly Ser
            180                 185                 190

Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Val Leu Leu Gln Gly Gln
        195                 200                 205

Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu Ala
    210                 215                 220

Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly Thr
225                 230                 235                 240

Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn Ala
                245                 250                 255

Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly Tyr
            260                 265                 270

Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly Val
        275                 280                 285

Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln Phe
    290                 295                 300

Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile Ile Tyr Ala
305                 310                 315                 320

Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr Pro
                325                 330                 335

Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val Pro
            340                 345                 350

Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr Arg
        355                 360                 365
```

```
Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys Arg
    370                 375                 380

Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile Ile
385                 390                 395                 400

Thr Thr Thr Val Pro Glu Asp Ile Met Ser Asn Arg Gly Asn Asp Leu
                405                 410                 415

Leu Leu Lys Leu Leu Gln His Arg Tyr Pro Arg Val Met Ala Glu Glu
            420                 425                 430

Gly Leu Arg Val Val Arg Gln Trp Leu Glu Ala Ser Ser Gln Leu Glu
        435                 440                 445

Glu Ala Ser Ile Tyr Ser Arg Trp Glu Val Glu Glu Asp Trp Cys Leu
    450                 455                 460

Ser Val Leu Arg Ser Tyr Gln Ala Glu His Gly Pro Asp Phe Pro Trp
465                 470                 475                 480

Ser Val Gly Glu Asp Met Ser Ala Asp Gly Arg Arg Gln Leu Ala Leu
                485                 490                 495

Phe Leu Ala Arg Lys His Leu His Asn Phe Glu Ala Thr His Cys Thr
            500                 505                 510

Pro Leu Pro Ala Gln Asn Phe Gln Met Pro Trp His Leu
        515                 520                 525


<210> 815
<211> 469
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
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domain containing 16B; "

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<220>
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<223> /note="ENSP ID: ENSP00000358932"

<400> 815

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Met Cys Val Ile Cys Phe Val Lys Ala Leu Val Arg Val Phe Lys Ile
1               5                  10                  15

Tyr Leu Thr Ala Ser Tyr Thr Tyr Pro Phe Arg Gly Trp Pro Val Ala
            20                  25                  30

Phe Arg Trp Asp Asp Val Arg Ala Val Gly Arg Ser Ser Ser His Arg
        35                  40                  45

Ala Leu Thr Cys Ala Ala Ala Ala Ala Gly Val Trp Leu Leu Arg Asp
    50                  55                  60

Glu Thr Leu Gly Gly Asp Ala Leu Gly Arg Pro Pro Arg Gly Ala Arg
65                  70                  75                  80

Ser Gln Ala Gln Cys Leu Leu Gln Gln Leu Arg Glu Leu Pro Gly Gln
                85                  90                  95

Leu Ala Ser Tyr Ala Leu Ala His Ser Leu Gly Arg Trp Leu Val Tyr
            100                 105                 110

Pro Gly Ser Val Ser Leu Met Thr Arg Ala Leu Leu Pro Leu Leu Gln
        115                 120                 125

Gln Gly Gln Glu Arg Leu Val Glu Arg Tyr His Gly Arg Arg Ala Lys
    130                 135                 140

Leu Val Ala Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Met Asp Arg
145                 150                 155                 160

Arg Gln His Pro Gly Ser His Val His Gly Pro Arg Leu Val Ile Cys
                165                 170                 175
```

```
Cys Glu Gly Asn Ala Gly Phe Tyr Glu Met Gly Cys Leu Ser Ala Pro
            180                 185                 190

Leu Glu Ala Gly Tyr Ser Val Leu Gly Trp Asn His Pro Gly Phe Gly
        195                 200                 205

Ser Ser Thr Gly Val Pro Phe Pro Gln His Asp Ala Asn Ala Met Asp
    210                 215                 220

Val Val Val Glu Tyr Ala Leu His Arg Leu His Phe Pro Pro Ala His
225                 230                 235                 240

Leu Val Val Tyr Gly Trp Ser Val Gly Gly Phe Thr Ala Thr Trp Ala
                245                 250                 255

Thr Met Thr Tyr Pro Glu Leu Gly Ala Leu Val Leu Asp Ala Thr Phe
            260                 265                 270

Asp Asp Leu Val Pro Leu Ala Leu Lys Val Met Pro His Ser Trp Lys
        275                 280                 285

Gly Leu Val Val Arg Thr Val Arg Glu His Phe Asn Leu Asn Val Ala
    290                 295                 300

Glu Gln Leu Cys Cys Tyr Pro Gly Pro Val Leu Leu Leu Arg Arg Thr
305                 310                 315                 320

Gln Asp Asp Val Val Ser Thr Ser Gly Arg Leu Arg Pro Leu Ser Pro
                325                 330                 335

Gly Asp Val Glu Gly Asn Arg Gly Asn Glu Leu Leu Leu Arg Leu Leu
            340                 345                 350

Glu His Arg Tyr Pro Val Val Met Ala Arg Glu Gly Arg Ala Val Val
        355                 360                 365

Thr Arg Trp Leu Arg Ala Gly Ser Leu Ala Gln Glu Ala Ala Phe Tyr
    370                 375                 380

Ala Arg Tyr Arg Val Asp Glu Asp Trp Cys Leu Ala Leu Leu Arg Ser
385                 390                 395                 400

Tyr Arg Ala Arg Cys Glu Glu Glu Leu Glu Gly Glu Glu Ala Leu Gly
```

405 410 415

Pro His Gly Pro Ala Phe Pro Trp Leu Val Gly Gln Gly Leu Ser Ser
420 425 430

Arg Arg Arg Arg Arg Leu Ala Leu Phe Leu Ala Arg Lys His Leu Lys
435 440 445

Asn Val Glu Ala Thr His Phe Ser Pro Leu Glu Pro Glu Glu Phe Gln
450 455 460

Leu Pro Trp Arg Leu
465

<210> 816
<211> 361
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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domain containing 17A; "

<220>
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<223> /note="Uniprot ID: Q96GS6; "

<220>
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<400> 816
Met Asn Gly Leu Ser Leu Ser Glu Leu Cys Cys Leu Phe Cys Cys Pro
1 5 10 15

Pro Cys Pro Gly Arg Ile Ala Ala Lys Leu Ala Phe Leu Pro Pro Glu
20 25 30

Ala Thr Tyr Ser Leu Val Pro Glu Pro Glu Pro Gly Pro Gly Gly Ala
35 40 45

```
Gly Ala Ala Pro Leu Gly Thr Leu Arg Ala Ser Ser Gly Ala Pro Gly
    50                  55                  60

Arg Trp Lys Leu His Leu Thr Glu Arg Ala Asp Phe Gln Tyr Ser Gln
65                  70                  75                  80

Arg Glu Leu Asp Thr Ile Glu Val Phe Pro Thr Lys Ser Ala Arg Gly
                85                  90                  95

Asn Arg Val Ser Cys Met Tyr Val Arg Cys Val Pro Gly Ala Arg Gln
            100                 105                 110

Gly His Gln Ala Gln Gly Gly His Pro Gln Leu Ala Trp Val Gly Arg
        115                 120                 125

Leu Gly Asp Ser Asn Asn Pro Ala Pro Gly Gly Cys Leu Leu Gly Lys
    130                 135                 140

Ser Trp Gly Thr Gly Ala Ala Leu Ala Cys Gly Tyr Ile His Leu Leu
145                 150                 155                 160

Ala Arg Tyr Thr Val Leu Phe Ser His Gly Asn Ala Val Asp Leu Gly
                165                 170                 175

Gln Met Ser Ser Phe Tyr Ile Gly Leu Gly Ser Arg Leu His Cys Asn
            180                 185                 190

Ile Phe Ser Tyr Asp Tyr Ser Gly Tyr Gly Ala Ser Ser Gly Arg Pro
        195                 200                 205

Ser Glu Arg Asn Leu Tyr Ala Asp Ile Asp Ala Ala Trp Gln Ala Leu
    210                 215                 220

Arg Thr Arg Tyr Gly Ile Ser Pro Asp Ser Ile Ile Leu Tyr Gly Gln
225                 230                 235                 240

Ser Ile Gly Thr Val Pro Thr Val Asp Leu Ala Ser Arg Tyr Glu Cys
                245                 250                 255

Ala Ala Val Val Leu His Ser Pro Leu Thr Ser Gly Met Arg Val Ala
            260                 265                 270
```

```
Phe Pro Asp Thr Lys Lys Thr Tyr Cys Phe Asp Ala Phe Pro Asn Ile
        275                 280                 285

Glu Lys Val Ser Lys Ile Thr Ser Pro Val Leu Ile Ile His Gly Thr
    290                 295                 300

Glu Asp Glu Val Ile Asp Phe Ser His Gly Leu Ala Leu Tyr Glu Arg
305                 310                 315                 320

Cys Pro Lys Ala Val Glu Pro Leu Trp Val Glu Gly Ala Gly His Asn
                325                 330                 335

Asp Ile Glu Leu Tyr Ser Gln Tyr Leu Glu Arg Leu Arg Arg Phe Ile
            340                 345                 350

Ser Gln Glu Leu Pro Ser Gln Arg Ala
        355                 360


<210> 817
<211> 310
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 137; "

<220>
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<223> /note="Gene Symbol: ABHD17A; "

<220>
<221> source
<223> /note="Gene Name:
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      domain containing 17A; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96GS6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000292577"

<400> 817
Met Asn Gly Leu Ser Leu Ser Glu Leu Cys Cys Leu Phe Cys Cys Pro
1               5                   10                  15
```

```
Pro Cys Pro Gly Arg Ile Ala Ala Lys Leu Ala Phe Leu Pro Pro Glu
            20                  25                  30

Ala Thr Tyr Ser Leu Val Pro Glu Pro Glu Pro Gly Pro Gly Gly Ala
        35                  40                  45

Gly Ala Ala Pro Leu Gly Thr Leu Arg Ala Ser Ser Gly Ala Pro Gly
    50                  55                  60

Arg Trp Lys Leu His Leu Thr Glu Arg Ala Asp Phe Gln Tyr Ser Gln
65                  70                  75                  80

Arg Glu Leu Asp Thr Ile Glu Val Phe Pro Thr Lys Ser Ala Arg Gly
                85                  90                  95

Asn Arg Val Ser Cys Met Tyr Val Arg Cys Val Pro Gly Ala Arg Tyr
            100                 105                 110

Thr Val Leu Phe Ser His Gly Asn Ala Val Asp Leu Gly Gln Met Ser
        115                 120                 125

Ser Phe Tyr Ile Gly Leu Gly Ser Arg Leu His Cys Asn Ile Phe Ser
    130                 135                 140

Tyr Asp Tyr Ser Gly Tyr Gly Ala Ser Ser Gly Arg Pro Ser Glu Arg
145                 150                 155                 160

Asn Leu Tyr Ala Asp Ile Asp Ala Ala Trp Gln Ala Leu Arg Thr Arg
                165                 170                 175

Tyr Gly Ile Ser Pro Asp Ser Ile Ile Leu Tyr Gly Gln Ser Ile Gly
            180                 185                 190

Thr Val Pro Thr Val Asp Leu Ala Ser Arg Tyr Glu Cys Ala Ala Val
        195                 200                 205

Val Leu His Ser Pro Leu Thr Ser Gly Met Arg Val Ala Phe Pro Asp
    210                 215                 220

Thr Lys Lys Thr Tyr Cys Phe Asp Ala Phe Pro Asn Ile Glu Lys Val
225                 230                 235                 240

Ser Lys Ile Thr Ser Pro Val Leu Ile Ile His Gly Thr Glu Asp Glu
```

```
                245                 250                 255

Val Ile Asp Phe Ser His Gly Leu Ala Leu Tyr Glu Arg Cys Pro Lys
            260                 265                 270

Ala Val Glu Pro Leu Trp Val Glu Gly Ala Gly His Asn Asp Ile Glu
        275                 280                 285

Leu Tyr Ser Gln Tyr Leu Glu Arg Leu Arg Arg Phe Ile Ser Gln Glu
    290                 295                 300

Leu Pro Ser Gln Arg Ala
305                 310


<210> 818
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 137; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17A; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 17A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466977"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 818
Xaa Tyr Asp Tyr Ser Gly Tyr Gly Ala Ser Ser Gly Arg Pro Ser Glu
1               5                   10                  15

Arg Asn Leu Tyr Ala Asp Ile Asp Ala Ala Trp Gln Ala Leu Arg Thr
            20                  25                  30
```

Arg Asn Leu Gly Pro Glu Leu
        35

<210> 819
<211> 225
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 137; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17A; "

<220>
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<223> /note="Gene Name:
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      domain containing 17A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467638"

<400> 819
Met Asn Gly Leu Ser Leu Ser Glu Leu Cys Cys Leu Phe Cys Cys Pro
1   5   10   15

Pro Cys Pro Gly Arg Ile Ala Ala Lys Leu Ala Phe Leu Pro Pro Glu
            20   25   30

Ala Thr Tyr Ser Leu Val Pro Glu Pro Glu Pro Gly Pro Gly Gly Ala
        35   40   45

Gly Ala Ala Pro Leu Gly Thr Leu Arg Ala Ser Ser Gly Ala Pro Gly
    50   55   60

Arg Trp Lys Leu His Leu Thr Glu Arg Ala Asp Phe Gln Tyr Ser Gln
65   70   75   80

Arg Glu Leu Asp Thr Ile Glu Val Phe Pro Thr Lys Ser Ala Arg Gly
                85   90   95

Asn Arg Val Ser Cys Met Tyr Val Arg Cys Val Pro Gly Ala Ser Phe
            100   105   110

Tyr Ile Gly Leu Gly Ser Arg Leu His Cys Asn Ile Phe Ser Tyr Asp

```
        115                 120                 125

Tyr Ser Gly Tyr Gly Ala Ser Ser Gly Arg Pro Ser Glu Arg Asn Leu
    130                 135                 140

Tyr Ala Asp Ile Asp Ala Ala Trp Gln Ala Leu Arg Thr Arg Ala Ser
145                 150                 155                 160

Ala Arg Cys Pro Pro Trp Thr Trp Pro Arg Ala Thr Ser Val Pro Arg
                165                 170                 175

Trp Cys Cys Thr Arg Arg Ser Pro Arg Ala Cys Ala Ser Pro Ser Pro
            180                 185                 190

Thr Pro Arg Arg Pro Thr Ala Ser Thr Pro Ser Leu Thr Ser Arg Arg
        195                 200                 205

Cys Pro Arg Ser Arg Leu Pro Cys Ser Ser Ser Thr Ala Arg Arg Thr
    210                 215                 220

Arg
225


<210> 820
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 138; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17B; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 17B; "

<220>
<221> source
<223> /note="Uniprot ID:  Q5VST6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000330222"
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<400> 820
Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe Cys Cys Pro
1 5 10 15

Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu Pro Pro Asp
20 25 30

Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Arg Trp Thr Leu
35 40 45

His Leu Ser Glu Arg Ala Asp Trp Gln Tyr Ser Ser Arg Glu Lys Asp
50 55 60

Ala Ile Glu Cys Phe Met Thr Arg Thr Ser Lys Gly Asn Arg Ile Ala
65 70 75 80

Cys Met Phe Val Arg Cys Ser Pro Asn Ala Lys Tyr Thr Leu Leu Phe
85 90 95

Ser His Gly Asn Ala Val Asp Leu Gly Gln Met Ser Ser Phe Tyr Ile
100 105 110

Gly Leu Gly Ser Arg Ile Asn Cys Asn Ile Phe Ser Tyr Asp Tyr Ser
115 120 125

Gly Tyr Gly Ala Ser Ser Gly Lys Pro Thr Glu Lys Asn Leu Tyr Ala
130 135 140

Asp Ile Glu Ala Ala Trp Leu Ala Leu Arg Thr Arg Tyr Gly Ile Arg
145 150 155 160

Pro Glu Asn Val Ile Ile Tyr Gly Gln Ser Ile Gly Thr Val Pro Ser
165 170 175

Val Asp Leu Ala Ala Arg Tyr Glu Ser Ala Ala Val Ile Leu His Ser
180 185 190

Pro Leu Thr Ser Gly Met Arg Val Ala Phe Pro Asp Thr Lys Lys Thr
195 200 205

Tyr Cys Phe Asp Ala Phe Pro Asn Ile Asp Lys Ile Ser Lys Ile Thr
210 215 220

Ser Pro Val Leu Ile Ile His Gly Thr Glu Asp Glu Val Ile Asp Phe
225 230 235 240

Ser His Gly Leu Ala Leu Phe Glu Arg Cys Gln Arg Pro Val Glu Pro
245 250 255

Leu Trp Val Glu Gly Ala Gly His Asn Asp Val Glu Leu Tyr Gly Gln
260 265 270

Tyr Leu Glu Arg Leu Lys Gln Phe Val Ser Gln Glu Leu Val Asn Leu
275 280 285

<210> 821
<211> 293
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 138; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17B; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 17B; "

<220>
<221> source
<223> /note="Uniprot ID: Q5VST6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000366240"

<400> 821
Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe Cys Cys Pro
1 5 10 15

Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu Pro Pro Asp
20 25 30

Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Arg Trp Thr Leu
35 40 45

```
His Leu Ser Glu Arg Ala Asp Trp Gln Tyr Ser Ser Arg Glu Lys Asp
    50                  55                  60

Ala Ile Glu Cys Phe Met Thr Arg Thr Ser Lys Gly Asn Arg Ile Ala
65                  70                  75                  80

Cys Met Phe Val Arg Cys Ser Pro Asn Ala Lys Tyr Thr Leu Leu Phe
                85                  90                  95

Ser His Gly Asn Ala Val Asp Leu Gly Gln Met Ser Ser Phe Tyr Ile
            100                 105                 110

Gly Leu Gly Ser Arg Ile Asn Cys Asn Ile Phe Ser Tyr Asp Tyr Ser
        115                 120                 125

Gly Tyr Gly Ala Ser Ser Gly Lys Pro Thr Glu Lys Asn Leu Tyr Ala
    130                 135                 140

Asp Ile Glu Ala Ala Trp Leu Ala Leu Arg Thr Arg Tyr Gly Ile Arg
145                 150                 155                 160

Pro Glu Asn Val Ile Ile Tyr Gly Gln Ser Ile Gly Thr Val Pro Ser
                165                 170                 175

Val Asp Leu Ala Ala Arg Tyr Glu Ser Ala Ala Val Ile Leu His Ser
            180                 185                 190

Pro Leu Thr Ser Gly Met Arg Val Ala Phe Pro Asp Thr Lys Lys Thr
        195                 200                 205

Tyr Cys Phe Asp Ala Phe Pro Asn Ile Asp Lys Ile Ser Lys Ile Thr
    210                 215                 220

Ser Pro Val Leu Ile Ile His Gly Thr Glu Asp Glu Val Ile Asp Phe
225                 230                 235                 240

Ser His Gly Leu Ala Leu Phe Glu Arg Cys Gln Arg Pro Val Glu Pro
                245                 250                 255

Leu Trp Val Glu Gly Ala Gly His Asn Asp Val Glu Leu Tyr Gly Gln
            260                 265                 270

Tyr Leu Glu Arg Leu Lys Gln Phe Val Ser Gln Glu Leu Val Gln Lys
```

```
        275                 280                 285

His Lys Glu Gly Lys
    290


<210> 822
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 139; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17C; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 17C; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6PCB6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000258884"

<400> 822
Met Pro Glu Pro Gly Pro Arg Met Asn Gly Phe Ser Leu Gly Glu Leu
1               5                  10                  15


Cys Trp Leu Phe Cys Cys Pro Pro Cys Pro Ser Arg Ile Ala Ala Lys
            20                  25                  30


Leu Ala Phe Leu Pro Pro Glu Pro Thr Tyr Thr Val Leu Ala Pro Glu
        35                  40                  45


Gln Arg Gly Ala Gly Ala Ser Ala Pro Ala Pro Ala Gln Ala Thr Ala
    50                  55                  60


Ala Ala Ala Ala Ala Gln Pro Ala Pro Gln Gln Pro Glu Glu Gly Ala
65                  70                  75                  80


Gly Ala Gly Pro Gly Ala Cys Ser Leu His Leu Ser Glu Arg Ala Asp
                85                  90                  95
```

```
Trp Gln Tyr Ser Gln Arg Glu Leu Asp Ala Val Glu Val Phe Phe Ser
            100                 105                 110

Arg Thr Ala Arg Asp Asn Arg Leu Gly Cys Met Phe Val Arg Cys Ala
        115                 120                 125

Pro Ser Ser Arg Tyr Thr Leu Leu Phe Ser His Gly Asn Ala Val Asp
    130                 135                 140

Leu Gly Gln Met Cys Ser Phe Tyr Ile Gly Leu Gly Ser Arg Ile Asn
145                 150                 155                 160

Cys Asn Ile Phe Ser Tyr Asp Tyr Ser Gly Tyr Gly Val Ser Ser Gly
                165                 170                 175

Lys Pro Ser Glu Lys Asn Leu Tyr Ala Asp Ile Asp Ala Ala Trp Gln
            180                 185                 190

Ala Leu Arg Thr Arg Tyr Gly Val Ser Pro Glu Asn Ile Ile Leu Tyr
        195                 200                 205

Gly Gln Ser Ile Gly Thr Val Pro Thr Val Asp Leu Ala Ser Arg Tyr
    210                 215                 220

Glu Cys Ala Ala Val Ile Leu His Ser Pro Leu Met Ser Gly Leu Arg
225                 230                 235                 240

Val Ala Phe Pro Asp Thr Arg Lys Thr Tyr Cys Phe Asp Ala Phe Pro
                245                 250                 255

Ser Ile Asp Lys Ile Ser Lys Val Thr Ser Pro Val Leu Val Ile His
            260                 265                 270

Gly Thr Glu Asp Glu Val Ile Asp Phe Ser His Gly Leu Ala Met Tyr
        275                 280                 285

Glu Arg Cys Pro Arg Ala Val Glu Pro Leu Trp Val Glu Gly Ala Gly
    290                 295                 300

His Asn Asp Ile Glu Leu Tyr Ala Gln Tyr Leu Glu Arg Leu Lys Gln
305                 310                 315                 320
```

```
Phe Ile Ser His Glu Leu Pro Asn Ser
                325


<210> 823
<211> 295
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 139; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17C; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 17C; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6PCB6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452778"

<400> 823
Met Pro Glu Pro Gly Pro Arg Met Asn Gly Phe Ser Leu Gly Glu Leu
1               5                  10                  15


Cys Trp Leu Phe Cys Cys Pro Pro Cys Pro Ser Arg Ile Ala Ala Lys
            20                  25                  30


Leu Ala Phe Leu Pro Pro Glu Pro Thr Tyr Thr Val Leu Ala Pro Glu
        35                  40                  45


Gln Arg Gly Ala Gly Ala Ser Ala Pro Ala Pro Ala Gln Ala Thr Ala
    50                  55                  60


Ala Ala Ala Ala Ala Gln Pro Ala Pro Gln Gln Pro Glu Glu Gly Ala
65                  70                  75                  80


Gly Ala Gly Pro Gly Ala Cys Ser Leu His Leu Ser Glu Arg Ala Asp
                85                  90                  95
```

```
Trp Gln Tyr Ser Gln Arg Glu Leu Asp Ala Val Glu Val Phe Phe Ser
            100                 105                 110

Arg Thr Ala Arg Asp Asn Arg Leu Gly Cys Met Phe Val Arg Cys Ala
        115                 120                 125

Pro Ser Ser Arg Tyr Thr Leu Leu Phe Ser His Gly Asn Ala Val Asp
    130                 135                 140

Leu Gly Gln Met Cys Ser Phe Tyr Ile Gly Leu Gly Ser Arg Ile Asn
145                 150                 155                 160

Cys Asn Ile Phe Ser Tyr Asp Tyr Ser Gly Tyr Gly Val Ser Ser Gly
                165                 170                 175

Lys Pro Ser Glu Lys Asn Leu Tyr Ala Asp Ile Asp Ala Ala Trp Gln
            180                 185                 190

Ala Leu Arg Thr Arg Tyr Gly Val Ser Pro Glu Asn Ile Ile Leu Tyr
        195                 200                 205

Gly Gln Ser Ile Gly Thr Val Pro Thr Val Asp Leu Ala Ser Ser Ile
    210                 215                 220

Asp Lys Ile Ser Lys Val Thr Ser Pro Val Leu Val Ile His Gly Thr
225                 230                 235                 240

Glu Asp Glu Val Ile Asp Phe Ser His Gly Leu Ala Met Tyr Glu Arg
                245                 250                 255

Cys Pro Arg Ala Val Glu Pro Leu Trp Val Glu Gly Ala Gly His Asn
            260                 265                 270

Asp Ile Glu Leu Tyr Ala Gln Tyr Leu Glu Arg Leu Lys Gln Phe Ile
        275                 280                 285

Ser His Glu Leu Pro Asn Ser
    290                 295
```

<210> 824
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 139; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD17C; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 17C; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453923"

<400> 824
Met Ser Gly Leu Arg Val Ala Phe Pro Asp Thr Arg Lys Thr Tyr Cys
1 5 10 15

Phe Asp Ala Phe Pro Ser Ile Asp Lys Ile Ser Lys Val Thr Ser Pro
20 25 30

Val Leu Val Ile His Gly Thr Glu Asp Glu Val Ile Asp Phe Ser His
35 40 45

Gly Leu Ala Met Tyr Glu Arg Cys Pro Arg Ala Val Glu Pro Leu Trp
50 55 60

Val Glu Gly Ala Gly His Asn Asp Ile Glu Leu Tyr Ala Gln Tyr Leu
65 70 75 80

Glu Arg Leu Lys Gln Phe Ile Ser His Glu Leu Pro Asn Ser
85 90

<210> 825
<211> 382
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 140; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD18; "

<220>

<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373447"

<400> 825
Met Leu Asp Thr Asn Leu Ile Leu Leu Pro Leu Phe Gln Phe Ile Val
1 5 10 15

Pro Lys Glu Trp Asn Ser Lys Tyr Arg Pro Val Cys Ile His Leu Ala
20 25 30

Gly Thr Gly Asp His His Tyr Trp Arg Arg Arg Thr Leu Met Ala Arg
35 40 45

Pro Met Ile Lys Glu Ala Arg Met Ala Ser Leu Leu Leu Glu Asn Pro
50 55 60

Tyr Tyr Gly Cys Arg Lys Pro Lys Asp Gln Val Arg Ser Ser Leu Lys
65 70 75 80

Asn Val Ser Asp Leu Phe Val Met Gly Gly Ala Leu Val Leu Glu Ser
85 90 95

Ala Ala Leu Leu His Trp Leu Glu Arg Glu Gly Tyr Gly Pro Leu Gly
100 105 110

Met Thr Gly Ile Ser Met Gly Gly His Met Ala Ser Leu Ala Val Ser
115 120 125

Asn Trp Pro Lys Pro Met Pro Leu Ile Pro Cys Leu Ser Trp Ser Thr
130 135 140

Ala Ser Gly Val Phe Thr Thr Gly Val Leu Ser Lys Ser Ile Asn Trp
145 150 155 160

Arg Glu Leu Glu Lys Gln Tyr Tyr Thr Gln Thr Val Tyr Glu Glu Glu
165 170 175

Ile Ile His Met Leu Glu Tyr Cys Gly Thr Asp Ser Phe Lys Met Gly
180 185 190

```
Gln Glu Phe Val Lys His Phe Thr Ser Ser Ala Asp Lys Leu Thr Asn
        195                 200                 205

Leu Asn Leu Val Ser Arg Thr Leu Asn Leu Asp Ile Ser Asn Gln Val
    210                 215                 220

Val Ser Gln Lys Pro Ala Asp Cys His Asn Ser Ser Lys Thr Ser Val
225                 230                 235                 240

Ser Ala Thr Ser Glu Gly Leu Leu Leu Gln Asp Thr Ser Lys Met Lys
                245                 250                 255

Arg Phe Asn Gln Thr Leu Ser Thr Asn Lys Ser Gly Tyr Thr Ser Arg
            260                 265                 270

Asn Pro Gln Ser Tyr His Leu Leu Ser Lys Glu Gln Ser Arg Asn Ser
        275                 280                 285

Leu Arg Lys Glu Ser Leu Ile Phe Met Lys Gly Val Met Asp Glu Cys
    290                 295                 300

Thr His Val Ala Asn Phe Ser Val Pro Val Asp Pro Ser Leu Ile Ile
305                 310                 315                 320

Val Val Gln Ala Lys Glu Asp Ala Tyr Ile Pro Arg Thr Gly Val Arg
                325                 330                 335

Ser Leu Gln Glu Ile Trp Pro Gly Cys Glu Ile Arg Tyr Leu Glu Gly
            340                 345                 350

Gly His Ile Ser Ala Tyr Leu Phe Lys Gln Gly Leu Phe Arg Gln Ala
        355                 360                 365

Ile Tyr Asp Ala Phe Asp Arg Phe Leu His Lys Tyr Ala Asn
    370                 375                 380


<210> 826
<211> 414
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 140; "
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<220>
<221> source
<223> /note="Gene Symbol: ABHD18; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 18; "

<220>
<221> source
<223> /note="Uniprot ID: Q0P651; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000381937"

<400> 826
Met Gly Val Ser Lys Leu Asp Ile Leu Tyr Arg Arg Leu Leu Leu Thr
1   5   10   15

Lys Leu Phe Ile Arg Gly Trp Gly Arg Pro Glu Asp Leu Lys Arg Leu
            20   25   30

Phe Glu Phe Arg Lys Met Ile Gly Asn Arg Glu Arg Cys Gln Asn Leu
        35   40   45

Val Ser Ser Asp Tyr Pro Val His Ile Asp Lys Ile Glu Glu Gln Ser
    50   55   60

Asp Cys Lys Ile Leu Asp Gly His Phe Val Ser Pro Met Ala His Tyr
65   70   75   80

Val Pro Asp Ile Met Pro Ile Glu Ser Val Ile Ala Arg Phe Gln Phe
                85   90   95

Ile Val Pro Lys Glu Trp Asn Ser Lys Tyr Arg Pro Val Cys Ile His
            100   105   110

Leu Ala Gly Thr Gly Asp His His Tyr Trp Arg Arg Arg Thr Leu Met
        115   120   125

Ala Arg Pro Met Ile Lys Glu Ala Arg Met Ala Ser Leu Leu Leu Glu
    130   135   140

Asn Pro Tyr Tyr Gly Cys Arg Lys Pro Lys Asp Gln Val Arg Ser Ser

145 150 155 160

Leu Lys Asn Val Ser Asp Leu Phe Val Met Gly Gly Ala Leu Val Leu
165 170 175

Glu Ser Ala Ala Leu Leu His Trp Leu Glu Arg Glu Gly Tyr Gly Pro
180 185 190

Leu Gly Met Thr Gly Ile Ser Met Gly Gly His Met Ala Ser Leu Ala
195 200 205

Val Ser Asn Trp Pro Lys Pro Met Pro Leu Ile Pro Cys Leu Ser Trp
210 215 220

Ser Thr Ala Ser Gly Val Phe Thr Thr Thr Asp Ser Phe Lys Met Gly
225 230 235 240

Gln Glu Phe Val Lys His Phe Thr Ser Ser Ala Asp Lys Leu Thr Asn
245 250 255

Leu Asn Leu Val Ser Arg Thr Leu Asn Leu Asp Ile Ser Asn Gln Val
260 265 270

Val Ser Gln Lys Pro Ala Asp Cys His Asn Ser Ser Lys Thr Ser Val
275 280 285

Ser Ala Thr Ser Glu Gly Leu Leu Leu Gln Asp Thr Ser Lys Met Lys
290 295 300

Arg Phe Asn Gln Thr Leu Ser Thr Asn Lys Ser Gly Tyr Thr Ser Arg
305 310 315 320

Asn Pro Gln Ser Tyr His Leu Leu Ser Lys Glu Gln Ser Arg Asn Ser
325 330 335

Leu Arg Lys Glu Ser Leu Ile Phe Met Lys Gly Val Met Asp Glu Cys
340 345 350

Thr His Val Ala Asn Phe Ser Val Pro Val Asp Pro Ser Leu Ile Ile
355 360 365

Val Val Gln Ala Lys Glu Asp Ala Tyr Ile Pro Arg Thr Gly Val Arg
370 375 380

Ser Leu Gln Glu Ile Trp Pro Gly Cys Glu Ile Arg Tyr Leu Glu Gly
385 390 395 400

Gly His Ile Ser Ala Tyr Leu Phe Lys Gln Gly Leu Phe Arg
405 410

<210> 827
<211> 414
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 140; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD18; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 18; "

<220>
<221> source
<223> /note="Uniprot ID: Q0P651; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397229"

<400> 827
Met Gly Val Ser Lys Leu Asp Ile Leu Tyr Arg Arg Leu Leu Leu Thr
1 5 10 15

Lys Leu Phe Ile Arg Gly Trp Gly Arg Pro Glu Asp Leu Lys Arg Leu
20 25 30

Phe Glu Phe Arg Lys Met Ile Gly Asn Arg Glu Arg Cys Gln Asn Leu
35 40 45

Val Ser Ser Asp Tyr Pro Val His Ile Asp Lys Ile Glu Glu Gln Ser
50 55 60

Asp Cys Lys Ile Leu Asp Gly His Phe Val Ser Pro Met Ala His Tyr
65 70 75 80

```
Val Pro Asp Ile Met Pro Ile Glu Ser Val Ile Ala Arg Phe Gln Phe
                85                  90                  95

Ile Val Pro Lys Glu Trp Asn Ser Lys Tyr Arg Pro Val Cys Ile His
            100                 105                 110

Leu Ala Gly Thr Gly Asp His His Tyr Trp Arg Arg Arg Thr Leu Met
        115                 120                 125

Ala Arg Pro Met Ile Lys Glu Ala Arg Met Ala Ser Leu Leu Leu Glu
    130                 135                 140

Asn Pro Tyr Tyr Gly Cys Arg Lys Pro Lys Asp Gln Val Arg Ser Ser
145                 150                 155                 160

Leu Lys Asn Val Ser Asp Leu Phe Val Met Gly Gly Ala Leu Val Leu
                165                 170                 175

Glu Ser Ala Ala Leu Leu His Trp Leu Glu Arg Glu Gly Tyr Gly Pro
            180                 185                 190

Leu Gly Met Thr Gly Ile Ser Met Gly Gly His Met Ala Ser Leu Ala
        195                 200                 205

Val Ser Asn Trp Pro Lys Pro Met Pro Leu Ile Pro Cys Leu Ser Trp
    210                 215                 220

Ser Thr Ala Ser Gly Val Phe Thr Thr Thr Asp Ser Phe Lys Met Gly
225                 230                 235                 240

Gln Glu Phe Val Lys His Phe Thr Ser Ser Ala Asp Lys Leu Thr Asn
                245                 250                 255

Leu Asn Leu Val Ser Arg Thr Leu Asn Leu Asp Ile Ser Asn Gln Val
            260                 265                 270

Val Ser Gln Lys Pro Ala Asp Cys His Asn Ser Ser Lys Thr Ser Val
        275                 280                 285

Ser Ala Thr Ser Glu Gly Leu Leu Leu Gln Asp Thr Ser Lys Met Lys
    290                 295                 300
```

```
Arg Phe Asn Gln Thr Leu Ser Thr Asn Lys Ser Gly Tyr Thr Ser Arg
305                 310                 315                 320

Asn Pro Gln Ser Tyr His Leu Leu Ser Lys Glu Gln Ser Arg Asn Ser
                325                 330                 335

Leu Arg Lys Glu Ser Leu Ile Phe Met Lys Gly Val Met Asp Glu Cys
            340                 345                 350

Thr His Val Ala Asn Phe Ser Val Pro Val Asp Pro Ser Leu Ile Ile
        355                 360                 365

Val Val Gln Ala Lys Glu Asp Ala Tyr Ile Pro Arg Thr Gly Val Arg
    370                 375                 380

Ser Leu Gln Glu Ile Trp Pro Gly Cys Glu Ile Arg Tyr Leu Glu Gly
385                 390                 395                 400

Gly His Ile Ser Ala Tyr Leu Phe Lys Gln Gly Leu Phe Arg
                405                 410


<210> 828
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 140; "

<220>
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<223> /note="Gene Symbol: ABHD18; "

<220>
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<223> /note="Gene Name:
      abhydrolase
      domain containing 18; "

<220>
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<223> /note="ENSP ID: ENSP00000421129"

<400> 828
Met Gly Val Ser Lys Leu Asp Ile Leu Tyr Arg Arg Leu Leu Leu Thr
1               5                   10                  15

Lys Leu Phe Ile Arg Gly Trp Gly Arg Pro Glu Asp Leu Lys Arg Leu
```

```
            20                  25                  30

Phe Glu Phe Arg Lys Met Ile Gly Asn Arg Glu Arg Cys Gln Asn Leu
        35                  40                  45

Val Ser Ser Asp Tyr Pro Val His Ile Asp Lys Ile Glu Glu Gln Ser
    50                  55                  60

Asp Cys Lys Ile Leu Asp Gly His Phe Val Ser Pro Met Ala His Tyr
65                  70                  75                  80

Val Pro Asp Ile Met Pro Ile Glu Ser Val Ile Ala Arg Phe Gln Phe
                85                  90                  95

Ile Val Pro Lys Glu Trp Asn Ser Lys
            100                 105


<210> 829
<211> 65
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 18; "

<220>
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<223> /note="ENSP ID: ENSP00000425434"

<400> 829
Met Gly Val Ser Lys Leu Asp Ile Leu Tyr Arg Arg Leu Leu Leu Thr
1               5                   10                  15

Lys Leu Phe Ile Arg Gly Trp Gly Arg Pro Glu Asp Leu Lys Arg Leu
            20                  25                  30

Phe Glu Phe Arg Lys Met Ile Gly Asn Arg Glu Arg Cys Gln Asn Leu
        35                  40                  45
```

```
Val Ser Ser Asp Tyr Pro Val His Ile Asp Lys Val Pro Ile Tyr Cys
    50                  55                  60


Ala
65


<210> 830
<211> 321
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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      domain containing 18; "

<220>
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<223> /note="Uniprot ID:  Q0P651; "

<220>
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<223> /note="ENSP ID: ENSP00000480015"

<400> 830
Met Ala Arg Pro Met Ile Lys Glu Ala Arg Met Ala Ser Leu Leu Leu
1               5                   10                  15


Glu Asn Pro Tyr Tyr Gly Cys Arg Lys Pro Lys Asp Gln Val Arg Ser
            20                  25                  30


Ser Leu Lys Asn Val Ser Asp Leu Phe Val Met Gly Gly Ala Leu Val
        35                  40                  45


Leu Glu Ser Ala Ala Leu Leu His Trp Leu Glu Arg Glu Gly Tyr Gly
    50                  55                  60


Pro Leu Gly Met Thr Gly Ile Ser Met Gly Gly His Met Ala Ser Leu
65                  70                  75                  80
```

```
Ala Val Ser Asn Trp Pro Lys Pro Met Pro Leu Ile Pro Cys Leu Ser
                85                  90                  95

Trp Ser Thr Ala Ser Gly Val Phe Thr Thr Gly Val Leu Ser Lys Ser
            100                 105                 110

Ile Asn Trp Arg Glu Leu Glu Lys Gln Tyr Tyr Thr Gln Thr Val Tyr
        115                 120                 125

Glu Glu Glu Ile Ile His Met Leu Glu Tyr Cys Gly Thr Asp Ser Phe
    130                 135                 140

Lys Met Gly Gln Glu Phe Val Lys His Phe Thr Ser Ser Ala Asp Lys
145                 150                 155                 160

Leu Thr Asn Leu Asn Leu Val Ser Arg Thr Leu Asn Leu Asp Ile Ser
                165                 170                 175

Asn Gln Val Val Ser Gln Lys Pro Ala Asp Cys His Asn Ser Ser Lys
            180                 185                 190

Thr Ser Val Ser Ala Thr Ser Glu Gly Leu Leu Leu Gln Asp Thr Ser
        195                 200                 205

Lys Met Lys Arg Phe Asn Gln Thr Leu Ser Thr Asn Lys Ser Gly Tyr
    210                 215                 220

Thr Ser Arg Asn Pro Gln Ser Tyr His Leu Leu Ser Lys Glu Gln Ser
225                 230                 235                 240

Arg Asn Ser Leu Arg Lys Glu Ser Leu Ile Phe Met Lys Gly Val Met
                245                 250                 255

Asp Glu Cys Thr His Val Ala Asn Phe Ser Val Pro Val Asp Pro Ser
            260                 265                 270

Leu Ile Ile Val Val Gln Ala Lys Glu Asp Ala Tyr Ile Pro Arg Thr
        275                 280                 285

Gly Val Arg Ser Leu Gln Glu Ile Trp Pro Gly Cys Glu Ile Arg Tyr
    290                 295                 300
```

Leu Glu Gly Gly His Ile Ser Ala Tyr Leu Phe Lys Gln Gly Leu Phe
305 310 315 320

Arg

<210> 831
<211> 425
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 141; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD2; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: P08910; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000268129"

<400> 831
Met Asn Ala Met Leu Glu Thr Pro Glu Leu Pro Ala Val Phe Asp Gly
1 5 10 15

Val Lys Leu Ala Ala Val Ala Ala Val Leu Tyr Val Ile Val Arg Cys
20 25 30

Leu Asn Leu Lys Ser Pro Thr Ala Pro Pro Asp Leu Tyr Phe Gln Asp
35 40 45

Ser Gly Leu Ser Arg Phe Leu Leu Lys Ser Cys Pro Leu Leu Thr Lys
50 55 60

Glu Tyr Ile Pro Pro Leu Ile Trp Gly Lys Ser Gly His Ile Gln Thr
65 70 75 80

Ala Leu Tyr Gly Lys Met Gly Arg Val Arg Ser Pro His Pro Tyr Gly

```
                85                  90                  95

His Arg Lys Phe Ile Thr Met Ser Asp Gly Ala Thr Ser Thr Phe Asp
            100                 105                 110

Leu Phe Glu Pro Leu Ala Glu His Cys Val Gly Asp Asp Ile Thr Met
        115                 120                 125

Val Ile Cys Pro Gly Ile Ala Asn His Ser Glu Lys Gln Tyr Ile Arg
    130                 135                 140

Thr Phe Val Asp Tyr Ala Gln Lys Asn Gly Tyr Arg Cys Ala Val Leu
145                 150                 155                 160

Asn His Leu Gly Ala Leu Pro Asn Ile Glu Leu Thr Ser Pro Arg Met
                165                 170                 175

Phe Thr Tyr Gly Cys Thr Trp Glu Phe Gly Ala Met Val Asn Tyr Ile
            180                 185                 190

Lys Lys Thr Tyr Pro Leu Thr Gln Leu Val Val Val Gly Phe Ser Leu
        195                 200                 205

Gly Gly Asn Ile Val Cys Lys Tyr Leu Gly Glu Thr Gln Ala Asn Gln
    210                 215                 220

Glu Lys Val Leu Cys Cys Val Ser Val Cys Gln Gly Tyr Ser Ala Leu
225                 230                 235                 240

Arg Ala Gln Glu Thr Phe Met Gln Trp Asp Gln Cys Arg Arg Phe Tyr
                245                 250                 255

Asn Phe Leu Met Ala Asp Asn Met Lys Lys Ile Ile Leu Ser His Arg
            260                 265                 270

Gln Ala Leu Phe Gly Asp His Val Lys Lys Pro Gln Ser Leu Glu Asp
        275                 280                 285

Thr Asp Leu Ser Arg Leu Tyr Thr Ala Thr Ser Leu Met Gln Ile Asp
    290                 295                 300

Asp Asn Val Met Arg Lys Phe His Gly Tyr Asn Ser Leu Lys Glu Tyr
305                 310                 315                 320
```

```
Tyr Glu Glu Glu Ser Cys Met Arg Tyr Leu His Arg Ile Tyr Val Pro
                325                 330                 335

Leu Met Leu Val Asn Ala Ala Asp Asp Pro Leu Val His Glu Ser Leu
            340                 345                 350

Leu Thr Ile Pro Lys Ser Leu Ser Glu Lys Arg Glu Asn Val Met Phe
        355                 360                 365

Val Leu Pro Leu His Gly Gly His Leu Gly Phe Phe Glu Gly Ser Val
    370                 375                 380

Leu Phe Pro Glu Pro Leu Thr Trp Met Asp Lys Leu Val Val Glu Tyr
385                 390                 395                 400

Ala Asn Ala Ile Cys Gln Trp Glu Arg Asn Lys Leu Gln Cys Ser Asp
                405                 410                 415

Thr Glu Gln Val Glu Ala Asp Leu Glu
            420                 425


<210> 832
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 141; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD2; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 2; "

<220>
<221> source
<223> /note="Uniprot ID:  P08910; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000347217"
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<400> 832
Met Asn Ala Met Leu Glu Thr Pro Glu Leu Pro Ala Val Phe Asp Gly
1 5 10 15

Val Lys Leu Ala Ala Val Ala Ala Val Leu Tyr Val Ile Val Arg Cys
20 25 30

Leu Asn Leu Lys Ser Pro Thr Ala Pro Pro Asp Leu Tyr Phe Gln Asp
35 40 45

Ser Gly Leu Ser Arg Phe Leu Leu Lys Ser Cys Pro Leu Leu Thr Lys
50 55 60

Glu Tyr Ile Pro Pro Leu Ile Trp Gly Lys Ser Gly His Ile Gln Thr
65 70 75 80

Ala Leu Tyr Gly Lys Met Gly Arg Val Arg Ser Pro His Pro Tyr Gly
85 90 95

His Arg Lys Phe Ile Thr Met Ser Asp Gly Ala Thr Ser Thr Phe Asp
100 105 110

Leu Phe Glu Pro Leu Ala Glu His Cys Val Gly Asp Asp Ile Thr Met
115 120 125

Val Ile Cys Pro Gly Ile Ala Asn His Ser Glu Lys Gln Tyr Ile Arg
130 135 140

Thr Phe Val Asp Tyr Ala Gln Lys Asn Gly Tyr Arg Cys Ala Val Leu
145 150 155 160

Asn His Leu Gly Ala Leu Pro Asn Ile Glu Leu Thr Ser Pro Arg Met
165 170 175

Phe Thr Tyr Gly Cys Thr Trp Glu Phe Gly Ala Met Val Asn Tyr Ile
180 185 190

Lys Lys Thr Tyr Pro Leu Thr Gln Leu Val Val Val Gly Phe Ser Leu
195 200 205

Gly Gly Asn Ile Val Cys Lys Tyr Leu Gly Glu Thr Gln Ala Asn Gln
210 215 220

```
Glu Lys Val Leu Cys Cys Val Ser Val Cys Gln Gly Tyr Ser Ala Leu
225                 230                 235                 240

Arg Ala Gln Glu Thr Phe Met Gln Trp Asp Gln Cys Arg Arg Phe Tyr
                245                 250                 255

Asn Phe Leu Met Ala Asp Asn Met Lys Lys Ile Ile Leu Ser His Arg
            260                 265                 270

Gln Ala Leu Phe Gly Asp His Val Lys Lys Pro Gln Ser Leu Glu Asp
        275                 280                 285

Thr Asp Leu Ser Arg Leu Tyr Thr Ala Thr Ser Leu Met Gln Ile Asp
    290                 295                 300

Asp Asn Val Met Arg Lys Phe His Gly Tyr Asn Ser Leu Lys Glu Tyr
305                 310                 315                 320

Tyr Glu Glu Glu Ser Cys Met Arg Tyr Leu His Arg Ile Tyr Val Pro
                325                 330                 335

Leu Met Leu Val Asn Ala Ala Asp Asp Pro Leu Val His Glu Ser Leu
            340                 345                 350

Leu Thr Ile Pro Lys Ser Leu Ser Glu Lys Arg Glu Asn Val Met Phe
        355                 360                 365

Val Leu Pro Leu His Gly Gly His Leu Gly Phe Phe Glu Gly Ser Val
    370                 375                 380

Leu Phe Pro Glu Pro Leu Thr Trp Met Asp Lys Leu Val Val Glu Tyr
385                 390                 395                 400

Ala Asn Ala Ile Cys Gln Trp Glu Arg Asn Lys Leu Gln Cys Ser Asp
                405                 410                 415

Thr Glu Gln Val Glu Ala Asp Leu Glu
            420                 425


<210> 833
<211> 123
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 141; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD2; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 2; "

<220>
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<223> /note="ENSP ID: ENSP00000454531"

<400> 833
Met Asn Ala Met Leu Glu Thr Pro Glu Leu Pro Ala Val Phe Asp Gly
1 5 10 15

Val Lys Leu Ala Ala Val Ala Ala Val Leu Tyr Val Ile Val Arg Cys
20 25 30

Leu Asn Leu Lys Ser Pro Thr Ala Pro Pro Asp Leu Tyr Phe Gln Asp
35 40 45

Ser Gly Leu Ser Arg Phe Leu Leu Lys Ser Cys Pro Leu Leu Thr Lys
50 55 60

Glu Tyr Ile Pro Pro Leu Ile Trp Gly Lys Ser Gly His Ile Gln Thr
65 70 75 80

Ala Leu Tyr Gly Lys Met Gly Arg Val Arg Ser Pro His Pro Tyr Gly
85 90 95

His Arg Lys Phe Ile Thr Met Ser Asp Gly Ala Thr Ser Thr Phe Asp
100 105 110

Leu Phe Glu Pro Leu Ala Glu His Cys Val Gly
115 120

<210> 834
<211> 55
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 141; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD2; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454645"

<400> 834
Met Asn Ala Met Leu Glu Thr Pro Glu Leu Pro Ala Val Phe Asp Gly
1 5 10 15

Val Lys Leu Ala Ala Val Ala Ala Val Leu Tyr Val Ile Val Arg Cys
20 25 30

Leu Asn Leu Lys Ser Pro Thr Ala Pro Pro Asp Leu Tyr Phe Gln Asp
35 40 45

Ser Gly Leu Ser Arg Phe Leu
50 55

<210> 835
<211> 425
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 141; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD2; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: P08910; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455639"

<400> 835
Met Asn Ala Met Leu Glu Thr Pro Glu Leu Pro Ala Val Phe Asp Gly
1   5   10   15

Val Lys Leu Ala Ala Val Ala Ala Val Leu Tyr Val Ile Val Arg Cys
            20   25   30

Leu Asn Leu Lys Ser Pro Thr Ala Pro Pro Asp Leu Tyr Phe Gln Asp
        35   40   45

Ser Gly Leu Ser Arg Phe Leu Leu Lys Ser Cys Pro Leu Leu Thr Lys
    50   55   60

Glu Tyr Ile Pro Pro Leu Ile Trp Gly Lys Ser Gly His Ile Gln Thr
65   70   75   80

Ala Leu Tyr Gly Lys Met Gly Arg Val Arg Ser Pro His Pro Tyr Gly
                85   90   95

His Arg Lys Phe Ile Thr Met Ser Asp Gly Ala Thr Ser Thr Phe Asp
            100   105   110

Leu Phe Glu Pro Leu Ala Glu His Cys Val Gly Asp Asp Ile Thr Met
        115   120   125

Val Ile Cys Pro Gly Ile Ala Asn His Ser Glu Lys Gln Tyr Ile Arg
    130   135   140

Thr Phe Val Asp Tyr Ala Gln Lys Asn Gly Tyr Arg Cys Ala Val Leu
145   150   155   160

Asn His Leu Gly Ala Leu Pro Asn Ile Glu Leu Thr Ser Pro Arg Met
                165   170   175

Phe Thr Tyr Gly Cys Thr Trp Glu Phe Gly Ala Met Val Asn Tyr Ile
            180   185   190

Lys Lys Thr Tyr Pro Leu Thr Gln Leu Val Val Val Gly Phe Ser Leu
        195   200   205

```
Gly Gly Asn Ile Val Cys Lys Tyr Leu Gly Glu Thr Gln Ala Asn Gln
    210                 215                 220

Glu Lys Val Leu Cys Cys Val Ser Val Cys Gln Gly Tyr Ser Ala Leu
225                 230                 235                 240

Arg Ala Gln Glu Thr Phe Met Gln Trp Asp Gln Cys Arg Arg Phe Tyr
                245                 250                 255

Asn Phe Leu Met Ala Asp Asn Met Lys Lys Ile Ile Leu Ser His Arg
            260                 265                 270

Gln Ala Leu Phe Gly Asp His Val Lys Lys Pro Gln Ser Leu Glu Asp
        275                 280                 285

Thr Asp Leu Ser Arg Leu Tyr Thr Ala Thr Ser Leu Met Gln Ile Asp
    290                 295                 300

Asp Asn Val Met Arg Lys Phe His Gly Tyr Asn Ser Leu Lys Glu Tyr
305                 310                 315                 320

Tyr Glu Glu Glu Ser Cys Met Arg Tyr Leu His Arg Ile Tyr Val Pro
                325                 330                 335

Leu Met Leu Val Asn Ala Ala Asp Asp Pro Leu Val His Glu Ser Leu
            340                 345                 350

Leu Thr Ile Pro Lys Ser Leu Ser Glu Lys Arg Glu Asn Val Met Phe
        355                 360                 365

Val Leu Pro Leu His Gly Gly His Leu Gly Phe Phe Glu Gly Ser Val
    370                 375                 380

Leu Phe Pro Glu Pro Leu Thr Trp Met Asp Lys Leu Val Val Glu Tyr
385                 390                 395                 400

Ala Asn Ala Ile Cys Gln Trp Glu Arg Asn Lys Leu Gln Cys Ser Asp
                405                 410                 415

Thr Glu Gln Val Glu Ala Asp Leu Glu
            420                 425
```

<210> 836

<211> 131
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 141; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD2; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457882"

<400> 836

Met	Asn	Ala	Met	Leu	Glu	Thr	Pro	Glu	Leu	Pro	Ala	Val	Phe	Asp	Gly
1				5				10						15	

Val	Lys	Leu	Ala	Ala	Val	Ala	Ala	Val	Leu	Tyr	Val	Ile	Val	Arg	Cys
			20					25					30		

Leu	Asn	Leu	Lys	Ser	Pro	Thr	Ala	Pro	Pro	Asp	Leu	Tyr	Phe	Gln	Asp
		35					40					45			

Ser	Gly	Leu	Ser	Arg	Phe	Leu	Leu	Lys	Ser	Cys	Pro	Leu	Leu	Thr	Lys
	50					55					60				

Glu	Tyr	Ile	Pro	Pro	Leu	Ile	Trp	Gly	Lys	Ser	Gly	His	Ile	Gln	Thr
65					70					75					80

Ala	Leu	Tyr	Gly	Lys	Met	Gly	Arg	Val	Arg	Ser	Pro	His	Pro	Tyr	Gly
				85					90					95	

His	Arg	Lys	Phe	Ile	Thr	Met	Ser	Asp	Gly	Ala	Thr	Ser	Thr	Phe	Asp
			100					105					110		

Leu	Phe	Glu	Pro	Leu	Ala	Glu	His	Cys	Val	Gly	Asp	Asp	Ile	Thr	Met
		115					120					125			

Val	Ile	Cys													
	130														

<210> 837
<211> 409
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 142; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD3; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q8WU67; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000289119"

<400> 837
Met Gln Arg Leu Ala Met Asp Leu Arg Met Leu Ser Arg Glu Leu Ser
1   5   10   15

Leu Tyr Leu Glu His Gln Val Arg Val Gly Phe Phe Gly Ser Gly Val
            20   25   30

Gly Leu Ser Leu Ile Leu Gly Phe Ser Val Ala Tyr Ala Phe Tyr Tyr
        35   40   45

Leu Ser Ser Ile Ala Lys Lys Pro Gln Leu Val Thr Gly Gly Glu Ser
    50   55   60

Phe Ser Arg Phe Leu Gln Asp His Cys Pro Val Val Thr Glu Thr Tyr
65   70   75   80

Tyr Pro Thr Val Trp Cys Trp Glu Gly Arg Gly Gln Thr Leu Leu Arg
                85   90   95

Pro Phe Ile Thr Ser Lys Pro Pro Val Gln Tyr Arg Asn Glu Leu Ile
            100   105   110

```
Lys Thr Ala Asp Gly Gly Gln Ile Ser Leu Asp Trp Phe Asp Asn Asp
        115                 120                 125

Asn Ser Thr Cys Tyr Met Asp Ala Ser Thr Arg Pro Thr Ile Leu Leu
    130                 135                 140

Leu Pro Gly Leu Thr Gly Thr Ser Lys Glu Ser Tyr Ile Leu His Met
145                 150                 155                 160

Ile His Leu Ser Glu Glu Leu Gly Tyr Arg Cys Val Val Phe Asn Asn
                165                 170                 175

Arg Gly Val Ala Gly Glu Asn Leu Leu Thr Pro Arg Thr Tyr Cys Cys
            180                 185                 190

Ala Asn Thr Glu Asp Leu Glu Thr Val Ile His His Val His Ser Leu
        195                 200                 205

Tyr Pro Ser Ala Pro Phe Leu Ala Ala Gly Val Ser Met Gly Gly Met
    210                 215                 220

Leu Leu Leu Asn Tyr Leu Gly Lys Ile Gly Ser Lys Thr Pro Leu Met
225                 230                 235                 240

Ala Ala Ala Thr Phe Ser Val Gly Trp Asn Thr Phe Ala Cys Ser Glu
                245                 250                 255

Ser Leu Glu Lys Pro Leu Asn Trp Leu Leu Phe Asn Tyr Tyr Leu Thr
            260                 265                 270

Thr Cys Leu Gln Ser Ser Val Asn Lys His Arg His Met Phe Val Lys
        275                 280                 285

Gln Val Asp Met Asp His Val Met Lys Ala Lys Ser Ile Arg Glu Phe
    290                 295                 300

Asp Lys Arg Phe Thr Ser Val Met Phe Gly Tyr Gln Thr Ile Asp Asp
305                 310                 315                 320

Tyr Tyr Thr Asp Ala Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile
                325                 330                 335
```

```
Pro Val Leu Cys Leu Asn Ser Val Asp Asp Val Phe Ser Pro Ser His
            340                 345                 350

Ala Ile Pro Ile Glu Thr Ala Lys Gln Asn Pro Asn Val Ala Leu Val
        355                 360                 365

Leu Thr Ser Tyr Gly Gly His Ile Gly Phe Leu Glu Gly Ile Trp Pro
    370                 375                 380

Arg Gln Ser Thr Tyr Met Asp Arg Val Phe Lys Gln Phe Val Gln Ala
385                 390                 395                 400

Met Val Glu His Gly His Glu Leu Ser
                405
```

<210> 838
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 142; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD3; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462578"

<400> 838

```
Met Thr Phe Ile Thr Pro Val Thr Glu Ile Ile Thr Tyr Cys Ser Leu
1               5                  10                  15

Gln Leu Gln Trp Pro Ser Lys Leu Phe Phe Pro Arg Met Leu Leu Leu
            20                  25                  30

Asn Tyr Leu Gly Lys Ile Gly Ser Lys Thr Pro Leu Met Ala Ala Ala
        35                  40                  45

Thr Phe Ser Val Gly Trp Asn Thr Phe Ala Cys Ser Glu Ser Leu Glu
```

```
    50                  55                  60

Lys Pro Leu Asn Trp Leu Leu Phe Asn Tyr Tyr Leu Thr Thr Cys Leu
65                  70                  75                  80

Gln Ser Ser Val Asn Lys His Arg His Met Phe Val Lys Gln Val Asp
                85                  90                  95

Met Asp His Val Met Lys Ala Lys Ser Ile Arg Glu Phe Asp Lys Arg
            100                 105                 110

Phe Thr Ser Val Met Phe Gly Tyr Gln Thr Ile Asp Asp Tyr Tyr Thr
        115                 120                 125

Asp Ala Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile Pro Val Leu
    130                 135                 140

Cys Leu Asn Ser Val Asp Asp Val Phe Ser Pro Ser His Ala Ile Pro
145                 150                 155                 160

Ile Glu Thr Ala Lys Gln Asn Pro Asn Val Ala Leu Val Leu Thr Ser
                165                 170                 175

Tyr Gly Gly His Ile Gly Phe Leu Glu Gly Ile Trp Pro Arg Gln Ser
            180                 185                 190

Thr Tyr Met Asp Arg Val Phe Lys Gln Phe Val Gln Ala Met Val Glu
        195                 200                 205

His Gly His Glu Leu Ser
    210


<210> 839
<211> 356
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 142; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD3; "

<220>
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<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462935"

<400> 839

```
Met Gln Arg Leu Ala Met Asp Leu Arg Met Leu Ser Arg Glu Leu Ser
1               5                  10                  15

Leu Tyr Leu Glu His Gln Val Arg Val Gly Phe Phe Gly Ser Gly Val
            20                  25                  30

Gly Leu Ser Leu Ile Leu Gly Phe Ser Val Ala Tyr Ala Phe Tyr Tyr
        35                  40                  45

Leu Ser Ser Ile Ala Lys Lys Pro Gln Leu Val Thr Gly Gly Glu Ser
    50                  55                  60

Phe Ser Arg Phe Leu Gln Asp His Cys Pro Val Val Thr Glu Thr Tyr
65                  70                  75                  80

Tyr Pro Thr Val Trp Cys Trp Glu Gly Arg Gly Gln Thr Leu Leu Arg
                85                  90                  95

Pro Phe Ile Thr Ser Lys Pro Pro Val Gln Tyr Arg Asn Glu Leu Ile
            100                 105                 110

Lys Thr Ala Asp Gly Gly Gln Ile Ser Leu Asp Trp Phe Asp Asn Asp
        115                 120                 125

Asn Ser Thr Cys Tyr Met Asp Ala Ser Thr Arg Pro Thr Ile Leu Leu
    130                 135                 140

Leu Pro Gly Leu Thr Gly Thr Ser Lys Glu Ser Tyr Ile Leu His Met
145                 150                 155                 160

Ile His Leu Ser Glu Glu Leu Gly Tyr Arg Met Leu Leu Leu Asn Tyr
                165                 170                 175

Leu Gly Lys Ile Gly Ser Lys Thr Pro Leu Met Ala Ala Ala Thr Phe
            180                 185                 190
```

```
Ser Val Gly Trp Asn Thr Phe Ala Cys Ser Glu Ser Leu Glu Lys Pro
        195                 200                 205

Leu Asn Trp Leu Leu Phe Asn Tyr Tyr Leu Thr Thr Cys Leu Gln Ser
    210                 215                 220

Ser Val Asn Lys His Arg His Met Phe Val Lys Gln Val Asp Met Asp
225                 230                 235                 240

His Val Met Lys Ala Lys Ser Ile Arg Glu Phe Asp Lys Arg Phe Thr
                245                 250                 255

Ser Val Met Phe Gly Tyr Gln Thr Ile Asp Asp Tyr Tyr Thr Asp Ala
            260                 265                 270

Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile Pro Val Leu Cys Leu
        275                 280                 285

Asn Ser Val Asp Asp Val Phe Ser Pro Ser His Ala Ile Pro Ile Glu
    290                 295                 300

Thr Ala Lys Gln Asn Pro Asn Val Ala Leu Val Leu Thr Ser Tyr Gly
305                 310                 315                 320

Gly His Ile Gly Phe Leu Glu Gly Ile Trp Pro Arg Gln Ser Thr Tyr
                325                 330                 335

Met Asp Arg Val Phe Lys Gln Phe Val Gln Ala Met Val Glu His Gly
            340                 345                 350

His Glu Leu Ser
        355


<210> 840
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 142; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD3; "
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<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q8WU67; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463365"

<400> 840
Met Gln Arg Leu Ala Met Asp Leu Arg Met Leu Ser Arg Glu Leu Ser
1   5   10   15

Leu Tyr Leu Glu His Gln Val Arg Val Gly Phe Phe Gly Ser Gly Val
            20   25   30

Gly Leu Ser Leu Ile Leu Gly Phe Ser Val Ala Tyr Ala Phe Tyr Tyr
        35   40   45

Leu Ser Ser Ile Ala Lys Lys Arg Thr Thr Arg Arg Ser Gly Ala Gly
    50   55   60

Arg Val Glu Asp Arg Pro Cys Leu Asp Leu Ser Ser Leu Arg Ser Pro
65   70   75   80

Arg Cys Ser Thr Gly Met Asn Leu Leu Lys Leu Gln Met Glu Asp Arg
                85   90   95

Phe His Trp Thr Gly Leu Ile Met Ile Thr Val Arg Val Ile Trp Met
            100   105   110

Pro Ala Pro Asp Leu Leu Ser Tyr Cys Cys Leu Ala Ser Arg Glu Gln
        115   120   125

Ala Arg Ser His Ile Ser Phe Ile
    130   135

<210> 841
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 142; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD3; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463848"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 841
Xaa Val Val Thr Glu Thr Tyr Tyr Pro Thr Val Trp Cys Trp Glu Gly
1 5 10 15

Arg Gly Gln Thr Leu Leu Arg Pro Phe Ile Thr Ser Lys Pro Pro Val
20 25 30

Gln Tyr Arg Asn Glu Leu Ile Lys Thr Ala Asp Gly Gly Gln Ile Ser
35 40 45

Leu Asp Trp Phe Asp Asn Asp Asn Ser Thr Cys Tyr Met Asp Ala Ser
50 55 60

Thr Arg Pro Thr Ile Leu Leu Leu Pro Gly Leu Thr Gly Thr Ser Lys
65 70 75 80

Glu Ser Tyr Ile Leu His Met Ile His Leu Ser Glu Glu Leu Gly Tyr
85 90 95

Arg Cys Val Val Phe Asn Asn Arg Gly Val Ala Gly Glu Asn Leu Leu
100 105 110

<210> 842
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 142; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD3; "

<220>
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<223> /note="Gene Name:
abhydrolase
domain containing 3; "

<220>
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<223> /note="ENSP ID: ENSP00000463996"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 842
Xaa Tyr Thr Asp Ala Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile
1 5 10 15

Pro Val Leu Cys Leu Asn Ser Val Asp Asp Val Phe Ser Pro Ser His
20 25 30

Gly Asn Leu Arg Ser
35

<210> 843
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 143; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000216327"

<400> 843
Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
1   5   10   15

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
            20   25   30

Ala Arg Ile Leu Gln Cys Phe Gly Arg Ser Ser Arg Pro Ala Phe Pro
        35   40   45

Arg Asp Pro Glu Gly Ala Glu Asp Glu Phe Val Thr Ser Ile Glu Thr
    50   55   60

Trp Arg Glu Thr Met Gly Ile Pro Ser Met Ile Leu Leu Gly His Ser
65   70   75   80

Leu Gly Gly Phe Leu Ala Thr Ser Tyr Ser Ile Lys Tyr Pro Asp Arg
                85   90   95

Val Lys His Leu Ile Leu Val Asp Pro Trp Gly Phe Pro Leu Arg Pro
            100   105   110

Thr Asn Pro Ser Glu Ile Arg Ala Pro Pro Ala Trp Val Lys Ala Val
        115   120   125

Ala Ser Val Leu Gly Arg Ser Asn Pro Leu Ala Val Leu Arg Val Ala
    130   135   140

Gly Pro Trp Gly Glu
145

<210> 844
<211> 181
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 143; "

<220>
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<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TB40; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388751"

<400> 844
Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
1   5   10   15

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
            20   25   30

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
        35   40   45

Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
    50   55   60

Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
65   70   75   80

Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Ser Ala Arg Arg Thr
                85   90   95

Leu His Thr Phe Asp Leu Leu Gly Phe Gly Arg Ser Ser Arg Pro Ala
            100   105   110

Phe Pro Arg Asp Pro Glu Gly Ala Glu Asp Glu Phe Val Thr Ser Ile
        115   120   125

Glu Thr Trp Arg Glu Thr Met Gly Ile Pro Ser Met Ile Leu Leu Gly
    130   135   140

His Ser Leu Gly Gly Phe Leu Ala Thr Ser Tyr Ser Ile Lys Tyr Pro
145   150   155   160

Asp Arg Ala Trp Ser Gly Ala Ala Ile Pro Ala Gly Leu Gln Thr Gln

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                165                 170                 175

Val Cys Arg Leu Leu
            180


<210> 845
<211> 342
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 143; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TB40; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414558"

<400> 845
Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
1               5                   10                  15


Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
            20                  25                  30


Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
        35                  40                  45


Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
    50                  55                  60


Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
65                  70                  75                  80


Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Ser Ala Arg Arg Thr
                85                  90                  95
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Leu His Thr Phe Asp Leu Leu Gly Phe Gly Arg Ser Ser Arg Pro Ala
            100                 105                 110

Phe Pro Arg Asp Pro Glu Gly Ala Glu Asp Glu Phe Val Thr Ser Ile
        115                 120                 125

Glu Thr Trp Arg Glu Thr Met Gly Ile Pro Ser Met Ile Leu Leu Gly
    130                 135                 140

His Ser Leu Gly Gly Phe Leu Ala Thr Ser Tyr Ser Ile Lys Tyr Pro
145                 150                 155                 160

Asp Arg Val Lys His Leu Ile Leu Val Asp Pro Trp Gly Phe Pro Leu
                165                 170                 175

Arg Pro Thr Asn Pro Ser Glu Ile Arg Ala Pro Pro Ala Trp Val Lys
            180                 185                 190

Ala Val Ala Ser Val Leu Gly Arg Ser Asn Pro Leu Ala Val Leu Arg
        195                 200                 205

Val Ala Gly Pro Trp Gly Pro Gly Leu Val Gln Arg Phe Arg Pro Asp
    210                 215                 220

Phe Lys Arg Lys Phe Ala Asp Phe Phe Glu Asp Asp Thr Ile Ser Glu
225                 230                 235                 240

Tyr Ile Tyr His Cys Asn Ala Gln Asn Pro Ser Gly Glu Thr Ala Phe
                245                 250                 255

Lys Ala Met Met Glu Ser Phe Gly Trp Ala Arg Arg Pro Met Leu Glu
            260                 265                 270

Arg Ile His Leu Ile Arg Lys Asp Val Pro Ile Thr Met Ile Tyr Gly
        275                 280                 285

Ser Asp Thr Trp Ile Asp Thr Ser Thr Gly Lys Lys Val Lys Met Gln
    290                 295                 300

Arg Pro Asp Ser Tyr Val Arg Asp Met Glu Ile Lys Gly Ala Ser His
305                 310                 315                 320
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His Val Tyr Ala Asp Gln Pro His Ile Phe Asn Ala Val Val Glu Glu
                325                 330                 335


Ile Cys Asp Ser Val Asp
            340


<210> 846
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 143; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437385"

<400> 846
Met Ser Gln Leu Lys Asn Val Glu Ala Arg Ile Leu Gln Cys Leu Gln
1               5                   10                  15


Asn Lys Phe Leu Ala Arg Tyr Val Ser Leu Pro Asn Gln Asn Lys Ile
            20                  25                  30


Trp Thr Val Thr Val Ser Pro Glu Gln Asn Asp Arg Thr Pro Leu Val
        35                  40                  45


Met Val His Gly Phe Gly Gly Gly Val Gly Leu Trp Ile Leu Asn Met
    50                  55                  60


Asp Ser Leu Ser Ala Arg Arg Thr Leu His Thr Phe Asp Leu Leu Gly
65                  70                  75                  80


Phe Gly Arg Ser Ser Arg Pro Ala Phe Pro
                85                  90
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<210> 847
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 143; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438014"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 847
Xaa Ser Gln Gly Trp Leu Ser Ser Trp Leu Pro Thr Trp Arg Pro Thr
1 5 10 15

Ser Met Ser Gln Leu Lys Asn Val Glu Ala Arg Ile Leu Gln Cys Leu
20 25 30

Gln Asn Lys Phe Leu Ala Arg Tyr Val Ser Leu Pro Asn Gln Asn Lys
35 40 45

Ile Trp Thr Val Thr Ser
50

<210> 848
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 143; "

<220>
<221> source

<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438332"

<400> 848
Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
1 5 10 15

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
20 25 30

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
35 40 45

Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
50 55 60

Gln Asn Asp Arg Thr Pro Leu Val Met Leu Lys Ala Ser Ile Pro Lys
65 70 75 80

Gly Pro Gly Gly Gly
85

<210> 849
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 143; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD4; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 4; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000444550"

<400> 849
Met Cys Pro Gln Ser His Cys Trp Ser Gln Gly Trp Leu Ser Ser Trp
1   5   10   15

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
            20   25   30

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu
        35   40

<210> 850
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 144; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD5; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000013894"

<400> 850
Met Ala Ala Glu Glu Glu Glu Val Asp Ser Ala Asp Thr Gly Glu Arg
1   5   10   15

Ser Gly Trp Leu Thr Gly Trp Leu Pro Thr Trp Cys Pro Thr Ser Ile
            20   25   30

Ser His Leu Lys Glu Ala Glu Glu Lys Met Leu Lys
        35   40

<210> 851
<211> 349
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 144; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD5; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 5; "

<220>
<221> source
<223> /note="Uniprot ID: Q8WTS1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000390849"

<400> 851
Met Ala Ala Glu Glu Glu Glu Val Asp Ser Ala Asp Thr Gly Glu Arg
1   5   10   15

Ser Gly Trp Leu Thr Gly Trp Leu Pro Thr Trp Cys Pro Thr Ser Ile
            20   25   30

Ser His Leu Lys Glu Ala Glu Glu Lys Met Leu Lys Cys Val Pro Cys
        35   40   45

Thr Tyr Lys Lys Glu Pro Val Arg Ile Ser Asn Gly Asn Lys Ile Trp
    50   55   60

Thr Leu Lys Phe Ser His Asn Ile Ser Asn Lys Thr Pro Leu Val Leu
65   70   75   80

Leu His Gly Phe Gly Gly Gly Leu Gly Leu Trp Ala Leu Asn Phe Gly
                85   90   95

Asp Leu Cys Thr Asn Arg Pro Val Tyr Ala Phe Asp Leu Leu Gly Phe
            100   105   110

Gly Arg Ser Ser Arg Pro Arg Phe Asp Ser Asp Ala Glu Glu Val Glu
        115   120   125

Asn Gln Phe Val Glu Ser Ile Glu Glu Trp Arg Cys Ala Leu Gly Leu
    130   135   140

```
Asp Lys Met Ile Leu Leu Gly His Asn Leu Gly Gly Phe Leu Ala Ala
145                 150                 155                 160

Ala Tyr Ser Leu Lys Tyr Pro Ser Arg Val Asn His Leu Ile Leu Val
                165                 170                 175

Glu Pro Trp Gly Phe Pro Glu Arg Pro Asp Leu Ala Asp Gln Asp Arg
            180                 185                 190

Pro Ile Pro Val Trp Ile Arg Ala Leu Gly Ala Ala Leu Thr Pro Phe
        195                 200                 205

Asn Pro Leu Ala Gly Leu Arg Ile Ala Gly Pro Phe Gly Leu Ser Leu
    210                 215                 220

Val Gln Arg Leu Arg Pro Asp Phe Lys Arg Lys Tyr Ser Ser Met Phe
225                 230                 235                 240

Glu Asp Asp Thr Val Thr Glu Tyr Ile Tyr His Cys Asn Val Gln Thr
                245                 250                 255

Pro Ser Gly Glu Thr Ala Phe Lys Asn Met Thr Ile Pro Tyr Gly Trp
            260                 265                 270

Ala Lys Arg Pro Met Leu Gln Arg Ile Gly Lys Met His Pro Asp Ile
        275                 280                 285

Pro Val Ser Val Ile Phe Gly Ala Arg Ser Cys Ile Asp Gly Asn Ser
    290                 295                 300

Gly Thr Ser Ile Gln Ser Leu Arg Pro His Ser Tyr Val Lys Thr Ile
305                 310                 315                 320

Ala Ile Leu Gly Ala Gly His Tyr Val Tyr Ala Asp Gln Pro Glu Glu
                325                 330                 335

Phe Asn Gln Lys Val Lys Glu Ile Cys Asp Thr Val Asp
            340                 345
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<210> 852
<211> 126
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 144; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD5; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391582"

<400> 852
Met Leu Lys Cys Val Pro Cys Thr Tyr Lys Lys Glu Pro Val Arg Ile
1 5 10 15

Ser Asn Gly Asn Lys Ile Trp Thr Leu Lys Phe Ser His Asn Ile Ser
20 25 30

Asn Lys Thr Pro Leu Val Leu Leu His Gly Phe Gly Gly Gly Leu Gly
35 40 45

Leu Trp Ala Leu Asn Phe Gly Asp Leu Cys Thr Asn Arg Pro Val Tyr
50 55 60

Ala Phe Asp Leu Leu Gly Phe Gly Arg Ser Ser Arg Pro Arg Phe Asp
65 70 75 80

Ser Asp Ala Glu Glu Val Glu Asn Gln Phe Val Glu Ser Ile Glu Glu
85 90 95

Trp Arg Cys Ala Leu Gly Leu Asp Lys Met Ile Leu Leu Gly His Asn
100 105 110

Leu Gly Gly Phe Leu Ala Ala Ala Tyr Ser Leu Lys Tyr Pro
115 120 125

<210> 853
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 144; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD5; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392159"

<400> 853
Arg Val Asn His Leu Ile Leu Val Glu Pro Trp Gly Phe Pro Glu Arg
1 5 10 15

Pro Asp Leu Ala Asp Gln Asp Arg Pro Ile Pro Val Trp Ile Arg Ala
20 25 30

Leu Gly Ala Ala Leu Thr Pro Phe Asn Pro Leu Ala Gly Leu Arg Ile
35 40 45

Ala Gly Pro Phe Gly Leu Ser Leu Val Gln Arg Leu Arg Pro Asp Phe
50 55 60

Lys Arg Lys Tyr Ser Ser Met Phe Glu Asp Asp Thr Val Thr Glu Tyr
65 70 75 80

Ile Tyr His Cys Asn Val Gln Thr Pro Ser Phe Ser Asp Leu Trp Arg
85 90 95

Pro Ile Leu His Arg Trp Gln Phe Trp His Gln His Pro Val Leu Thr
100 105 110

Thr Thr Phe Ile Cys Glu Asp Asn Ser Tyr Ser Trp Gly Arg Thr Leu
115 120 125

Cys Ile Cys Arg Ser Thr Arg Arg Ile Gln Pro Glu Ser Lys Gly Asp
130 135 140

Leu Arg His Cys Gly Leu Asn Thr Leu Lys Leu

145 150 155

<210> 854
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 144; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD5; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412014"

<400> 854
Met Leu Lys Cys Val Pro Cys Thr Tyr Lys Lys Glu Pro Val Arg Ile
1 5 10 15

Ser Asn Gly Asn Lys Ile Trp Thr Leu Lys Phe Ser His Asn Ile Ser
20 25 30

Asn Lys Thr Pro Leu Val Leu Leu His Gly Phe Gly Gly
35 40 45

<210> 855
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 145; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD6; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BV23; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000295962"

<400> 855
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1   5   10   15

Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
            20   25   30

Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
        35   40   45

Gln Val Arg Tyr Val His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
    50   55   60

Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65   70   75   80

Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
                85   90   95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
            100   105   110

Arg Ser Ser Leu Asp Asp Leu Ser Ile Asp Gly Gln Val Lys Arg Ile
        115   120   125

His Gln Phe Val Glu Cys Leu Lys Leu Asn Lys Lys Pro Phe His Leu
    130   135   140

Val Gly Thr Ser Met Gly Gly Gln Val Ala Gly Val Tyr Ala Ala Tyr
145   150   155   160

Tyr Pro Ser Asp Val Ser Ser Leu Cys Leu Val Cys Pro Ala Gly Leu
                165   170   175

Gln Tyr Ser Thr Asp Asn Gln Phe Val Gln Arg Leu Lys Glu Leu Gln
            180   185   190

```
Gly Ser Ala Ala Val Glu Lys Ile Pro Leu Ile Pro Ser Thr Pro Glu
        195                 200                 205

Glu Met Ser Glu Met Leu Gln Leu Cys Ser Tyr Val Arg Phe Lys Val
    210                 215                 220

Pro Gln Gln Ile Leu Gln Gly Leu Val Asp Val Arg Ile Pro His Asn
225                 230                 235                 240

Asn Phe Tyr Arg Lys Leu Phe Leu Glu Ile Val Ser Glu Lys Ser Arg
                245                 250                 255

Tyr Ser Leu His Gln Asn Met Asp Lys Ile Lys Val Pro Thr Gln Ile
            260                 265                 270

Ile Trp Gly Lys Gln Asp Gln Val Leu Asp Val Ser Gly Ala Asp Met
        275                 280                 285

Leu Ala Lys Ser Ile Ala Asn Cys Gln Val Glu Leu Leu Glu Asn Cys
    290                 295                 300

Gly His Ser Val Val Met Glu Arg Pro Arg Lys Thr Ala Lys Leu Ile
305                 310                 315                 320

Ile Asp Phe Leu Ala Ser Val His Asn Thr Asp Asn Asn Lys Lys Leu
                325                 330                 335

Asp
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<210> 856
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 145; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD6; "

<220>
<221> source
<223> /note="Gene Name:

abhydrolase
domain containing 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418209"

<400> 856
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1 5 10 15

Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
20 25 30

Ala Leu Ile Arg Ile Tyr Tyr Cys Met Ser Ser Val Lys Asp Val Ala
35 40 45

Ala Leu Ser
50

<210> 857
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 145; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD6; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418934"

<400> 857
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1 5 10 15

Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
20 25 30

Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met

```
        35                  40                  45

Gln Val Arg Tyr Val His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
    50                  55                  60

Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65                  70                  75                  80

Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
                85                  90                  95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
            100                 105                 110

Arg Ser Ser Leu Asp Asp Leu Ser Ile Asp Gly Gln Val Lys Arg Ile
        115                 120                 125

His Gln Phe Val Glu Cys Leu Lys Leu Asn Lys Lys Pro Phe His Leu
    130                 135                 140

Val Gly Thr Ser Met Gly Gly Gln Val Ala Gly Val Tyr Ala Ala Tyr
145                 150                 155                 160

Tyr Pro Ser Asp Val Ser Ser Leu Cys Leu Val Cys Pro
                165                 170


<210> 858
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 145; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD6; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 6; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9BV23; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000420315"

<400> 858
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1   5   10   15

Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
            20   25   30

Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
        35   40   45

Gln Val Arg Tyr Val His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
    50   55   60

Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65   70   75   80

Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
                85   90   95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
            100   105   110

Arg Ser Ser Leu Asp Asp Leu Ser Ile Asp Gly Gln Val Lys Arg Ile
        115   120   125

His Gln Phe Val Glu Cys Leu Lys Leu Asn Lys Lys Pro Phe His Leu
    130   135   140

Val Gly Thr Ser Met Gly Gly Gln Val Ala Gly Val Tyr Ala Ala Tyr
145   150   155   160

Tyr Pro Ser Asp Val Ser Ser Leu Cys Leu Val Cys Pro Ala Gly Leu
                165   170   175

Gln Tyr Ser Thr Asp Asn Gln Phe Val Gln Arg Leu Lys Glu Leu Gln
            180   185   190

Gly Ser Ala Ala Val Glu Lys Ile Pro Leu Ile Pro Ser Thr Pro Glu
        195   200   205

```
Glu Met Ser Glu Met Leu Gln Leu Cys Ser Tyr Val Arg Phe Lys Val
    210                 215                 220

Pro Gln Gln Ile Leu Gln Gly Leu Val Asp Val Arg Ile Pro His Asn
225                 230                 235                 240

Asn Phe Tyr Arg Lys Leu Phe Leu Glu Ile Val Ser Glu Lys Ser Arg
                245                 250                 255

Tyr Ser Leu His Gln Asn Met Asp Lys Ile Lys Val Pro Thr Gln Ile
            260                 265                 270

Ile Trp Gly Lys Gln Asp Gln Val Leu Asp Val Ser Gly Ala Asp Met
        275                 280                 285

Leu Ala Lys Ser Ile Ala Asn Cys Gln Val Glu Leu Leu Glu Asn Cys
    290                 295                 300

Gly His Ser Val Val Met Glu Arg Pro Arg Lys Thr Ala Lys Leu Ile
305                 310                 315                 320

Ile Asp Phe Leu Ala Ser Val His Asn Thr Asp Asn Asn Lys Lys Leu
                325                 330                 335

Asp
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<210> 859
<211> 225
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 145; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD6; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 6; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000420408"

<400> 859
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1 5 10 15

Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
20 25 30

Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
35 40 45

Gln Val Arg Tyr Val His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
50 55 60

Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65 70 75 80

Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
85 90 95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
100 105 110

Arg Ser Ser Leu Asp Asp Leu Ser Ile Asp Gly Gln Val Lys Arg Ile
115 120 125

His Gln Phe Val Glu Cys Leu Lys Leu Asn Lys Lys Pro Phe His Leu
130 135 140

Val Gly Thr Ser Met Gly Gly Gln Val Ala Gly Val Tyr Ala Ala Tyr
145 150 155 160

Tyr Pro Ser Asp Val Ser Ser Leu Cys Leu Val Cys Pro Ala Gly Leu
165 170 175

Gln Tyr Ser Thr Asp Asn Gln Phe Val Gln Arg Leu Lys Glu Leu Gln
180 185 190

Gly Ser Ala Ala Val Glu Lys Ile Pro Leu Ile Pro Ser Thr Pro Glu
195 200 205

Glu Met Ser Glu Met Leu Gln Leu Cys Ser Tyr Val Arg Phe Lys Val

210 215 220

Pro
225

<210> 860
<211> 318
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 145; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD6; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484876"

<400> 860
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1 5 10 15

Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
20 25 30

Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
35 40 45

Gln Val Arg Tyr Val His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
50 55 60

Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65 70 75 80

Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
85 90 95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
100 105 110

```
Arg Ser Ser Leu Asp Asp Leu Ser Ile Asp Gly Gln Val Lys Arg Ile
        115                 120                 125

His Gln Phe Val Glu Cys Leu Lys Leu Asn Lys Lys Pro Phe His Leu
    130                 135                 140

Val Gly Thr Ser Met Gly Gly Gln Val Ala Gly Val Tyr Ala Ala Tyr
145                 150                 155                 160

Tyr Pro Ser Asp Val Ser Ser Leu Cys Leu Val Cys Pro Ala Gly Leu
                165                 170                 175

Gln Tyr Ser Thr Asp Asn Gln Phe Val Gln Arg Leu Lys Glu Leu Gln
            180                 185                 190

Gly Ser Ala Ala Val Glu Lys Ile Pro Leu Ile Pro Ser Thr Pro Glu
        195                 200                 205

Glu Met Ser Glu Met Leu Gln Leu Cys Ser Tyr Val Arg Phe Lys Val
    210                 215                 220

Pro Gln Gln Ile Leu Gln Gly Leu Val Asp Val Arg Ile Pro His Asn
225                 230                 235                 240

Asn Phe Tyr Arg Lys Leu Phe Leu Glu Ile Val Ser Glu Lys Ser Arg
                245                 250                 255

Tyr Ser Leu His Gln Asn Met Asp Lys Ile Lys Val Pro Thr Gln Ile
            260                 265                 270

Ile Trp Gly Lys Gln Asp Gln Val Leu Asp Val Ser Gly Ala Asp Val
        275                 280                 285

Gly Gln Val Asn Cys Gln Leu Pro Gly Gly Ala Ser Gly Lys Leu Trp
    290                 295                 300

Ala Leu Ser Ser Asp Gly Lys Pro Gly Arg Gln Pro Ser Ser
305                 310                 315
```

<210> 861
<211> 439
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 146; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD8; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 8; "

<220>
<221> source
<223> /note="Uniprot ID: Q96I13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000247706"

<400> 861

Met	Leu	Thr	Gly	Val	Thr	Asp	Gly	Ile	Phe	Cys	Cys	Leu	Leu	Gly	Thr
1				5				10						15	
Pro	Pro	Asn	Ala	Val	Gly	Pro	Leu	Glu	Ser	Val	Glu	Ser	Ser	Asp	Gly
			20					25					30		
Tyr	Thr	Phe	Val	Glu	Val	Lys	Pro	Gly	Arg	Val	Leu	Arg	Val	Lys	His
		35					40					45			
Ala	Gly	Pro	Ala	Pro	Ala	Ala	Ala	Pro	Pro	Pro	Pro	Ser	Ser	Ala	Ser
	50					55					60				
Ser	Asp	Ala	Ala	Gln	Gly	Asp	Leu	Ser	Gly	Leu	Val	Arg	Cys	Gln	Arg
65					70					75					80
Arg	Ile	Thr	Val	Tyr	Arg	Asn	Gly	Arg	Leu	Leu	Val	Glu	Asn	Leu	Gly
				85					90					95	
Arg	Ala	Pro	Arg	Ala	Asp	Leu	Leu	His	Gly	Gln	Asn	Gly	Ser	Gly	Glu
			100					105					110		
Pro	Pro	Ala	Ala	Leu	Glu	Val	Glu	Leu	Ala	Asp	Pro	Ala	Gly	Ser	Asp
		115					120					125			

```
Gly Arg Leu Ala Pro Gly Ser Ala Gly Ser Gly Ser Gly Ser Gly Ser
    130                 135                 140

Gly Gly Arg Arg Arg Arg Ala Arg Arg Pro Lys Arg Thr Ile His Ile
145                 150                 155                 160

Asp Cys Glu Lys Arg Ile Thr Ser Cys Lys Gly Ala Gln Ala Asp Val
                165                 170                 175

Val Leu Phe Phe Ile His Gly Val Gly Gly Ser Leu Ala Ile Trp Lys
            180                 185                 190

Glu Gln Leu Asp Phe Phe Val Arg Leu Gly Tyr Glu Val Val Ala Pro
        195                 200                 205

Asp Leu Ala Gly His Gly Ala Ser Ser Ala Pro Gln Val Ala Ala Ala
    210                 215                 220

Tyr Thr Phe Tyr Ala Leu Ala Glu Asp Met Arg Ala Ile Phe Lys Arg
225                 230                 235                 240

Tyr Ala Lys Lys Arg Asn Val Leu Ile Gly His Ser Tyr Gly Val Ser
                245                 250                 255

Phe Cys Thr Phe Leu Ala His Glu Tyr Pro Asp Leu Val His Lys Val
            260                 265                 270

Ile Met Ile Asn Gly Gly Gly Pro Thr Ala Leu Glu Pro Ser Phe Cys
        275                 280                 285

Ser Ile Phe Asn Met Pro Thr Cys Val Leu His Cys Leu Ser Pro Cys
    290                 295                 300

Leu Ala Trp Ser Phe Leu Lys Ala Gly Phe Ala Arg Gln Gly Ala Lys
305                 310                 315                 320

Glu Lys Gln Leu Leu Lys Glu Gly Asn Ala Phe Asn Val Ser Ser Phe
                325                 330                 335

Val Leu Arg Ala Met Met Ser Gly Gln Tyr Trp Pro Glu Gly Asp Glu
            340                 345                 350

Val Tyr His Ala Glu Leu Thr Val Pro Val Leu Leu Val His Gly Met
```

```
        355                 360                 365

His Asp Lys Phe Val Pro Val Glu Glu Asp Gln Arg Met Ala Glu Ile
    370                 375                 380

Leu Leu Leu Ala Phe Leu Lys Leu Ile Asp Glu Gly Ser His Met Val
385                 390                 395                 400

Met Leu Glu Cys Pro Glu Thr Val Asn Thr Leu Leu His Glu Phe Leu
                405                 410                 415

Leu Trp Glu Pro Glu Pro Ser Pro Lys Ala Leu Pro Glu Pro Leu Pro
            420                 425                 430

Ala Pro Pro Glu Asp Lys Lys
        435
```

<210> 862
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 146; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD8; "

<220>
<221> source
<223> /note="Gene Name:
abhydrolase
domain containing 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468883"

<400> 862

```
Met Arg Ile Gly Asp Lys Ser Phe Ser Phe Leu Glu Ala Gly His Thr
1               5                   10                  15

Met Leu Thr Gly Val Thr Asp Gly Ile Phe Cys Cys Leu Leu Gly Thr
            20                  25                  30

Pro Pro Asn Ala Val Gly Pro Leu Glu Ser Val Glu Ser Ser Asp Gly
        35                  40                  45
```

```
Tyr Thr Phe Val Glu Val Lys Pro Gly Arg Val Leu Arg Val Lys His
    50                  55                  60

Ala Gly Pro Ala Pro Ala Ala Ala Pro Pro Pro Pro Ser Ser Ala Ser
65                  70                  75                  80

Ser Asp Ala Ala Gln Gly Asp Leu Ser Gly Leu Val Arg Cys Gln Arg
                85                  90                  95

Arg Ile Thr Val Tyr Arg Asn Gly Arg Leu Leu Val Glu Asn Leu Gly
            100                 105                 110

Arg Ala Pro Arg Ala Asp Leu Leu His Gly Gln Asn Gly Ser Gly Glu
        115                 120                 125

Pro Pro Ala Ala Leu Glu Val Glu Leu Ala Asp Pro Ala Gly Ser Asp
    130                 135                 140

Gly Arg Leu Ala Pro Gly Ser Ala Gly Ser Gly Ser Gly Ser Gly Ser
145                 150                 155                 160

Gly Gly Arg Arg Arg Arg Ala Arg Arg Pro Lys Arg Thr Ile His
                165                 170                 175


<210> 863
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 146; "

<220>
<221> source
<223> /note="Gene Symbol: ABHD8; "

<220>
<221> source
<223> /note="Gene Name:
      abhydrolase
      domain containing 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470413"
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<400> 863
Met Arg Asn Ile Pro Thr Gln Asp Ala Thr Thr Phe Pro Val Asp Thr
1   5   10   15

Leu Trp Gly His Thr Met Leu Thr Gly Val Thr Asp Gly Ile Phe Cys
            20   25   30

Cys Leu Leu Gly Thr Pro Pro Asn Ala Val Gly Pro Leu Glu Ser Val
        35   40   45

Glu Ser Ser Asp Gly Tyr Thr Phe Val Glu Val Lys Pro Gly Arg Val
    50   55   60

Leu Arg Val Lys His Ala Gly Pro Ala Pro Ala Ala Ala Pro Pro Pro
65   70   75   80

Pro Ser Ser Ala Ser Ser Asp Ala Ala Gln Gly Asp Leu Ser Gly Leu
                85   90   95

Val Arg Cys Gln Arg Arg Ile Thr Val Tyr Arg Asn Gly Arg Leu Leu
            100   105   110

Val Glu Asn Leu Gly Arg Ala Pro Arg Ala Asp Leu Leu His Gly Gln
        115   120   125

Asn Gly
    130

<210> 864
<211> 366
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 147; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3; "

<220>

<221> source
<223> /note="Uniprot ID: Q9P2A4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000225941"

<400> 864
Met Ala Glu Leu Gln Gln Leu Gln Glu Phe Glu Ile Pro Thr Gly Arg
1   5   10   15

Glu Ala Leu Arg Gly Asn His Ser Ala Leu Leu Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asp Asn Tyr Val Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35   40   45

Glu Thr Met Ala Phe Thr Thr Gln Ala Leu Ala Ser Val Ala Tyr Gln
    50   55   60

Val Gly Asn Leu Ala Gly His Thr Leu Arg Met Leu Asp Leu Gln Gly
65   70   75   80

Ala Ala Leu Arg Gln Val Glu Ala Arg Val Ser Thr Leu Gly Gln Met
                85   90   95

Val Asn Met His Met Glu Lys Val Ala Arg Arg Glu Ile Gly Thr Leu
            100   105   110

Ala Thr Val Gln Arg Leu Pro Pro Gly Gln Lys Val Ile Ala Pro Glu
        115   120   125

Asn Leu Pro Pro Leu Thr Pro Tyr Cys Arg Arg Pro Leu Asn Phe Gly
    130   135   140

Cys Leu Asp Asp Ile Gly His Gly Ile Lys Asp Leu Ser Thr Gln Leu
145   150   155   160

Ser Arg Thr Gly Thr Leu Ser Arg Lys Ser Ile Lys Ala Pro Ala Thr
                165   170   175

Pro Ala Ser Ala Thr Leu Gly Arg Pro Pro Arg Ile Pro Glu Pro Val
            180   185   190

His Leu Pro Val Val Pro Asp Gly Arg Leu Ser Ala Ala Ser Ser Ala

```
        195                 200                 205

Phe Ser Leu Ala Ser Ala Gly Ser Ala Glu Gly Val Gly Gly Ala Pro
    210                 215                 220

Thr Pro Lys Gly Gln Ala Ala Pro Pro Ala Pro Pro Leu Pro Ser Ser
225                 230                 235                 240

Leu Asp Pro Pro Pro Pro Pro Ala Ala Val Glu Val Phe Gln Arg Pro
                245                 250                 255

Pro Thr Leu Glu Glu Leu Ser Pro Pro Pro Pro Asp Glu Glu Leu Pro
            260                 265                 270

Leu Pro Leu Asp Leu Pro Pro Pro Pro Pro Leu Asp Gly Asp Glu Leu
        275                 280                 285

Gly Leu Pro Pro Pro Pro Pro Gly Phe Gly Pro Asp Glu Pro Ser Trp
    290                 295                 300

Val Pro Ala Ser Tyr Leu Glu Lys Val Val Thr Leu Tyr Pro Tyr Thr
305                 310                 315                 320

Ser Gln Lys Asp Asn Glu Leu Ser Phe Ser Glu Gly Thr Val Ile Cys
                325                 330                 335

Val Thr Arg Arg Tyr Ser Asp Gly Trp Cys Glu Gly Val Ser Ser Glu
            340                 345                 350

Gly Thr Gly Phe Phe Pro Gly Asn Tyr Val Glu Pro Ser Cys
        355                 360                 365


<210> 865
<211> 360
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 147; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3; "

<220>
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<221> source
<223> /note="Gene Name:
ABI
family, member 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9P2A4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000406651"

<400> 865

```
Met Ala Glu Leu Gln Gln Leu Gln Glu Phe Glu Ile Pro Thr Gly Arg
1               5                  10                  15

Glu Ala Leu Arg Gly Asn His Ser Ala Leu Leu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asp Asn Tyr Val Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35                  40                  45

Glu Thr Met Ala Phe Thr Thr Gln Ala Leu Ala Ser Val Ala Tyr Gln
    50                  55                  60

Val Gly Asn Leu Ala Gly His Thr Leu Arg Met Leu Asp Leu Gln Gly
65                  70                  75                  80

Ala Ala Leu Arg Gln Val Glu Ala Arg Met Val Asn Met His Met Glu
                85                  90                  95

Lys Val Ala Arg Arg Glu Ile Gly Thr Leu Ala Thr Val Gln Arg Leu
            100                 105                 110

Pro Pro Gly Gln Lys Val Ile Ala Pro Glu Asn Leu Pro Pro Leu Thr
        115                 120                 125

Pro Tyr Cys Arg Arg Pro Leu Asn Phe Gly Cys Leu Asp Asp Ile Gly
    130                 135                 140

His Gly Ile Lys Asp Leu Ser Thr Gln Leu Ser Arg Thr Gly Thr Leu
145                 150                 155                 160

Ser Arg Lys Ser Ile Lys Ala Pro Ala Thr Pro Ala Ser Ala Thr Leu
                165                 170                 175
```

```
Gly Arg Pro Pro Arg Ile Pro Glu Pro Val His Leu Pro Val Val Pro
            180                 185                 190

Asp Gly Arg Leu Ser Ala Ala Ser Ser Ala Phe Ser Leu Ala Ser Ala
        195                 200                 205

Gly Ser Ala Glu Gly Val Gly Gly Ala Pro Thr Pro Lys Gly Gln Ala
    210                 215                 220

Ala Pro Pro Ala Pro Pro Leu Pro Ser Ser Leu Asp Pro Pro Pro Pro
225                 230                 235                 240

Pro Ala Ala Val Glu Val Phe Gln Arg Pro Pro Thr Leu Glu Glu Leu
                245                 250                 255

Ser Pro Pro Pro Pro Asp Glu Glu Leu Pro Leu Pro Leu Asp Leu Pro
            260                 265                 270

Pro Pro Pro Pro Leu Asp Gly Asp Glu Leu Gly Leu Pro Pro Pro Pro
        275                 280                 285

Pro Gly Phe Gly Pro Asp Glu Pro Ser Trp Val Pro Ala Ser Tyr Leu
    290                 295                 300

Glu Lys Val Val Thr Leu Tyr Pro Tyr Thr Ser Gln Lys Asp Asn Glu
305                 310                 315                 320

Leu Ser Phe Ser Glu Gly Thr Val Ile Cys Val Thr Arg Arg Tyr Ser
                325                 330                 335

Asp Gly Trp Cys Glu Gly Val Ser Ser Glu Gly Thr Gly Phe Phe Pro
            340                 345                 350

Gly Asn Tyr Val Glu Pro Ser Cys
        355                 360


<210> 866
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 147; "
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<220>
<221> source
<223> /note="Gene Symbol: ABI3; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459171"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 866
Xaa Arg Pro Pro Arg Ile Pro Glu Pro Val His Leu Pro Val Val Pro
1 5 10 15

Asp Gly Arg Leu Ser Ala Ala Ser Ser Ala Phe Ser Leu Ala Ser Ala
20 25 30

Gly Ser Ala Glu Gly Val Gly Gly Ala Pro Thr Pro Lys Gly Gln Ala
35 40 45

Ala Pro Pro Ala Pro Pro Leu Pro Ser Ser Leu Asp Pro Pro Pro Pro
50 55 60

Pro Ala Ala Val Glu Val Phe Gln Arg Pro Pro Thr Leu Glu Glu Leu
65 70 75 80

Ser Pro Pro Pro Pro Ala Phe Leu Leu Phe Pro Gln Asp Glu Glu Leu
85 90 95

Pro Leu Pro Leu Asp Leu Pro Pro Pro Pro Pro Leu Asp Gly Asp Glu
100 105 110

Leu Gly Leu Pro Pro Pro Pro Pro Gly Phe Gly Pro Asp Glu Pro Ser
115 120 125

Trp Val Pro Ala Ser Tyr Leu Glu Lys Val Val Thr Leu Tyr Pro Tyr
130 135 140

```
Thr Ser Gln Lys Asp Asn Glu Leu Ser Phe Ser Glu Gly Thr Val Ile
145                 150                 155                 160


Cys Val Thr Arg Arg Tyr Ser Asp Gly Trp Cys Glu Gly Val Ser Ser
                165                 170                 175


Glu Gly Thr Gly Phe Phe Pro Gly Asn Tyr Val Glu Pro Ser Cys
            180                 185                 190


<210> 867
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 147; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460776"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 867
Xaa Thr Gly Thr Leu Ser Arg Lys Ser Ile Lys Ala Pro Ala Thr Pro
1               5                   10                  15


Ala Ser Ala Thr Leu Gly Arg Pro Pro Arg Ile Pro Glu Pro Val His
            20                  25                  30


Leu Pro Val Val Pro Asp Gly Arg Leu Ser Ala Ala Ser Ser Ala Phe
        35                  40                  45


Ser Leu Ala Ser Ala Gly Ser Ala Glu Gly Val Gly Gly Ala Pro Thr
    50                  55                  60
```

```
Pro Lys Gly Gln Ala Ala Pro Pro Ala Pro Pro Leu Pro Ser Ser Leu
65                  70                  75                  80

Asp Pro Pro Pro Pro Pro Ala Ala Val Glu Val Phe Gln Arg Pro Pro
                85                  90                  95

Thr Leu Glu Glu Leu Ser Pro Pro Pro Pro Ala Phe Leu Leu Phe Pro
            100                 105                 110

Gln Asp Glu Glu Leu Pro Leu Pro Leu Asp Leu Pro Pro Pro Pro Pro
        115                 120                 125

Leu Asp Gly Asp Glu Leu Gly Leu Pro Pro Pro Pro Pro Gly Phe Gly
    130                 135                 140

Pro Asp Glu Pro Ser Trp Val Pro Ala Ser Tyr Leu Glu Lys Gly Thr
145                 150                 155                 160


<210> 868
<211> 1075
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="Uniprot ID:  Q7Z7G0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000284322"

<400> 868
Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu Gly Cys Leu Leu
1               5                   10                  15
```

```
Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala Gln Lys Leu Pro
            20                  25                  30

Lys Gly Lys Arg Pro Asn Leu Lys Val His Ile Asn Thr Thr Ser Asp
        35                  40                  45

Ser Ile Leu Leu Lys Phe Leu Arg Pro Ser Pro Asn Val Lys Leu Glu
    50                  55                  60

Gly Leu Leu Leu Gly Tyr Gly Ser Asn Val Ser Pro Asn Gln Tyr Phe
65                  70                  75                  80

Pro Leu Pro Ala Glu Gly Lys Phe Thr Glu Ala Ile Val Asp Ala Glu
                85                  90                  95

Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro Pro Ser Gln Lys
            100                 105                 110

Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro Leu Gln Leu Val
        115                 120                 125

Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser Trp Gly Phe Leu
    130                 135                 140

Ile Asn Pro His His Asp Trp Thr Leu Pro Ser His Cys Pro Asn Asp
145                 150                 155                 160

Arg Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys Glu Lys Lys Trp
                165                 170                 175

Ile Phe Gln Ile Cys Pro Ala Thr Glu Thr Ile Val Glu Asn Leu Lys
            180                 185                 190

Pro Asn Thr Val Tyr Glu Phe Gly Val Lys Asp Asn Val Glu Gly Gly
        195                 200                 205

Ile Trp Ser Lys Ile Phe Asn His Lys Thr Val Val Gly Ser Lys Lys
    210                 215                 220

Val Asn Gly Lys Ile Gln Ser Thr Tyr Asp Gln Asp His Thr Val Pro
225                 230                 235                 240
```

```
Ala Tyr Val Pro Arg Lys Leu Ile Pro Ile Thr Ile Ile Lys Gln Val
                245                 250                 255

Ile Gln Asn Val Thr His Lys Asp Ser Ala Lys Ser Pro Glu Lys Ala
            260                 265                 270

Pro Leu Gly Gly Val Ile Leu Val His Leu Ile Ile Pro Gly Leu Asn
        275                 280                 285

Glu Thr Thr Val Lys Leu Pro Ala Ser Leu Met Phe Glu Ile Ser Asp
    290                 295                 300

Ala Leu Lys Thr Gln Leu Ala Lys Asn Glu Thr Leu Ala Leu Pro Ala
305                 310                 315                 320

Glu Ser Lys Thr Pro Glu Val Glu Lys Ile Ser Ala Arg Pro Thr Thr
                325                 330                 335

Val Thr Pro Glu Thr Val Pro Arg Ser Thr Lys Pro Thr Thr Ser Ser
            340                 345                 350

Ala Leu Asp Val Ser Glu Thr Thr Leu Ala Ser Ser Glu Lys Pro Trp
        355                 360                 365

Ile Val Pro Thr Ala Lys Ile Ser Glu Asp Ser Lys Val Leu Gln Pro
    370                 375                 380

Gln Thr Ala Thr Tyr Asp Val Phe Ser Ser Pro Thr Thr Ser Asp Glu
385                 390                 395                 400

Pro Glu Ile Ser Asp Ser Tyr Thr Ala Thr Ser Asp Arg Ile Leu Asp
                405                 410                 415

Ser Ile Pro Pro Lys Thr Ser Arg Thr Leu Glu Gln Pro Arg Ala Thr
            420                 425                 430

Leu Ala Pro Ser Glu Thr Pro Phe Val Pro Gln Lys Leu Glu Ile Phe
        435                 440                 445

Thr Ser Pro Glu Met Gln Pro Thr Thr Pro Ala Pro Gln Gln Thr Thr
    450                 455                 460

Ser Ile Pro Ser Thr Pro Lys Arg Arg Pro Arg Pro Lys Pro Pro Arg
```

```
465                 470                 475                 480

Thr Lys Pro Glu Arg Thr Thr Ser Ala Gly Thr Ile Thr Pro Lys Ile
                485                 490                 495

Ser Lys Ser Pro Glu Pro Thr Trp Thr Thr Pro Ala Pro Gly Lys Thr
            500                 505                 510

Gln Phe Ile Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val Thr
        515                 520                 525

His Thr Lys Pro Ala Pro Lys Gln Thr Pro Arg Ala Pro Pro Lys Pro
    530                 535                 540

Lys Thr Ser Pro Arg Pro Arg Ile Pro Gln Thr Gln Pro Val Pro Lys
545                 550                 555                 560

Val Pro Gln Arg Val Thr Ala Lys Pro Lys Thr Ser Pro Ser Pro Glu
                565                 570                 575

Val Ser Tyr Thr Thr Pro Ala Pro Lys Asp Val Leu Leu Pro His Lys
            580                 585                 590

Pro Tyr Pro Glu Val Ser Gln Ser Glu Pro Ala Pro Leu Glu Thr Arg
        595                 600                 605

Gly Ile Pro Phe Ile Pro Met Ile Ser Pro Ser Pro Ser Gln Glu Glu
    610                 615                 620

Leu Gln Thr Thr Leu Glu Glu Thr Asp Gln Ser Thr Gln Glu Pro Phe
625                 630                 635                 640

Thr Thr Lys Ile Pro Arg Thr Thr Glu Leu Ala Lys Thr Thr Gln Ala
                645                 650                 655

Pro His Arg Phe Tyr Thr Thr Val Arg Pro Arg Thr Ser Asp Lys Pro
            660                 665                 670

His Ile Arg Pro Gly Val Lys Gln Ala Pro Arg Pro Ser Gly Ala Asp
        675                 680                 685

Arg Asn Val Ser Val Asp Ser Thr His Pro Thr Lys Lys Pro Gly Thr
    690                 695                 700
```

```
Arg Arg Pro Pro Leu Pro Pro Arg Pro Thr His Pro Arg Arg Lys Pro
705                 710                 715                 720

Leu Pro Pro Asn Asn Val Thr Gly Lys Pro Gly Ser Ala Gly Ile Ile
                725                 730                 735

Ser Ser Gly Pro Ile Thr Thr Pro Pro Leu Arg Ser Thr Pro Arg Pro
            740                 745                 750

Thr Gly Thr Pro Leu Glu Arg Ile Glu Thr Asp Ile Lys Gln Pro Thr
        755                 760                 765

Val Pro Ala Ser Gly Glu Glu Leu Glu Asn Ile Thr Asp Phe Ser Ser
    770                 775                 780

Ser Pro Thr Arg Glu Thr Asp Pro Leu Gly Lys Pro Arg Phe Lys Gly
785                 790                 795                 800

Pro His Val Arg Tyr Ile Gln Lys Pro Asp Asn Ser Pro Cys Ser Ile
                805                 810                 815

Thr Asp Ser Val Lys Arg Phe Pro Lys Glu Glu Ala Thr Glu Gly Asn
            820                 825                 830

Ala Thr Ser Pro Pro Gln Asn Pro Pro Thr Asn Leu Thr Val Val Thr
        835                 840                 845

Val Glu Gly Cys Pro Ser Phe Val Ile Leu Asp Trp Glu Lys Pro Leu
    850                 855                 860

Asn Asp Thr Val Thr Glu Tyr Glu Val Ile Ser Arg Glu Asn Gly Ser
865                 870                 875                 880

Phe Ser Gly Lys Asn Lys Ser Ile Gln Met Thr Asn Gln Thr Phe Ser
                885                 890                 895

Thr Val Glu Asn Leu Lys Pro Asn Thr Ser Tyr Glu Phe Gln Val Lys
            900                 905                 910

Pro Lys Asn Pro Leu Gly Glu Gly Pro Val Ser Asn Thr Val Ala Phe
        915                 920                 925
```

```
Ser Thr Glu Ser Ala Asp Pro Arg Val Ser Glu Pro Val Ser Ala Gly
    930                 935                 940

Arg Asp Ala Ile Trp Thr Glu Arg Pro Phe Asn Ser Asp Ser Tyr Ser
945                 950                 955                 960

Glu Cys Lys Gly Lys Gln Tyr Val Lys Arg Thr Trp Tyr Lys Lys Phe
                965                 970                 975

Val Gly Val Gln Leu Cys Asn Ser Leu Arg Tyr Lys Ile Tyr Leu Ser
            980                 985                 990

Asp Ser Leu Thr Gly Lys Phe Tyr  Asn Ile Gly Asp Gln  Arg Gly
His
        995                 1000                1005

Gly Glu  Asp His Cys Gln Phe  Val Asp Ser Phe Leu  Asp Gly Arg
    1010                1015                1020

Thr Gly  Gln Gln Leu Thr Ser  Asp Gln Leu Pro Ile  Lys Glu Gly
    1025                1030                1035

Tyr Phe  Arg Ala Val Arg Gln  Glu Pro Val Gln Phe  Gly Glu Ile
    1040                1045                1050

Gly Gly  His Thr Gln Ile Asn  Tyr Val Gln Trp Tyr  Glu Cys Gly
    1055                1060                1065

Thr Thr  Ile Pro Gly Lys Trp
    1070                1075


<210> 869
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
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<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417325"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 869
Xaa Phe Glu Lys Pro Arg Gly Thr Leu Ala Ser Ser Glu Lys Pro Trp
1 5 10 15

Ile Val Pro Thr Ala Lys Ile Ser Glu Asp Ser Lys Val Leu Gln Pro
20 25 30

Gln Thr Ala Thr Ser Asp Arg Ile Leu Asp Ser Ile Pro Pro Lys Thr
35 40 45

Ser Arg Thr Leu Glu Gln Pro Arg Ala Thr Leu Ala Pro Ser Glu Thr
50 55 60

Pro Phe Val Pro Gln Lys Leu Glu Ile Phe Thr Ser Pro Glu Met Gln
65 70 75 80

Pro Thr Thr Pro

<210> 870
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417745"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 870
Xaa Lys Thr Thr Pro His Pro Glu Val Pro Gln Thr Lys Leu Ala Pro
1 5 10 15

Lys Val Pro Gln Arg Thr His Arg Pro His Pro Lys Pro Lys Thr Thr
20 25 30

Leu Ser Pro Glu Glu Leu Gln Thr Glu Leu Val Pro Ala Thr Ile Phe
35 40 45

Glu Pro Val Ser Pro Ile Lys Glu Ala Pro Gly Thr Thr Phe Val Pro
50 55 60

Val Thr Asp Leu Glu Pro Val Thr Phe Arg Thr Glu Ile Pro Ala Thr
65 70 75 80

Thr Leu Ala Thr Lys Thr Ser Lys Arg Thr Arg Pro Pro Arg Pro Arg
85 90 95

Pro Lys Thr Thr Pro Ser Pro Gln Ala Pro Glu Thr Lys Pro Ala Pro
100 105 110

Lys Gln Thr Pro Arg Ala Pro Pro Lys Pro Lys Thr Ser Pro Arg Pro
115 120 125

Arg Ile Pro Gln Thr Gln Pro Val Pro Lys Val Pro Gln Arg Val Thr
130 135 140

Ala Lys Pro Lys Thr Ser Pro Ser Pro Glu Val Ser Tyr Thr Thr Pro
145 150 155 160

Ala Pro Leu Glu Thr Arg Gly Ile Pro Phe Ile Pro Met Ile Ser Pro
165 170 175

Ser Pro Ser Gln Glu Glu Leu Gln Thr Thr Leu

180 185

<210> 871
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418024"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 871
Xaa Pro Lys Pro Lys Thr Thr Pro His Pro Glu Val Pro Gln Thr Lys
1 5 10 15

Leu Ala Thr Lys Thr Ser Lys Arg Thr Arg Pro Pro Arg Pro Arg Pro
20 25 30

Lys Thr Thr Pro Ser Pro Gln Ala Pro Glu Thr Lys Pro Val Pro Ala
35 40 45

Thr Val Leu Glu Pro Val Thr Leu Arg Pro Glu Ala Ser Thr Thr Leu
50 55 60

Ala Ser Lys Thr Ser Gln Arg Thr Arg Arg Pro Arg Leu Arg Thr Lys
65 70 75 80

Thr Thr Pro Arg Pro Glu Ala Pro Glu Ser Lys Pro Val Pro Thr Ala
85 90 95

```
Glu Leu Lys Pro Val Thr Leu Arg Thr Glu Thr Trp Val Thr Thr Gln
            100                 105                 110

Ala Pro Lys Gln Thr Pro Arg Ala Pro Pro Lys Pro Lys Thr Ser Pro
        115                 120                 125

Arg Pro Arg Ile Pro Gln Thr Gln Pro Val Pro Lys Val Pro Gln Arg
    130                 135                 140

Val Thr Ala Lys Pro Lys Thr Ser Pro Ser Pro Glu Val Ser Tyr Thr
145                 150                 155                 160

Thr Pro Ala Pro Lys Asp Val Leu Leu Pro His Lys Pro Tyr Pro Glu
                165                 170                 175

Val Ser Gln Ser Glu Pro Ala Pro Leu Glu Thr Arg Gly Ile Pro Phe
            180                 185                 190

Ile Pro Met Ile Ser Pro Ser Pro Ser Gln Glu Glu Leu Gln Thr Thr
        195                 200                 205

Leu Glu Glu Thr Asp Gln Ser Thr Gln Glu Pro Phe Thr Thr Lys Ile
    210                 215                 220

Pro Arg Thr Thr Glu Leu Ala Lys Thr Thr Gln Ala Pro His Arg Phe
225                 230                 235                 240

Tyr Thr Thr Val Arg Pro Arg Thr Ser Asp Lys Pro His Ile Arg Pro
                245                 250                 255

Val Leu Asn Arg Thr Thr Thr Arg Pro Thr Arg Pro Lys Pro Ser Gly
            260                 265                 270

Met Pro Ser Gly Asn Gly Val Gly Thr Gly Val Lys Gln Ala Pro Arg
        275                 280                 285

Pro Ser Gly Ala Asp Arg Asn Val Ser Val Asp Ser Thr His Pro Thr
    290                 295                 300

Lys Lys Pro
305
```

<210> 872

<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418063"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 872
Xaa Phe Ile Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val Thr
1 5 10 15

His Thr Lys Pro Ala Pro Lys Thr Ser Gln Arg Thr Arg Thr Arg Arg
20 25 30

Pro Arg Pro Lys His Lys Thr Thr Pro Arg Pro Glu Thr Leu Gln Thr
35 40 45

Lys Leu Asp Phe Gly Pro Ile Thr Pro Gly Thr Ser Ser Ala Pro Thr
50 55 60

Thr Thr Thr Lys Arg Thr Arg Arg Pro His Pro Lys Pro Lys Thr Thr
65 70 75 80

Pro His Pro Glu Val Pro Gln Thr Lys Leu Ala Pro Lys Gln Thr Pro
85 90 95

Arg Ala Pro Pro Lys Pro Lys Thr Ser Pro Arg Pro Arg Ile Pro Gln
100 105 110

```
Thr Gln Pro Val Pro Lys Val Pro Gln Arg Val Thr Ala Lys Pro Lys
        115                 120                 125

Thr Ser Pro Ser Pro Glu Val Ser Tyr Thr Thr Pro Ala Pro Lys Asp
    130                 135                 140

Val Leu Leu Pro His Lys Pro Tyr Pro Glu Val Ser Gln Ser Glu Pro
145                 150                 155                 160

Ala Pro Leu Glu Thr Arg Gly Ile Pro Phe Ile Pro Met Ile Ser Pro
                165                 170                 175

Ser Pro Ser Gln Glu Glu Leu Gln Thr Thr Leu
            180                 185


<210> 873
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418479"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 873
Xaa Asn Gly Lys Ile Gln Ser Thr Tyr Asp Gln Asp His Thr Val Pro
1               5                   10                  15

Ala Tyr Val Pro Arg Lys Leu Ile Pro Ile Thr Ile Ile Lys Gln Val
            20                  25                  30
```

```
Ile Gln Asn Val Thr His Lys Asp Ser Ala Lys Ser Pro Glu Lys Ala
        35                  40                  45

Pro Leu Gly Gly Val Ile Leu Val His Leu Ile Ile Pro Gly Leu Asn
    50                  55                  60

Glu Thr Thr Val Lys Leu Pro Ala Ser Leu Met Phe Glu Ile Ser Asp
65                  70                  75                  80

Ala Leu Lys Thr Gln Leu Ala Lys Asn Glu Thr Leu Ala Leu Pro Ala
                85                  90                  95

Glu Ser Lys Thr Pro Glu Val Glu Lys Ile Ser Ala Arg Pro Thr Thr
            100                 105                 110

Val Thr Pro Glu Thr Val Pro Arg Ser Thr Lys Pro Thr Thr Ser Ser
        115                 120                 125

Ala Leu Asp Val Ser Glu Thr Thr Leu Val Leu Ser Lys Arg Thr Pro
    130                 135                 140

Glu Thr Leu Gln Thr Ile Leu Ile Pro Gln Phe Glu Leu Pro Leu Ser
145                 150                 155                 160

Thr Leu Ala Ser Ser Glu Lys Pro Trp Ile Val Pro Thr Ala Lys Ile
                165                 170                 175

Ser Glu Asp Ser Lys Val Leu Gln Pro Gln Thr
            180                 185


<210> 874
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
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ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418800"

<400> 874

Val	Ser	Asp	Val	Leu	Glu	Ser	Val	Thr	Leu	Ser	Thr	Glu	Ser	Pro	Lys
1				5				10						15	
Glu	Thr	Ile	Ala	Pro	Ala	Lys	Thr	Asp	Tyr	Val	Tyr	Pro	Thr	Ala	Lys
			20					25					30		
Ala	Pro	Leu	Trp	Pro	Glu	Glu	Pro	Lys	Thr	Glu	Val	Val	Glu	Ser	Ile
		35					40					45			
Thr	Tyr	Val	Ser	Glu	Pro	Pro	Glu	Thr	Thr	Leu	Glu	Thr	Ser	Pro	Leu
	50					55					60				
Pro	Ser	Gln	Ser	Ile	Thr	Leu	Pro	Ser	Pro	Asp	Glu	Pro	Gln	Thr	Glu
65					70					75					80
Pro	Ala	Pro	Lys	Gln	Thr	Pro	Arg	Ala	Pro	Pro	Lys	Pro	Lys	Thr	Ser
				85					90					95	
Pro	Arg	Pro	Arg	Ile	Pro	Gln	Thr	Gln	Pro	Val	Pro	Lys	Val	Pro	Gln
			100					105					110		
Arg	Val	Thr	Ala	Lys	Pro	Lys	Thr	Ser	Pro	Ser	Pro	Glu	Val	Ser	Tyr
		115					120					125			
Thr	Thr	Pro	Ala	Pro	Leu	Glu	Thr	Arg	Gly	Ile	Pro	Phe	Ile	Pro	Met
	130					135					140				
Ile	Ser	Pro	Ser	Pro	Ser	Gln	Glu	Glu	Leu	Gln	Thr	Thr	Leu		
145					150					155					

<210> 875
<211> 1131
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418817"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 875
Xaa Ile Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val Thr His
1 5 10 15

Thr Lys Pro Ala Pro Glu Pro Gln Thr Leu Leu Pro Ser Gln Ser Thr
20 25 30

Ile Gly Pro Glu Thr Pro Gly Thr Lys Pro Ser Thr Thr Leu Ala Leu
35 40 45

Glu Pro Ala Thr Ile Gln Pro Glu Pro Leu Val Pro Thr Thr Ala Ser
50 55 60

Lys Pro Ser Glu Arg Pro Lys Thr Thr His Arg Pro Asp Ala Pro Gln
65 70 75 80

Ile Gln Pro Gly Ser Lys Pro Pro Lys Gln Leu Leu Pro Lys Pro Gln
85 90 95

Thr Thr Ala Glu Pro Asp Met Pro Pro Thr Lys Ser Val Ser Glu Pro
100 105 110

Val Pro Phe Glu Thr Glu Ala Pro Ser Met Thr Ile Val Pro Thr Thr
115 120 125

Asp Ile Glu Pro Val Thr Val Arg Thr Glu Ala Thr Val Thr Thr Leu
130 135 140

Ala Pro Lys Thr Ser Gln Arg Thr Arg Thr Arg Arg Pro Arg Pro Lys
145 150 155 160

His Lys Thr Thr Pro Arg Pro Glu Thr Leu Gln Thr Lys Leu Asp Phe
165 170 175

Gly Pro Ile Thr Pro Gly Thr Ser Ser Ala Pro Thr Thr Thr Thr Lys
180 185 190

Arg Thr Arg Arg Pro His Pro Lys Pro Lys Thr Thr Pro His Pro Glu
195 200 205

Val Pro Gln Thr Lys Leu Val Pro Ala Thr Ile Leu Glu Pro Val Leu
210 215 220

Arg Thr Glu Ala Ser Gly Thr Thr Ala Val Pro Ala Thr Ile Phe Glu
225 230 235 240

Pro Val Ser Pro Ile Lys Glu Ala Pro Gly Thr Thr Phe Val Pro Val
245 250 255

Thr Asp Leu Glu Pro Val Thr Phe Arg Thr Glu Ile Pro Ala Thr Thr
260 265 270

Leu Ala Thr Lys Thr Ser Lys Arg Thr Arg Pro Pro Arg Pro Arg Pro
275 280 285

Lys Thr Thr Pro Ser Pro Gln Ala Pro Glu Thr Lys Pro Val Pro Ala
290 295 300

Thr Val Leu Glu Pro Val Thr Leu Arg Pro Glu Ala Ser Thr Thr Leu
305 310 315 320

Ala Ser Lys Thr Ser Gln Arg Thr Arg Arg Pro Arg Leu Arg Thr Lys
325 330 335

Thr Thr Pro Arg Pro Glu Ala Pro Glu Ser Lys Pro Val Pro Thr Ala
340 345 350

Glu Leu Lys Pro Val Thr Leu Arg Thr Glu Thr Trp Val Thr Thr Gln
355 360 365

Ala Pro Lys Thr Ser Gln Arg Thr Arg Arg Pro Arg Pro Lys Thr Lys

370 375 380

Thr Thr Pro Ser Pro Glu Val Pro Gln Thr Lys Leu Val Pro Ser Thr
385 390 395 400

Asp Leu Glu Pro Gly Thr Leu Arg Thr Glu Ala Pro Lys Thr Met Val
405 410 415

Val Thr Thr Val Leu Glu Pro Asp Thr Phe Arg Thr Lys Phe Pro Glu
420 425 430

Thr Thr Leu Ala Pro Lys Thr Gln Arg Thr Arg Arg Pro Arg Pro Arg
435 440 445

Pro Lys Thr Thr Ser Ser Pro Glu Val Pro Gln Asn Lys Ser Val Ser
450 455 460

Val Thr Gly Phe Glu Pro Val Val His Ser Thr Asp Ala Pro Gly Thr
465 470 475 480

Thr Phe Ala Leu Thr Glu Leu Gln Thr Leu Ile Leu Lys Pro Val Thr
485 490 495

Ser Pro Ser Leu Glu Met Thr Glu Ser Gln Pro Val Ser Asp Val Leu
500 505 510

Glu Ser Val Thr Leu Ser Thr Glu Ser Pro Lys Glu Thr Ile Ala Pro
515 520 525

Ala Lys Thr Asp Tyr Val Tyr Pro Thr Ala Lys Ala Pro Leu Trp Pro
530 535 540

Glu Glu Pro Lys Thr Glu Val Val Glu Ser Ile Thr Tyr Val Ser Glu
545 550 555 560

Pro Pro Glu Thr Thr Leu Glu Thr Ser Pro Leu Pro Ser Gln Ser Ile
565 570 575

Thr Leu Pro Ser Pro Asp Glu Pro Gln Thr Glu Pro Ala Pro Lys Gln
580 585 590

Thr Pro Arg Ala Pro Pro Lys Pro Lys Thr Ser Pro Arg Pro Arg Ile
595 600 605

```
Pro Gln Thr Gln Pro Val Pro Lys Val Pro Gln Arg Val Thr Ala Lys
    610                 615                 620

Pro Lys Thr Ser Pro Ser Pro Glu Val Ser Tyr Thr Thr Pro Ala Pro
625                 630                 635                 640

Lys Asp Val Leu Leu Pro His Lys Pro Tyr Pro Glu Val Ser Gln Ser
                645                 650                 655

Glu Pro Ala Pro Leu Glu Thr Arg Gly Ile Pro Phe Ile Pro Met Ile
            660                 665                 670

Ser Pro Ser Pro Ser Gln Glu Glu Leu Gln Thr Thr Leu Glu Glu Thr
        675                 680                 685

Asp Gln Ser Thr Gln Glu Pro Phe Thr Thr Lys Ile Pro Arg Thr Thr
    690                 695                 700

Glu Leu Ala Lys Thr Thr Gln Ala Pro His Arg Phe Tyr Thr Thr Val
705                 710                 715                 720

Arg Pro Arg Thr Ser Asp Lys Pro His Ile Arg Pro Gly Val Lys Gln
                725                 730                 735

Ala Pro Arg Pro Ser Gly Ala Asp Arg Asn Val Ser Val Asp Ser Thr
            740                 745                 750

His Pro Thr Lys Lys Pro Gly Thr Arg Arg Pro Pro Leu Pro Pro Arg
        755                 760                 765

Pro Thr His Pro Arg Arg Lys Pro Leu Pro Pro Asn Asn Val Thr Gly
    770                 775                 780

Lys Pro Gly Ser Ala Gly Ile Ile Ser Ser Gly Pro Ile Thr Thr Pro
785                 790                 795                 800

Pro Leu Arg Ser Thr Pro Arg Pro Thr Gly Thr Pro Leu Glu Arg Ile
                805                 810                 815

Glu Thr Asp Ile Lys Gln Pro Thr Val Pro Ala Ser Gly Glu Glu Leu
            820                 825                 830
```

```
Glu Asn Ile Thr Asp Phe Ser Ser Ser Pro Thr Arg Glu Thr Asp Pro
        835                 840                 845

Leu Gly Lys Pro Arg Phe Lys Gly Pro His Val Arg Tyr Ile Gln Lys
    850                 855                 860

Pro Asp Asn Ser Pro Cys Ser Ile Thr Asp Ser Val Lys Arg Phe Pro
865                 870                 875                 880

Lys Glu Glu Ala Thr Glu Gly Asn Ala Thr Ser Pro Pro Gln Asn Pro
                885                 890                 895

Pro Thr Asn Leu Thr Val Val Thr Val Glu Gly Cys Pro Ser Phe Val
            900                 905                 910

Ile Leu Asp Trp Glu Lys Pro Leu Asn Asp Thr Val Thr Glu Tyr Glu
        915                 920                 925

Val Ile Ser Arg Glu Asn Gly Ser Phe Ser Gly Lys Asn Lys Ser Ile
    930                 935                 940

Gln Met Thr Asn Gln Thr Phe Ser Thr Val Glu Asn Leu Lys Pro Asn
945                 950                 955                 960

Thr Ser Tyr Glu Phe Gln Val Lys Pro Lys Asn Pro Leu Gly Glu Gly
                965                 970                 975

Pro Val Ser Asn Thr Val Ala Phe Ser Thr Glu Ser Ala Asp Pro Arg
            980                 985                 990

Val Ser Glu Pro Val Ser Ala Gly  Arg Asp Ala Ile Trp  Thr Glu
Arg
        995                 1000                1005

Pro Phe  Asn Ser Asp Ser Tyr  Ser Glu Cys Lys Gly  Lys Gln Tyr
    1010                1015                1020

Val Lys  Arg Thr Trp Tyr Lys  Lys Phe Val Gly Val  Gln Leu Cys
    1025                1030                1035

Asn Ser  Leu Arg Tyr Lys Ile  Tyr Leu Ser Asp Ser  Leu Thr Gly
    1040                1045                1050
```

```
Lys Phe  Tyr Asn Ile Gly Asp  Gln Arg Gly His Gly  Glu Asp His
    1055                1060                1065

Cys Gln  Phe Val Asp Ser Phe  Leu Asp Gly Arg Thr  Gly Gln Gln
    1070                1075                1080

Leu Thr  Ser Asp Gln Leu Pro  Ile Lys Glu Gly Tyr  Phe Arg Ala
    1085                1090                1095

Val Arg  Gln Glu Pro Val Gln  Phe Gly Glu Ile Gly  Gly His Thr
    1100                1105                1110

Gln Ile  Asn Tyr Val Gln Trp  Tyr Glu Cys Gly Thr  Thr Ile Pro
    1115                1120                1125

Gly Lys  Trp
    1130


<210> 876
<211> 233
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419029"

<400> 876
Gln Arg Val Thr Ala Lys Pro Lys Thr Ser Pro Ser Pro Glu Val Ser
1               5                  10                  15

Tyr Thr Thr Pro Ala Pro Lys Asp Val Leu Leu Pro His Lys Pro Tyr
            20                  25                  30
```

```
Pro Glu Val Ser Gln Ser Glu Pro Ala Pro Leu Glu Thr Arg Gly Ile
        35                  40                  45

Pro Phe Ile Pro Met Ile Ser Pro Ser Pro Ser Gln Glu Glu Leu Gln
    50                  55                  60

Thr Thr Leu Ala Pro His Arg Phe Tyr Thr Thr Val Arg Pro Arg Thr
65                  70                  75                  80

Ser Asp Lys Pro His Ile Arg Pro Gly Val Lys Gln Ala Pro Arg Pro
                85                  90                  95

Ser Gly Ala Asp Arg Asn Val Ser Val Asp Ser Thr His Pro Thr Lys
            100                 105                 110

Lys Pro Gly Thr Arg Arg Pro Pro Leu Pro Pro Arg Pro Thr His Pro
        115                 120                 125

Arg Arg Lys Pro Leu Pro Pro Asn Asn Val Thr Gly Lys Pro Gly Ser
    130                 135                 140

Ala Gly Ile Ile Ser Ser Gly Pro Ile Thr Thr Pro Pro Leu Arg Ser
145                 150                 155                 160

Thr Pro Arg Pro Thr Gly Thr Pro Leu Glu Arg Ile Glu Thr Asp Ile
                165                 170                 175

Lys Gln Pro Thr Val Pro Ala Ser Gly Glu Glu Leu Glu Asn Ile Thr
            180                 185                 190

Asp Phe Ser Ser Ser Pro Thr Arg Glu Thr Asp Pro Leu Gly Lys Pro
        195                 200                 205

Arg Phe Lys Gly Pro His Val Arg Tyr Ile Gln Lys Pro Asp Asn Ser
    210                 215                 220

Pro Cys Ser Ile Thr Asp Ser Val Lys
225                 230
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<210> 877
<211> 1777
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420524"

<400> 877
Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu Gly Cys Leu Leu
1 5 10 15

Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala Gln Lys Leu Pro
20 25 30

Lys Gly Lys Arg Pro Asn Leu Lys Val His Ile Asn Thr Thr Ser Asp
35 40 45

Ser Ile Leu Leu Lys Phe Leu Arg Pro Ser Pro Asn Val Lys Leu Glu
50 55 60

Gly Leu Leu Leu Gly Tyr Gly Ser Asn Val Ser Pro Asn Gln Tyr Phe
65 70 75 80

Pro Leu Pro Ala Glu Gly Lys Phe Thr Glu Ala Ile Val Asp Ala Glu
85 90 95

Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro Pro Ser Gln Lys
100 105 110

Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro Leu Gln Leu Val
115 120 125

Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser Trp Gly Phe Leu
130 135 140

Ile Asn Pro His His Asp Trp Thr Leu Pro Ser His Cys Pro Asn Asp
145 150 155 160

```
Arg Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys Glu Lys Lys Trp
                165                 170                 175

Ile Phe Gln Ile Cys Pro Ala Thr Glu Thr Ile Val Glu Asn Leu Lys
            180                 185                 190

Pro Asn Thr Val Tyr Glu Phe Gly Val Lys Asp Asn Val Glu Gly Gly
        195                 200                 205

Ile Trp Ser Lys Ile Phe Asn His Lys Thr Val Val Gly Ser Lys Lys
    210                 215                 220

Val Asn Gly Lys Ile Gln Ser Thr Tyr Asp Gln Asp His Thr Val Pro
225                 230                 235                 240

Ala Tyr Val Pro Arg Lys Leu Ile Pro Ile Thr Ile Ile Lys Gln Val
                245                 250                 255

Ile Gln Asn Val Thr His Lys Asp Ser Ala Lys Ser Pro Glu Lys Ala
            260                 265                 270

Pro Leu Gly Gly Val Ile Leu Val His Leu Ile Ile Pro Gly Leu Asn
        275                 280                 285

Glu Thr Thr Val Lys Leu Pro Ala Ser Leu Met Phe Glu Ile Ser Asp
    290                 295                 300

Ala Leu Lys Thr Gln Leu Ala Lys Asn Glu Thr Leu Ala Leu Pro Ala
305                 310                 315                 320

Glu Ser Lys Thr Pro Glu Val Glu Lys Ile Ser Ala Arg Pro Thr Thr
                325                 330                 335

Val Thr Pro Glu Thr Val Pro Arg Ser Thr Lys Pro Thr Thr Ser Ser
            340                 345                 350

Ala Leu Asp Val Ser Glu Thr Thr Leu Val Leu Ser Lys Arg Thr Pro
        355                 360                 365

Glu Thr Leu Gln Thr Ile Leu Ile Pro Gln Phe Glu Leu Pro Leu Ser
    370                 375                 380
```

```
Thr Leu Ala Pro Lys Ser Leu Pro Glu Phe Pro Glu Ala Lys Thr Pro
385                 390                 395                 400

Phe Pro Phe Glu Lys Pro Arg Gly Thr Leu Ala Ser Ser Glu Lys Pro
                405                 410                 415

Trp Ile Val Pro Thr Ala Lys Ile Ser Glu Asp Ser Lys Val Leu Gln
            420                 425                 430

Pro Gln Thr Ala Thr Tyr Asp Val Phe Ser Ser Pro Thr Thr Ser Asp
        435                 440                 445

Glu Pro Glu Ile Ser Asp Ser Tyr Thr Ala Thr Ser Asp Arg Ile Leu
    450                 455                 460

Asp Ser Ile Pro Pro Lys Thr Ser Arg Thr Leu Glu Gln Pro Arg Ala
465                 470                 475                 480

Thr Leu Ala Pro Ser Glu Thr Pro Phe Val Pro Gln Lys Leu Glu Ile
                485                 490                 495

Phe Thr Ser Pro Glu Met Gln Pro Thr Thr Pro Ala Pro Gln Gln Thr
            500                 505                 510

Thr Ser Ile Pro Ser Thr Pro Lys Arg Arg Pro Arg Pro Lys Pro Pro
        515                 520                 525

Arg Thr Lys Pro Glu Arg Thr Thr Ser Ala Gly Thr Ile Thr Pro Lys
    530                 535                 540

Ile Ser Lys Ser Pro Glu Pro Thr Trp Thr Thr Pro Ala Pro Gly Lys
545                 550                 555                 560

Thr Gln Phe Ile Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val
                565                 570                 575

Thr His Thr Lys Pro Ala Pro Glu Pro Gln Thr Leu Leu Pro Ser Gln
            580                 585                 590

Ser Thr Ile Gly Pro Glu Thr Pro Gly Thr Lys Pro Ser Thr Thr Leu
        595                 600                 605
```

```
Ala Pro Arg Lys Thr Lys Arg Pro Gly Arg Arg Pro Arg Pro Arg Pro
    610                 615                 620

Arg Pro Lys Thr Thr Pro Ser Pro Glu Val Pro Lys Ser Lys Pro Ala
625                 630                 635                 640

Leu Glu Pro Ala Thr Ile Gln Pro Glu Pro Leu Val Pro Thr Thr Ala
                645                 650                 655

Ser Lys Pro Ser Glu Arg Pro Lys Thr Thr His Arg Pro Asp Ala Pro
            660                 665                 670

Gln Ile Gln Pro Gly Ser Lys Pro Pro Lys Gln Leu Leu Pro Lys Pro
        675                 680                 685

Gln Thr Thr Ala Glu Pro Asp Met Pro Pro Thr Lys Ser Val Ser Glu
    690                 695                 700

Pro Val Pro Phe Glu Thr Glu Ala Pro Ser Met Thr Ile Val Pro Thr
705                 710                 715                 720

Thr Asp Ile Glu Pro Val Thr Val Arg Thr Glu Ala Thr Val Thr Thr
                725                 730                 735

Leu Ala Pro Lys Thr Ser Gln Arg Thr Arg Thr Arg Arg Pro Arg Pro
            740                 745                 750

Lys His Lys Thr Thr Pro Arg Pro Glu Thr Leu Gln Thr Lys Leu Asp
        755                 760                 765

Phe Gly Pro Ile Thr Pro Gly Thr Ser Ser Ala Pro Thr Thr Thr Thr
    770                 775                 780

Lys Arg Thr Arg Arg Pro His Pro Lys Pro Lys Thr Thr Pro His Pro
785                 790                 795                 800

Glu Val Pro Gln Thr Lys Leu Val Pro Ala Thr Ile Leu Glu Pro Val
                805                 810                 815

Leu Arg Thr Glu Ala Ser Gly Thr Thr Ala Ala Pro Lys Val Pro Gln
            820                 825                 830

Arg Thr His Arg Pro His Pro Lys Pro Lys Thr Thr Leu Ser Pro Glu
```

```
        835                 840                 845

Glu Leu Gln Thr Glu Leu Val Pro Ala Thr Ile Phe Glu Pro Val Ser
    850                 855                 860

Pro Ile Lys Glu Ala Pro Gly Thr Thr Phe Val Pro Val Thr Asp Leu
865                 870                 875                 880

Glu Pro Val Thr Phe Arg Thr Glu Ile Pro Ala Thr Thr Leu Ala Thr
                885                 890                 895

Lys Thr Ser Lys Arg Thr Arg Pro Pro Arg Pro Arg Pro Lys Thr Thr
            900                 905                 910

Pro Ser Pro Gln Ala Pro Glu Thr Lys Pro Val Pro Ala Thr Val Leu
        915                 920                 925

Glu Pro Val Thr Leu Arg Pro Glu Ala Ser Thr Thr Leu Ala Ser Lys
    930                 935                 940

Thr Ser Gln Arg Thr Arg Arg Pro Arg Leu Arg Thr Lys Thr Thr Pro
945                 950                 955                 960

Arg Pro Glu Ala Pro Glu Ser Lys Pro Val Pro Thr Ala Glu Leu Lys
                965                 970                 975

Pro Val Thr Leu Arg Thr Glu Thr Trp Val Thr Thr Gln Ala Pro Lys
            980                 985                 990

Thr Ser Gln Arg Thr Arg Arg Pro  Arg Pro Lys Thr Lys  Thr Thr
Pro
        995                 1000                1005

Ser Pro  Glu Val Pro Gln Thr  Lys Leu Val Pro Ser  Thr Asp Leu
    1010                1015                1020

Glu Pro  Gly Thr Leu Arg Thr  Glu Ala Pro Lys Thr  Met Val Val
    1025                1030                1035

Thr Thr  Val Leu Glu Pro Asp  Thr Phe Arg Thr Lys  Phe Pro Glu
    1040                1045                1050

Thr Thr  Leu Ala Pro Lys Thr  Gln Arg Thr Arg Arg  Pro Arg Pro
```

1055 1060 1065

Arg Pro Lys Thr Thr Ser Ser Pro Glu Val Pro Gln Asn Lys Ser
1070 1075 1080

Val Ser Val Thr Gly Phe Glu Pro Val Val His Ser Thr Asp Ala
1085 1090 1095

Pro Gly Thr Thr Phe Ala Leu Thr Glu Leu Gln Thr Leu Ile Leu
1100 1105 1110

Lys Pro Val Thr Ser Pro Ser Leu Glu Met Thr Glu Ser Gln Pro
1115 1120 1125

Val Ser Asp Val Leu Glu Ser Val Thr Leu Ser Thr Glu Ser Pro
1130 1135 1140

Lys Glu Thr Ile Ala Pro Ala Lys Thr Asp Tyr Val Tyr Pro Thr
1145 1150 1155

Ala Lys Ala Pro Leu Trp Pro Glu Glu Pro Lys Thr Glu Val Val
1160 1165 1170

Glu Ser Ile Thr Tyr Val Ser Glu Pro Pro Glu Thr Thr Leu Glu
1175 1180 1185

Thr Ser Pro Leu Pro Ser Gln Ser Ile Thr Leu Pro Ser Pro Asp
1190 1195 1200

Glu Pro Gln Thr Glu Pro Ala Pro Lys Gln Thr Pro Arg Ala Pro
1205 1210 1215

Pro Lys Pro Lys Thr Ser Pro Arg Pro Arg Ile Pro Gln Thr Gln
1220 1225 1230

Pro Val Pro Lys Val Pro Gln Arg Val Thr Ala Lys Pro Lys Thr
1235 1240 1245

Ser Pro Ser Pro Glu Val Ser Tyr Thr Thr Pro Ala Pro Lys Asp
1250 1255 1260

Val Leu Leu Pro His Lys Pro Tyr Pro Glu Val Ser Gln Ser Glu
1265 1270 1275

```
Pro Ala  Pro Leu Glu Thr Arg  Gly Ile Pro Phe Ile  Pro Met Ile
    1280                 1285                 1290

Ser Pro  Ser Pro Ser Gln Glu  Glu Leu Gln Thr Thr  Leu Glu Glu
    1295                 1300                 1305

Thr Asp  Gln Ser Thr Gln Glu  Pro Phe Thr Thr Lys  Ile Pro Arg
    1310                 1315                 1320

Thr Thr  Glu Leu Ala Lys Thr  Thr Gln Ala Pro His  Arg Phe Tyr
    1325                 1330                 1335

Thr Thr  Val Arg Pro Arg Thr  Ser Asp Lys Pro His  Ile Arg Pro
    1340                 1345                 1350

Val Leu  Asn Arg Thr Thr Thr  Arg Pro Thr Arg Pro  Lys Pro Ser
    1355                 1360                 1365

Gly Met  Pro Ser Gly Asn Gly  Val Gly Thr Gly Val  Lys Gln Ala
    1370                 1375                 1380

Pro Arg  Pro Ser Gly Ala Asp  Arg Asn Val Ser Val  Asp Ser Thr
    1385                 1390                 1395

His Pro  Thr Lys Lys Pro Gly  Thr Arg Arg Pro Pro  Leu Pro Pro
    1400                 1405                 1410

Arg Pro  Thr His Pro Arg Arg  Lys Pro Leu Pro Pro  Asn Asn Val
    1415                 1420                 1425

Thr Gly  Lys Pro Gly Ser Ala  Gly Ile Ile Ser Ser  Gly Pro Ile
    1430                 1435                 1440

Thr Thr  Pro Pro Leu Arg Ser  Thr Pro Arg Pro Thr  Gly Thr Pro
    1445                 1450                 1455

Leu Glu  Arg Ile Glu Thr Asp  Ile Lys Gln Pro Thr  Val Pro Ala
    1460                 1465                 1470

Ser Gly  Glu Glu Leu Glu Asn  Ile Thr Asp Phe Ser  Ser Ser Pro
    1475                 1480                 1485
```

```
Thr Arg  Glu Thr Asp Pro Leu  Gly Lys Pro Arg Phe  Lys Gly Pro
    1490                1495                1500

His Val  Arg Tyr Ile Gln Lys  Pro Asp Asn Ser Pro  Cys Ser Ile
    1505                1510                1515

Thr Asp  Ser Val Lys Arg Phe  Pro Lys Glu Glu Ala  Thr Glu Gly
    1520                1525                1530

Asn Ala  Thr Ser Pro Pro Gln  Asn Pro Pro Thr Asn  Leu Thr Val
    1535                1540                1545

Val Thr  Val Glu Gly Cys Pro  Ser Phe Val Ile Leu  Asp Trp Glu
    1550                1555                1560

Lys Pro  Leu Asn Asp Thr Val  Thr Glu Tyr Glu Val  Ile Ser Arg
    1565                1570                1575

Glu Asn  Gly Ser Phe Ser Gly  Lys Asn Lys Ser Ile  Gln Met Thr
    1580                1585                1590

Asn Gln  Thr Phe Ser Thr Val  Glu Asn Leu Lys Pro  Asn Thr Ser
    1595                1600                1605

Tyr Glu  Phe Gln Val Lys Pro  Lys Asn Pro Leu Gly  Glu Gly Pro
    1610                1615                1620

Val Ser  Asn Thr Val Ala Phe  Ser Thr Glu Ser Ala  Asp Pro Arg
    1625                1630                1635

Val Ser  Glu Pro Val Ser Ala  Gly Arg Asp Ala Ile  Trp Thr Glu
    1640                1645                1650

Arg Pro  Phe Asn Ser Asp Ser  Tyr Ser Glu Cys Lys  Gly Lys Gln
    1655                1660                1665

Tyr Val  Lys Arg Thr Trp Tyr  Lys Lys Phe Val Gly  Val Gln Leu
    1670                1675                1680

Cys Asn  Ser Leu Arg Tyr Lys  Ile Tyr Leu Ser Asp  Ser Leu Thr
    1685                1690                1695
```

```
Gly Lys  Phe Tyr Asn Ile Gly  Asp Gln Arg Gly His  Gly Glu Asp
    1700                1705                1710

His Cys  Gln Phe Val Asp Ser  Phe Leu Asp Gly Arg  Thr Gly Gln
    1715                1720                1725

Gln Leu  Thr Ser Asp Gln Leu  Pro Ile Lys Glu Gly  Tyr Phe Arg
    1730                1735                1740

Ala Val  Arg Gln Glu Pro Val  Gln Phe Gly Glu Ile  Gly Gly His
    1745                1750                1755

Thr Gln  Ile Asn Tyr Val Gln  Trp Tyr Glu Cys Gly  Thr Thr Ile
    1760                1765                1770

Pro Gly  Lys Trp
    1775


<210> 878
<211> 189
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420704"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 878
Xaa Thr Ala Lys Pro Lys Thr Ser Pro Ser Pro Glu Val Ser Tyr Thr
1               5                   10                  15
```

```
Thr Pro Ala Pro Leu Glu Thr Arg Gly Ile Pro Phe Ile Pro Met Ile
            20                  25                  30

Ser Pro Ser Pro Ser Gln Glu Glu Leu Gln Thr Thr Leu Glu Glu Thr
        35                  40                  45

Asp Gln Ser Thr Gln Glu Pro Phe Thr Thr Lys Ile Pro Arg Thr Thr
    50                  55                  60

Glu Leu Ala Lys Thr Thr Gln Ala Pro His Arg Phe Tyr Thr Thr Val
65                  70                  75                  80

Arg Pro Arg Thr Ser Asp Lys Pro His Ile Arg Pro Val Leu Asn Arg
                85                  90                  95

Thr Thr Thr Arg Pro Thr Arg Pro Lys Pro Ser Gly Met Pro Ser Gly
            100                 105                 110

Asn Gly Val Gly Thr Gly Val Lys Gln Ala Pro Arg Pro Ser Gly Ala
        115                 120                 125

Asp Arg Asn Val Ser Val Asp Ser Thr His Pro Thr Lys Lys Pro Gly
    130                 135                 140

Thr Arg Arg Pro Pro Leu Pro Pro Arg Pro Thr His Pro Arg Arg Lys
145                 150                 155                 160

Pro Leu Pro Pro Asn Asn Val Thr Gly Lys Pro Gly Ser Ala Gly Ile
                165                 170                 175

Ile Ser Ser Gly Pro Ile Thr Thr Pro Pro Leu Arg Ser
            180                 185


<210> 879
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "
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<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431537"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 879
Xaa Val Glu Ser Ile Thr Tyr Val Ser Glu Pro Pro Glu Thr Thr Leu
1 5 10 15

Glu Thr Ser Pro Leu Pro Ser Gln Ser Ile Thr Leu Pro Ser Pro Asp
20 25 30

Glu Pro Gln Thr Glu Pro Ala Pro Lys Gln Thr Pro Arg Ala Pro Pro
35 40 45

Lys Pro Lys Thr Ser Pro Arg Pro Arg Ile Pro Gln Thr Gln Pro Val
50 55 60

Pro Lys Val Pro Gln Arg Val Thr Ala Lys Pro Lys Thr Ser Pro Ser
65 70 75 80

Pro Glu Val Ser Tyr Thr Thr Pro Ala Pro Lys Asp Val Leu Leu Pro
85 90 95

His Lys Pro Tyr Pro Glu Val Ser Gln Ser Glu Pro Val Leu Gln Pro
100 105 110

Val Thr Phe Arg Phe Glu Pro Pro Lys Thr Thr Ile Ala Pro Leu Glu
115 120 125

Thr Arg Gly Ile Pro Phe Ile Pro Met Ile Ser Pro Ser Pro Ser Gln
130 135 140

Glu Glu Leu Gln Thr Thr Leu
145 150

<210> 880
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
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<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432069"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 880
Xaa Lys Asn Glu Thr Leu Ala Leu Pro Ala Glu Ser Lys Thr Pro Glu
1 5 10 15

Val Glu Lys Ile Ser Ala Arg Pro Thr Thr Val Thr Pro Glu Thr Val
20 25 30

Pro Arg Ser Thr Lys Pro Thr Thr Ser Ser Ala Leu Asp Val Ser Glu
35 40 45

Thr Thr Leu Ala Pro Lys Ser Leu Pro Glu Phe Pro Glu Ala Lys Thr
50 55 60

Pro Phe Pro Phe Glu Lys Pro Arg Gly Thr Leu Ala Ser Ser Glu Lys
65 70 75 80

Pro Trp Ile Val Pro Thr Ala Lys Ile Ser Glu Asp Ser Lys Val Leu
85 90 95

Gln Pro Gln Thr Ala Leu Thr Glu Leu Gln Thr Leu Ile Leu Lys Pro
100 105 110

```
Val Thr Ser Pro Ser Leu Glu Met Thr Glu Ser Gln Pro
        115                 120                 125


<210> 881
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433981"

<400> 881
Pro Arg Lys Thr Lys Arg Pro Gly Arg Arg Pro Arg Pro Arg Pro Arg
1               5                   10                  15


Pro Lys Thr Thr Pro Ser Pro Glu Val Pro Lys Ser Lys Pro Ala Leu
            20                  25                  30


Glu Pro Ala Thr Ile Gln Pro Glu Pro Leu Val Pro Thr Thr Ala Ser
        35                  40                  45


Lys Pro Ser Glu Arg Pro Lys Thr Thr His Arg Pro Asp Ala Pro Gln
    50                  55                  60


Ile Gln Pro Val Ser Glu Pro Val Pro Phe Glu Thr Glu Ala Pro Ser
65                  70                  75                  80


Met Thr Ile Val Pro Thr Thr Asp Ile Glu Pro Val Thr Val Arg Thr
                85                  90                  95


Glu Ala Thr Val Thr Thr Leu Ala Pro Lys Thr Ser Gln Arg Thr Arg
            100                 105                 110
```

```
Thr Arg Arg Pro Arg Pro Lys His Lys Thr Thr Pro Arg Pro Glu Thr
        115                 120                 125

Leu Gln Thr Lys Leu Asp Phe Gly Pro Ile Thr Pro Gly Thr Ser Ser
    130                 135                 140

Ala Pro Thr Thr Thr Thr Lys Arg Thr Arg Arg Pro His Pro Lys Pro
145                 150                 155                 160

Lys Thr Thr Pro His Pro Glu Val Pro Gln Thr Lys Leu Ala Pro Lys
                165                 170                 175

Gln Thr Pro Arg Ala Pro Pro Lys Pro Lys Thr
            180                 185


<210> 882
<211> 1005
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433993"

<400> 882
Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu Gly Cys Leu Leu
1               5                   10                  15

Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala Gln Lys Leu Pro
            20                  25                  30

Lys Gly Lys Arg Pro Asn Leu Lys Val His Ile Asn Thr Thr Ser Asp
        35                  40                  45
```

```
Ser Ile Leu Leu Lys Phe Leu Arg Pro Ser Pro Asn Val Lys Leu Glu
    50                  55                  60

Gly Leu Leu Leu Gly Tyr Gly Ser Asn Val Ser Pro Asn Gln Tyr Phe
65                  70                  75                  80

Pro Leu Pro Ala Glu Gly Lys Phe Thr Glu Ala Ile Val Asp Ala Glu
                85                  90                  95

Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro Pro Ser Gln Lys
            100                 105                 110

Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro Leu Gln Leu Val
        115                 120                 125

Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser Trp Gly Phe Leu
    130                 135                 140

Ile Asn Pro His His Asp Trp Thr Leu Pro Ser His Cys Pro Asn Asp
145                 150                 155                 160

Arg Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys Glu Lys Lys Trp
                165                 170                 175

Ile Phe Gln Ile Cys Pro Ala Thr Glu Thr Ile Val Glu Asn Leu Lys
            180                 185                 190

Pro Asn Thr Val Tyr Glu Phe Gly Val Lys Asp Asn Val Glu Gly Gly
        195                 200                 205

Ile Trp Ser Lys Ile Phe Asn His Lys Thr Val Val Gly Ser Lys Lys
    210                 215                 220

Val Asn Gly Lys Ile Gln Ser Thr Tyr Asp Gln Asp His Thr Val Pro
225                 230                 235                 240

Ala Tyr Val Pro Arg Lys Leu Ile Pro Ile Thr Ile Ile Lys Gln Val
                245                 250                 255

Ile Gln Asn Val Thr His Lys Asp Ser Ala Lys Ser Pro Glu Lys Ala
            260                 265                 270

Pro Leu Gly Gly Val Ile Leu Val His Leu Ile Ile Pro Gly Leu Asn
```

```
        275                 280                 285

Glu Thr Thr Val Lys Leu Pro Ala Ser Leu Met Phe Glu Ile Ser Asp
    290                 295                 300

Ala Leu Lys Thr Gln Leu Ala Lys Asn Glu Thr Leu Ala Leu Pro Ala
305                 310                 315                 320

Glu Ser Lys Thr Pro Glu Val Glu Lys Ile Ser Ala Arg Pro Thr Thr
                325                 330                 335

Val Thr Pro Glu Thr Val Pro Arg Ser Thr Lys Pro Thr Thr Ser Ser
            340                 345                 350

Ala Leu Asp Val Ser Glu Thr Thr Leu Val Leu Ser Lys Arg Thr Pro
        355                 360                 365

Glu Thr Leu Gln Thr Ile Leu Ile Pro Gln Phe Glu Leu Pro Leu Ser
    370                 375                 380

Thr Leu Ala Pro Lys Ser Leu Pro Glu Phe Pro Glu Ala Lys Thr Pro
385                 390                 395                 400

Phe Pro Phe Glu Lys Pro Arg Gly Thr Leu Ala Ser Ser Glu Lys Pro
                405                 410                 415

Trp Ile Val Pro Thr Ala Lys Ile Ser Glu Asp Ser Lys Val Leu Gln
            420                 425                 430

Pro Gln Thr Ala Thr Tyr Asp Val Phe Ser Ser Pro Thr Thr Ser Asp
        435                 440                 445

Glu Pro Glu Ile Ser Asp Ser Tyr Thr Ala Thr Ser Asp Arg Ile Leu
    450                 455                 460

Asp Ser Ile Pro Pro Lys Thr Ser Arg Thr Leu Glu Gln Pro Arg Ala
465                 470                 475                 480

Thr Leu Ala Pro Ser Glu Thr Pro Phe Val Pro Gln Lys Leu Glu Ile
                485                 490                 495

Phe Thr Ser Pro Glu Met Gln Pro Thr Thr Pro Ala Pro Gln Gln Thr
            500                 505                 510
```

```
Thr Ser Ile Pro Ser Thr Pro Lys Arg Arg Pro Arg Pro Lys Pro Pro
        515                 520                 525

Arg Thr Lys Pro Glu Arg Thr Thr Ser Ala Gly Thr Ile Thr Pro Lys
    530                 535                 540

Ile Ser Lys Ser Pro Glu Pro Thr Trp Thr Thr Pro Ala Pro Gly Lys
545                 550                 555                 560

Thr Gln Phe Ile Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val
                565                 570                 575

Thr His Thr Lys Pro Ala Pro Glu Pro Gln Thr Leu Leu Pro Ser Gln
            580                 585                 590

Ser Thr Ile Gly Pro Glu Thr Pro Gly Thr Lys Pro Ser Thr Thr Leu
        595                 600                 605

Ala Pro Arg Lys Thr Lys Arg Pro Gly Arg Arg Pro Arg Pro Arg Pro
    610                 615                 620

Arg Pro Lys Thr Thr Pro Ser Pro Glu Val Pro Lys Ser Lys Pro Ala
625                 630                 635                 640

Leu Glu Pro Ala Thr Ile Gln Pro Glu Pro Leu Val Pro Thr Thr Ala
                645                 650                 655

Ser Lys Pro Ser Glu Arg Pro Lys Thr Thr His Arg Pro Asp Ala Pro
            660                 665                 670

Gln Ile Gln Pro Gly Ser Lys Pro Pro Lys Gln Leu Leu Pro Lys Pro
        675                 680                 685

Gln Thr Thr Ala Glu Pro Asp Met Pro Pro Thr Lys Ser Val Ser Glu
    690                 695                 700

Pro Val Pro Phe Glu Thr Glu Ala Pro Ser Met Thr Ile Val Pro Thr
705                 710                 715                 720

Thr Asp Ile Glu Pro Val Thr Val Arg Thr Glu Ala Thr Val Thr Thr
                725                 730                 735
```

```
Leu Ala Pro Lys Thr Ser Gln Arg Thr Arg Thr Arg Arg Pro Arg Pro
            740                 745                 750

Lys His Lys Thr Thr Pro Arg Pro Glu Thr Leu Gln Thr Lys Leu Asp
        755                 760                 765

Phe Gly Pro Ile Thr Pro Gly Thr Ser Ser Ala Pro Thr Thr Thr Thr
    770                 775                 780

Lys Arg Thr Arg Arg Pro His Pro Lys Pro Lys Thr Thr Pro His Pro
785                 790                 795                 800

Glu Val Pro Gln Thr Lys Leu Ala Thr Lys Thr Ser Lys Arg Thr Arg
                805                 810                 815

Pro Pro Arg Pro Arg Pro Lys Thr Thr Pro Ser Pro Gln Ala Pro Glu
            820                 825                 830

Thr Lys Pro Val Pro Ala Thr Val Leu Glu Pro Val Thr Leu Arg Pro
        835                 840                 845

Glu Ala Ser Thr Thr Leu Ala Ser Lys Thr Ser Gln Arg Thr Arg Arg
    850                 855                 860

Pro Arg Leu Arg Thr Lys Thr Thr Pro Arg Pro Glu Ala Pro Glu Ser
865                 870                 875                 880

Lys Pro Val Pro Thr Ala Glu Leu Lys Pro Val Thr Leu Arg Thr Glu
                885                 890                 895

Thr Trp Val Thr Thr Gln Ala Pro Lys Thr Ser Gln Arg Thr Arg Arg
            900                 905                 910

Pro Arg Pro Lys Thr Lys Thr Thr Pro Ser Pro Glu Val Pro Gln Thr
        915                 920                 925

Lys Leu Val Pro Ser Thr Asp Leu Glu Pro Gly Thr Leu Arg Thr Glu
    930                 935                 940

Ala Pro Lys Thr Met Val Val Thr Thr Val Leu Glu Pro Asp Thr Phe
945                 950                 955                 960
```

```
Arg Thr Lys Phe Pro Glu Thr Thr Leu Ala Pro Lys Thr Gln Arg Thr
                965                 970                 975

Arg Arg Pro Arg Pro Arg Pro Lys Thr Thr Ser Ser Pro Glu Val Pro
            980                 985                 990

Gln Asn Lys Ser Gly Lys Cys Met  Asn Pro Trp Leu Lys
        995                 1000                1005


<210> 883
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434256"

<400> 883
Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu Gly Cys Leu Leu
1               5                   10                  15

Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala Gln Lys Leu Pro
            20                  25                  30

Lys Ala Asn Lys Arg Thr Glu Leu Val Ile Gln His Gly Trp Met Ser
        35                  40                  45

Leu Ile Lys Met Met Leu Asn Glu Arg Ser Gln Val
    50                  55                  60


<210> 884
<211> 87
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434425"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 884
Xaa Gln Thr Leu Leu Pro Ser Gln Ser Thr Ile Gly Pro Glu Thr Pro
1 5 10 15

Gly Thr Lys Pro Ser Thr Thr Leu Ala Pro Arg Lys Thr Lys Arg Pro
20 25 30

Gly Arg Arg Pro Arg Pro Arg Pro Arg Pro Lys Thr Thr Pro Ser Pro
35 40 45

Glu Val Pro Lys Ser Lys Pro Ala Leu Glu Pro Ala Thr Ile Gln Pro
50 55 60

Glu Pro Leu Val Pro Thr Thr Val Ser Glu Pro Val Pro Phe Glu Thr
65 70 75 80

Glu Ala Pro Ser Met Thr Ile
85

<210> 885
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435319"

<400> 885
Cys Ile Val Val Leu Trp Tyr Gly Trp Leu His Phe Tyr Ala Glu Pro
1 5 10 15

Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro Pro Ser Gln Lys Lys
20 25 30

Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro Leu Gln Leu Val Val
35 40 45

Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser Trp Gly Phe Leu Ile
50 55 60

Asn Pro His His Asp Trp Thr Leu Pro Ser His Cys Pro Asn Asp Arg
65 70 75 80

Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys Glu Lys Lys Trp Ile
85 90 95

Phe Gln Ile Cys Pro Ala Thr Glu Thr Ile Val Glu Asn Leu Lys Pro
100 105 110

Asn Thr Val Tyr Glu Phe Gly Val Lys Asp Asn Val Glu Gly Gly Ile
115 120 125

Trp Ser Lys Ile Phe Asn His Lys Thr Val Val Gly Ser Lys Lys Val
130 135 140

Asn Gly Lys Ile Gln Ser Thr Tyr Asp Gln Asp His Thr Val Pro Ala
145 150 155 160

Tyr Val Pro Arg Lys Leu Ile Pro Ile Thr Ile Ile Lys Gln Val Ile

```
                165                 170                 175

Gln Asn Val Thr His Lys Asp Ser Ala Lys Ser Pro Glu Lys Ala
            180                 185                 190


<210> 886
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000436070"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 886
Xaa Arg Thr Thr Ser Ala Gly Thr Ile Thr Pro Lys Ile Ser Lys Ser
1               5                   10                  15


Pro Glu Pro Thr Trp Thr Thr Pro Ala Pro Gly Lys Thr Gln Phe Ile
            20                  25                  30


Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val Thr His Thr Lys
        35                  40                  45


Pro Val Pro Thr Thr Asp Ile Glu Pro Val Thr Val Arg Thr Glu Ala
    50                  55                  60


Thr Val Thr Thr Leu Ala Pro Lys Thr Ser Gln Arg Thr Arg Thr Arg
65                  70                  75                  80
```

```
Arg Pro Arg Pro Lys His Lys Thr Thr Pro Arg Pro Glu Thr Leu Gln
                85                  90                  95

Thr Lys Leu Asp Phe Gly Pro Ile Thr Pro Gly Thr Ser Ser Ala Pro
            100                 105                 110

Thr Thr Thr Thr Lys Arg Thr Arg Arg Pro His Pro Lys Pro Lys Thr
        115                 120                 125

Thr Pro His Pro Glu Val Pro Gln Thr Lys Leu Ala Pro Lys Val Pro
    130                 135                 140

Gln Arg Thr His Arg Pro His Pro Lys Pro Lys Thr Thr Leu Ser Pro
145                 150                 155                 160

Glu Glu Leu Gln Thr Glu Leu Val Pro Ala Thr Ile Phe Glu Pro Val
                165                 170                 175

Ser Pro Ile Lys Glu Ala Pro Gly Thr Thr Phe
            180                 185


<210> 887
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436918"

<400> 887
Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu Gly Cys Leu Leu
1               5                   10                  15

Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala Gln Lys Leu Pro
```

```
            20                  25                  30

Lys Asp Ala Glu Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro
        35                  40                  45

Pro Ser Gln Lys Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro
    50                  55                  60

Leu Gln Leu Val Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser
65                  70                  75                  80

Trp Gly Phe Leu Ile Asn Pro His His Asp Trp Thr Leu Pro Ser His
                85                  90                  95

Cys Pro Asn Asp Arg Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys
            100                 105                 110

Glu Lys Lys Trp Ile Phe Gln Ile Cys Pro Ala Thr Glu Thr Ile Val
        115                 120                 125

Glu Asn Leu Lys Pro Asn Thr Val Tyr Glu Phe Gly Val Lys Asp Asn
    130                 135                 140

Val Glu Gly Gly Ile Trp Ser Lys Ile Phe Asn His Lys Thr Val Val
145                 150                 155                 160

Gly
```

<210> 888
<211> 303
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
ABI
family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437031"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 888
Xaa Thr Pro Glu Val Glu Lys Ile Ser Ala Arg Pro Thr Thr Val Thr
1 5 10 15

Pro Glu Thr Val Pro Arg Ser Thr Lys Pro Thr Thr Ser Ser Ala Leu
20 25 30

Asp Val Ser Glu Thr Thr Leu Ala Ser Ser Glu Lys Pro Trp Ile Val
35 40 45

Pro Thr Ala Lys Ile Ser Glu Asp Ser Lys Val Leu Gln Pro Gln Thr
50 55 60

Ala Thr Tyr Asp Val Phe Ser Ser Pro Thr Thr Ser Asp Glu Pro Glu
65 70 75 80

Ile Ser Asp Ser Tyr Thr Ala Thr Ser Asp Arg Ile Leu Asp Ser Ile
85 90 95

Pro Pro Lys Thr Ser Arg Thr Leu Glu Gln Pro Arg Ala Thr Leu Ala
100 105 110

Pro Ser Glu Thr Pro Phe Val Pro Gln Lys Leu Glu Ile Phe Thr Ser
115 120 125

Pro Glu Met Gln Pro Thr Thr Pro Ala Pro Gln Gln Thr Thr Ser Ile
130 135 140

Pro Ser Thr Pro Lys Arg Arg Pro Arg Pro Lys Pro Pro Arg Thr Lys
145 150 155 160

Pro Glu Arg Thr Thr Ser Ala Gly Thr Ile Thr Pro Lys Ile Ser Lys
165 170 175

Ser Pro Glu Pro Thr Trp Thr Thr Pro Ala Pro Gly Lys Thr Gln Phe

```
            180                 185                 190

Ile Ser Leu Lys Pro Lys Ile Pro Leu Ser Pro Glu Val Thr His Thr
        195                 200                 205

Lys Pro Ala Pro Glu Pro Gln Thr Leu Leu Pro Ser Gln Ser Thr Ile
    210                 215                 220

Gly Pro Glu Thr Pro Gly Thr Lys Pro Ser Thr Thr Leu Ala Pro Arg
225                 230                 235                 240

Lys Thr Lys Arg Pro Gly Arg Arg Pro Arg Pro Arg Pro Arg Pro Lys
                245                 250                 255

Thr Thr Pro Ser Pro Glu Val Pro Lys Ser Lys Pro Ala Leu Glu Pro
            260                 265                 270

Ala Thr Ile Gln Pro Glu Pro Leu Val Pro Thr Thr Ala Ser Lys Pro
        275                 280                 285

Ser Glu Arg Pro Lys Thr Thr His Arg Pro Asp Ala Pro Gln Ile
    290                 295                 300


<210> 889
<211> 150
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 148; "

<220>
<221> source
<223> /note="Gene Symbol: ABI3BP; "

<220>
<221> source
<223> /note="Gene Name:
      ABI
      family, member 3 (NESH) binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437308"


<220>
<221> MOD_RES
```

<222> (1)..(1)
<223> Any amino acid

<400> 889
Xaa Pro Glu Thr Pro Gly Thr Lys Pro Ser Thr Thr Leu Ala Pro Arg
1 5 10 15

Lys Thr Lys Arg Pro Gly Arg Arg Pro Arg Pro Arg Pro Arg Pro Lys
20 25 30

Thr Thr Pro Ser Pro Glu Val Pro Lys Ser Lys Pro Ala Leu Glu Pro
35 40 45

Ala Thr Ile Gln Pro Glu Pro Leu Val Pro Thr Thr Val Pro Thr Thr
50 55 60

Asp Ile Glu Pro Val Thr Val Arg Thr Glu Ala Thr Val Thr Thr Leu
65 70 75 80

Ala Pro Lys Thr Ser Gln Arg Thr Arg Thr Arg Arg Pro Arg Pro Lys
85 90 95

His Lys Thr Thr Pro Arg Pro Glu Thr Leu Gln Thr Lys Leu Asp Phe
100 105 110

Gly Pro Ile Thr Pro Gly Thr Ser Ser Ala Pro Thr Thr Thr Thr Lys
115 120 125

Arg Thr Arg Arg Pro His Pro Lys Pro Lys Thr Thr Pro His Pro Glu
130 135 140

Val Pro Gln Thr Lys Leu
145 150

<210> 890
<211> 1130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 149; "

<220>
<221> source
<223> /note="Gene Symbol: ABL1; "

<220>
<221> source
<223> /note="Gene Name:
ABL proto-oncogene 1, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="Uniprot ID: P00519; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000323315"

<400> 890

```
Met Leu Glu Ile Cys Leu Lys Leu Val Gly Cys Lys Ser Lys Lys Gly
1               5                  10                  15

Leu Ser Ser Ser Ser Ser Cys Tyr Leu Glu Glu Ala Leu Gln Arg Pro
            20                  25                  30

Val Ala Ser Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala Ala Arg Trp
        35                  40                  45

Asn Ser Lys Glu Asn Leu Leu Ala Gly Pro Ser Glu Asn Asp Pro Asn
    50                  55                  60

Leu Phe Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu
65                  70                  75                  80

Ser Ile Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn His Asn
                85                  90                  95

Gly Glu Trp Cys Glu Ala Gln Thr Lys Asn Gly Gln Gly Trp Val Pro
            100                 105                 110

Ser Asn Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr
        115                 120                 125

His Gly Pro Val Ser Arg Asn Ala Ala Glu Tyr Leu Leu Ser Ser Gly
    130                 135                 140

Ile Asn Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Gly Gln
145                 150                 155                 160

Arg Ser Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile
                165                 170                 175
```

```
Asn Thr Ala Ser Asp Gly Lys Leu Tyr Val Ser Ser Glu Ser Arg Phe
            180                 185                 190

Asn Thr Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp Gly
        195                 200                 205

Leu Ile Thr Thr Leu His Tyr Pro Ala Pro Lys Arg Asn Lys Pro Thr
    210                 215                 220

Val Tyr Gly Val Ser Pro Asn Tyr Asp Lys Trp Glu Met Glu Arg Thr
225                 230                 235                 240

Asp Ile Thr Met Lys His Lys Leu Gly Gly Gly Gln Tyr Gly Glu Val
                245                 250                 255

Tyr Glu Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala Val Lys Thr
            260                 265                 270

Leu Lys Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys Glu Ala Ala
        275                 280                 285

Val Met Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu Leu Gly Val
    290                 295                 300

Cys Thr Arg Glu Pro Pro Phe Tyr Ile Ile Thr Glu Phe Met Thr Tyr
305                 310                 315                 320

Gly Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Gln Glu Val Asn
                325                 330                 335

Ala Val Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser Ala Met Glu
            340                 345                 350

Tyr Leu Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn
        355                 360                 365

Cys Leu Val Gly Glu Asn His Leu Val Lys Val Ala Asp Phe Gly Leu
    370                 375                 380

Ser Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala Gly Ala Lys
385                 390                 395                 400
```

```
Phe Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr Asn Lys Phe
                405                 410                 415

Ser Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu Trp Glu Ile
            420                 425                 430

Ala Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu Ser Gln Val
        435                 440                 445

Tyr Glu Leu Leu Glu Lys Asp Tyr Arg Met Glu Arg Pro Glu Gly Cys
    450                 455                 460

Pro Glu Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Gln Trp Asn Pro
465                 470                 475                 480

Ser Asp Arg Pro Ser Phe Ala Glu Ile His Gln Ala Phe Glu Thr Met
                485                 490                 495

Phe Gln Glu Ser Ser Ile Ser Asp Glu Val Glu Lys Glu Leu Gly Lys
            500                 505                 510

Gln Gly Val Arg Gly Ala Val Ser Thr Leu Leu Gln Ala Pro Glu Leu
        515                 520                 525

Pro Thr Lys Thr Arg Thr Ser Arg Arg Ala Ala Glu His Arg Asp Thr
    530                 535                 540

Thr Asp Val Pro Glu Met Pro His Ser Lys Gly Gln Gly Glu Ser Asp
545                 550                 555                 560

Pro Leu Asp His Glu Pro Ala Val Ser Pro Leu Leu Pro Arg Lys Glu
                565                 570                 575

Arg Gly Pro Pro Glu Gly Gly Leu Asn Glu Asp Glu Arg Leu Leu Pro
            580                 585                 590

Lys Asp Lys Lys Thr Asn Leu Phe Ser Ala Leu Ile Lys Lys Lys Lys
        595                 600                 605

Lys Thr Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe Arg Glu Met
    610                 615                 620

Asp Gly Gln Pro Glu Arg Arg Gly Ala Gly Glu Glu Glu Gly Arg Asp
```

625 630 635 640

Ile Ser Asn Gly Ala Leu Ala Phe Thr Pro Leu Asp Thr Ala Asp Pro
645 650 655

Ala Lys Ser Pro Lys Pro Ser Asn Gly Ala Gly Val Pro Asn Gly Ala
660 665 670

Leu Arg Glu Ser Gly Gly Ser Gly Phe Arg Ser Pro His Leu Trp Lys
675 680 685

Lys Ser Ser Thr Leu Thr Ser Ser Arg Leu Ala Thr Gly Glu Glu Glu
690 695 700

Gly Gly Gly Ser Ser Ser Lys Arg Phe Leu Arg Ser Cys Ser Ala Ser
705 710 715 720

Cys Val Pro His Gly Ala Lys Asp Thr Glu Trp Arg Ser Val Thr Leu
725 730 735

Pro Arg Asp Leu Gln Ser Thr Gly Arg Gln Phe Asp Ser Ser Thr Phe
740 745 750

Gly Gly His Lys Ser Glu Lys Pro Ala Leu Pro Arg Lys Arg Ala Gly
755 760 765

Glu Asn Arg Ser Asp Gln Val Thr Arg Gly Thr Val Thr Pro Pro Pro
770 775 780

Arg Leu Val Lys Lys Asn Glu Glu Ala Ala Asp Glu Val Phe Lys Asp
785 790 795 800

Ile Met Glu Ser Ser Pro Gly Ser Ser Pro Pro Asn Leu Thr Pro Lys
805 810 815

Pro Leu Arg Arg Gln Val Thr Val Ala Pro Ala Ser Gly Leu Pro His
820 825 830

Lys Glu Glu Ala Gly Lys Gly Ser Ala Leu Gly Thr Pro Ala Ala Ala
835 840 845

Glu Pro Val Thr Pro Thr Ser Lys Ala Gly Ser Gly Ala Pro Gly Gly
850 855 860

```
Thr Ser Lys Gly Pro Ala Glu Glu Ser Arg Val Arg Arg His Lys His
865                 870                 875                 880

Ser Ser Glu Ser Pro Gly Arg Asp Lys Gly Lys Leu Ser Arg Leu Lys
                885                 890                 895

Pro Ala Pro Pro Pro Pro Pro Ala Ala Ser Ala Gly Lys Ala Gly Gly
            900                 905                 910

Lys Pro Ser Gln Ser Pro Ser Gln Glu Ala Ala Gly Glu Ala Val Leu
        915                 920                 925

Gly Ala Lys Thr Lys Ala Thr Ser Leu Val Asp Ala Val Asn Ser Asp
    930                 935                 940

Ala Ala Lys Pro Ser Gln Pro Gly Glu Gly Leu Lys Lys Pro Val Leu
945                 950                 955                 960

Pro Ala Thr Pro Lys Pro Gln Ser Ala Lys Pro Ser Gly Thr Pro Ile
                965                 970                 975

Ser Pro Ala Pro Val Pro Ser Thr Leu Pro Ser Ala Ser Ser Ala Leu
            980                 985                 990

Ala Gly Asp Gln Pro Ser Ser Thr  Ala Phe Ile Pro Leu  Ile Ser
Thr
        995                 1000                1005

Arg Val  Ser Leu Arg Lys Thr  Arg Gln Pro Pro Glu  Arg Ile Ala
    1010                1015                1020

Ser Gly  Ala Ile Thr Lys Gly  Val Val Leu Asp Ser  Thr Glu Ala
    1025                1030                1035

Leu Cys  Leu Ala Ile Ser Arg  Asn Ser Glu Gln Met  Ala Ser His
    1040                1045                1050

Ser Ala  Val Leu Glu Ala Gly  Lys Asn Leu Tyr Thr  Phe Cys Val
    1055                1060                1065

Ser Tyr  Val Asp Ser Ile Gln  Gln Met Arg Asn Lys  Phe Ala Phe
    1070                1075                1080
```

```
Arg Glu  Ala Ile Asn Lys Leu  Glu Asn Asn Leu Arg  Glu Leu Gln
    1085                1090                1095


Ile Cys  Pro Ala Thr Ala Gly  Ser Gly Pro Ala Ala  Thr Gln Asp
    1100                1105                1110


Phe Ser  Lys Leu Leu Ser Ser  Val Lys Glu Ile Ser  Asp Ile Val
    1115                1120                1125


Gln Arg
    1130


<210> 891
<211> 1149
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 149; "

<220>
<221> source
<223> /note="Gene Symbol: ABL1; "

<220>
<221> source
<223> /note="Gene Name:
      ABL proto-oncogene 1, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="Uniprot ID:  P00519; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000361423"

<400> 891
Met Gly Gln Gln Pro Gly Lys Val Leu Gly Asp Gln Arg Arg Pro Ser
1               5                  10                  15


Leu Pro Ala Leu His Phe Ile Lys Gly Ala Gly Lys Lys Glu Ser Ser
            20                  25                  30


Arg His Gly Gly Pro His Cys Asn Val Phe Val Glu His Glu Ala Leu
        35                  40                  45
```

```
Gln Arg Pro Val Ala Ser Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala
    50                  55                  60

Ala Arg Trp Asn Ser Lys Glu Asn Leu Leu Ala Gly Pro Ser Glu Asn
65                  70                  75                  80

Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp
                85                  90                  95

Asn Thr Leu Ser Ile Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr
            100                 105                 110

Asn His Asn Gly Glu Trp Cys Glu Ala Gln Thr Lys Asn Gly Gln Gly
        115                 120                 125

Trp Val Pro Ser Asn Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His
    130                 135                 140

Ser Trp Tyr His Gly Pro Val Ser Arg Asn Ala Ala Glu Tyr Leu Leu
145                 150                 155                 160

Ser Ser Gly Ile Asn Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser
                165                 170                 175

Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His
            180                 185                 190

Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu Tyr Val Ser Ser Glu
        195                 200                 205

Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His His His Ser Thr Val
    210                 215                 220

Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala Pro Lys Arg Asn
225                 230                 235                 240

Lys Pro Thr Val Tyr Gly Val Ser Pro Asn Tyr Asp Lys Trp Glu Met
                245                 250                 255

Glu Arg Thr Asp Ile Thr Met Lys His Lys Leu Gly Gly Gly Gln Tyr
            260                 265                 270

Gly Glu Val Tyr Glu Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala
```

```
        275                 280                 285

Val Lys Thr Leu Lys Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys
    290                 295                 300

Glu Ala Ala Val Met Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu
305                 310                 315                 320

Leu Gly Val Cys Thr Arg Glu Pro Pro Phe Tyr Ile Ile Thr Glu Phe
                325                 330                 335

Met Thr Tyr Gly Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Gln
            340                 345                 350

Glu Val Asn Ala Val Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser
        355                 360                 365

Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala
    370                 375                 380

Ala Arg Asn Cys Leu Val Gly Glu Asn His Leu Val Lys Val Ala Asp
385                 390                 395                 400

Phe Gly Leu Ser Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala
                405                 410                 415

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr
            420                 425                 430

Asn Lys Phe Ser Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu
        435                 440                 445

Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu
    450                 455                 460

Ser Gln Val Tyr Glu Leu Leu Glu Lys Asp Tyr Arg Met Glu Arg Pro
465                 470                 475                 480

Glu Gly Cys Pro Glu Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Gln
                485                 490                 495

Trp Asn Pro Ser Asp Arg Pro Ser Phe Ala Glu Ile His Gln Ala Phe
            500                 505                 510
```

```
Glu Thr Met Phe Gln Glu Ser Ser Ile Ser Asp Glu Val Glu Lys Glu
        515                 520                 525

Leu Gly Lys Gln Gly Val Arg Gly Ala Val Ser Thr Leu Leu Gln Ala
    530                 535                 540

Pro Glu Leu Pro Thr Lys Thr Arg Thr Ser Arg Arg Ala Ala Glu His
545                 550                 555                 560

Arg Asp Thr Thr Asp Val Pro Glu Met Pro His Ser Lys Gly Gln Gly
                565                 570                 575

Glu Ser Asp Pro Leu Asp His Glu Pro Ala Val Ser Pro Leu Leu Pro
            580                 585                 590

Arg Lys Glu Arg Gly Pro Pro Glu Gly Gly Leu Asn Glu Asp Glu Arg
        595                 600                 605

Leu Leu Pro Lys Asp Lys Lys Thr Asn Leu Phe Ser Ala Leu Ile Lys
    610                 615                 620

Lys Lys Lys Lys Thr Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe
625                 630                 635                 640

Arg Glu Met Asp Gly Gln Pro Glu Arg Arg Gly Ala Gly Glu Glu Glu
                645                 650                 655

Gly Arg Asp Ile Ser Asn Gly Ala Leu Ala Phe Thr Pro Leu Asp Thr
            660                 665                 670

Ala Asp Pro Ala Lys Ser Pro Lys Pro Ser Asn Gly Ala Gly Val Pro
        675                 680                 685

Asn Gly Ala Leu Arg Glu Ser Gly Gly Ser Gly Phe Arg Ser Pro His
    690                 695                 700

Leu Trp Lys Lys Ser Ser Thr Leu Thr Ser Ser Arg Leu Ala Thr Gly
705                 710                 715                 720

Glu Glu Glu Gly Gly Gly Ser Ser Ser Lys Arg Phe Leu Arg Ser Cys
                725                 730                 735
```

Ser Ala Ser Cys Val Pro His Gly Ala Lys Asp Thr Glu Trp Arg Ser
740 745 750

Val Thr Leu Pro Arg Asp Leu Gln Ser Thr Gly Arg Gln Phe Asp Ser
755 760 765

Ser Thr Phe Gly Gly His Lys Ser Glu Lys Pro Ala Leu Pro Arg Lys
770 775 780

Arg Ala Gly Glu Asn Arg Ser Asp Gln Val Thr Arg Gly Thr Val Thr
785 790 795 800

Pro Pro Pro Arg Leu Val Lys Lys Asn Glu Glu Ala Ala Asp Glu Val
805 810 815

Phe Lys Asp Ile Met Glu Ser Ser Pro Gly Ser Ser Pro Pro Asn Leu
820 825 830

Thr Pro Lys Pro Leu Arg Arg Gln Val Thr Val Ala Pro Ala Ser Gly
835 840 845

Leu Pro His Lys Glu Glu Ala Gly Lys Gly Ser Ala Leu Gly Thr Pro
850 855 860

Ala Ala Ala Glu Pro Val Thr Pro Thr Ser Lys Ala Gly Ser Gly Ala
865 870 875 880

Pro Gly Gly Thr Ser Lys Gly Pro Ala Glu Glu Ser Arg Val Arg Arg
885 890 895

His Lys His Ser Ser Glu Ser Pro Gly Arg Asp Lys Gly Lys Leu Ser
900 905 910

Arg Leu Lys Pro Ala Pro Pro Pro Pro Pro Ala Ala Ser Ala Gly Lys
915 920 925

Ala Gly Gly Lys Pro Ser Gln Ser Pro Ser Gln Glu Ala Ala Gly Glu
930 935 940

Ala Val Leu Gly Ala Lys Thr Lys Ala Thr Ser Leu Val Asp Ala Val
945 950 955 960

Asn Ser Asp Ala Ala Lys Pro Ser Gln Pro Gly Glu Gly Leu Lys Lys
965 970 975

Pro Val Leu Pro Ala Thr Pro Lys Pro Gln Ser Ala Lys Pro Ser Gly
980 985 990

Thr Pro Ile Ser Pro Ala Pro Val Pro Ser Thr Leu Pro Ser Ala Ser
995 1000 1005

Ser Ala Leu Ala Gly Asp Gln Pro Ser Ser Thr Ala Phe Ile Pro
1010 1015 1020

Leu Ile Ser Thr Arg Val Ser Leu Arg Lys Thr Arg Gln Pro Pro
1025 1030 1035

Glu Arg Ile Ala Ser Gly Ala Ile Thr Lys Gly Val Val Leu Asp
1040 1045 1050

Ser Thr Glu Ala Leu Cys Leu Ala Ile Ser Arg Asn Ser Glu Gln
1055 1060 1065

Met Ala Ser His Ser Ala Val Leu Glu Ala Gly Lys Asn Leu Tyr
1070 1075 1080

Thr Phe Cys Val Ser Tyr Val Asp Ser Ile Gln Gln Met Arg Asn
1085 1090 1095

Lys Phe Ala Phe Arg Glu Ala Ile Asn Lys Leu Glu Asn Asn Leu
1100 1105 1110

Arg Glu Leu Gln Ile Cys Pro Ala Thr Ala Gly Ser Gly Pro Ala
1115 1120 1125

Ala Thr Gln Asp Phe Ser Lys Leu Leu Ser Ser Val Lys Glu Ile
1130 1135 1140

Ser Asp Ile Val Gln Arg
1145

<210> 892
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 149; "

<220>
<221> source
<223> /note="Gene Symbol: ABL1; "

<220>
<221> source
<223> /note="Gene Name:
ABL proto-oncogene 1, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376971"

<400> 892
Met Gly Gln Gln Pro Gly Lys Val Leu Gly Asp Gln Arg Arg Pro Ser
1 5 10 15

Leu Pro Ala Leu His Phe Ile Lys Gly Ala Gly Lys Lys Glu Ser Ser
20 25 30

Arg His Gly Gly Pro His Cys Asn Val Phe Val Glu His Ala Leu Gln
35 40 45

Arg Pro Val Ala Ser Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala Ala
50 55 60

<210> 893
<211> 1064
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 150; "

<220>
<221> source
<223> /note="Gene Symbol: ABL2; "

<220>
<221> source
<223> /note="Gene Name:
ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="Uniprot ID: P42684; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000339209"

<400> 893
Met Val Leu Gly Thr Val Leu Leu Pro Pro Asn Ser Tyr Gly Arg Asp
1   5   10   15

Gln Asp Thr Ser Leu Cys Cys Leu Cys Thr Glu Ala Ser Glu Ser Ala
            20   25   30

Leu Pro Asp Leu Thr Asp His Phe Ala Ser Cys Val Glu Asp Gly Phe
        35   40   45

Glu Gly Asp Lys Thr Gly Gly Ser Ser Pro Glu Ala Leu His Arg Pro
    50   55   60

Tyr Gly Cys Asp Val Glu Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp
65   70   75   80

Ser Ser Lys Glu Asn Leu Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu
                85   90   95

Phe Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser
            100   105   110

Ile Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly
        115   120   125

Glu Trp Ser Glu Val Arg Ser Lys Asn Gly Gln Gly Trp Val Pro Ser
    130   135   140

Asn Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr His
145   150   155   160

Gly Pro Val Ser Arg Ser Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile
                165   170   175

Asn Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu
            180   185   190

Ser Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile Asn
        195   200   205

```
Thr Thr Ala Asp Gly Lys Val Tyr Val Thr Ala Glu Ser Arg Phe Ser
    210                 215                 220

Thr Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp Gly Leu
225                 230                 235                 240

Val Thr Thr Leu His Tyr Pro Ala Pro Lys Cys Asn Lys Pro Thr Val
                245                 250                 255

Tyr Gly Val Ser Pro Ile His Asp Lys Trp Glu Met Glu Arg Thr Asp
            260                 265                 270

Ile Thr Met Lys His Lys Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr
        275                 280                 285

Val Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala Val Lys Thr Leu
    290                 295                 300

Lys Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys Glu Ala Ala Val
305                 310                 315                 320

Met Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu Leu Gly Val Cys
                325                 330                 335

Thr Leu Glu Pro Pro Phe Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly
            340                 345                 350

Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Glu Glu Val Thr Ala
        355                 360                 365

Val Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr
    370                 375                 380

Leu Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys
385                 390                 395                 400

Leu Val Gly Glu Asn His Val Val Lys Val Ala Asp Phe Gly Leu Ser
                405                 410                 415

Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala Gly Ala Lys Phe
            420                 425                 430

Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser
```

```
        435                 440                 445

Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu Trp Glu Ile Ala
    450                 455                 460

Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr
465                 470                 475                 480

Asp Leu Leu Glu Lys Gly Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro
                485                 490                 495

Pro Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Lys Trp Ser Pro Ala
            500                 505                 510

Asp Arg Pro Ser Phe Ala Glu Thr His Gln Ala Phe Glu Thr Met Phe
        515                 520                 525

His Asp Ser Ser Ile Ser Glu Glu Val Ala Glu Glu Leu Gly Arg Ala
    530                 535                 540

Ala Ser Ser Ser Ser Val Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu
545                 550                 555                 560

Pro Ser Lys Thr Arg Thr Leu Lys Lys Gln Val Glu Asn Lys Glu Asn
                565                 570                 575

Ile Glu Gly Ala Gln Asp Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala
            580                 585                 590

Pro Gly Phe Ile Arg Gly Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu
        595                 600                 605

Pro Arg Lys Gln Arg Asp Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala
    610                 615                 620

Lys Glu Thr Cys Phe Thr Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser
625                 630                 635                 640

Phe Met Lys Lys Arg Asn Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser
                645                 650                 655

Phe Arg Glu Met Glu Asn Gln Pro His Lys Lys Tyr Glu Leu Thr Gly
            660                 665                 670
```

```
Leu Pro Glu Gln Asp Arg Met Ala Met Thr Leu Pro Arg Asn Cys Gln
        675                 680                 685

Arg Ser Lys Leu Gln Leu Glu Arg Thr Val Ser Thr Ser Ser Gln Pro
    690                 695                 700

Glu Glu Asn Val Asp Arg Ala Asn Asp Met Leu Pro Lys Lys Ser Glu
705                 710                 715                 720

Glu Ser Ala Ala Pro Ser Arg Glu Arg Pro Lys Ala Lys Leu Leu Pro
                725                 730                 735

Arg Gly Ala Thr Ala Leu Pro Leu Arg Thr Pro Ser Gly Asp Leu Ala
            740                 745                 750

Ile Thr Glu Lys Asp Pro Pro Gly Val Gly Val Ala Gly Val Ala Ala
        755                 760                 765

Ala Pro Lys Gly Lys Glu Lys Asn Gly Gly Ala Arg Leu Gly Met Ala
    770                 775                 780

Gly Val Pro Glu Asp Gly Glu Gln Pro Gly Trp Pro Ser Pro Ala Lys
785                 790                 795                 800

Ala Ala Pro Val Leu Pro Thr Thr His Asn His Lys Val Pro Val Leu
                805                 810                 815

Ile Ser Pro Thr Leu Lys His Thr Pro Ala Asp Val Gln Leu Ile Gly
            820                 825                 830

Thr Asp Ser Gln Gly Asn Lys Phe Lys Leu Leu Ser Glu His Gln Val
        835                 840                 845

Thr Ser Ser Gly Asp Lys Asp Arg Pro Arg Arg Val Lys Pro Lys Cys
    850                 855                 860

Ala Pro Pro Pro Pro Pro Val Met Arg Leu Leu Gln His Pro Ser Ile
865                 870                 875                 880

Cys Ser Asp Pro Thr Glu Glu Pro Thr Ala Leu Thr Ala Gly Gln Ser
                885                 890                 895
```

```
Thr Ser Glu Thr Gln Glu Gly Gly Lys Lys Ala Ala Leu Gly Ala Val
            900                 905                 910

Pro Ile Ser Gly Lys Ala Gly Arg Pro Val Met Pro Pro Pro Gln Val
        915                 920                 925

Pro Leu Pro Thr Ser Ser Ile Ser Pro Ala Lys Met Ala Asn Gly Thr
    930                 935                 940

Ala Gly Thr Lys Val Ala Leu Arg Lys Thr Lys Gln Ala Ala Glu Lys
945                 950                 955                 960

Ile Ser Ala Asp Lys Ile Ser Lys Glu Ala Leu Leu Glu Cys Ala Asp
                965                 970                 975

Leu Leu Ser Ser Ala Leu Thr Glu Pro Val Pro Asn Ser Gln Leu Val
            980                 985                 990

Asp Thr Gly His Gln Leu Leu Asp  Tyr Cys Ser Gly Tyr  Val Asp
Cys
        995                 1000                1005

Ile Pro  Gln Thr Arg Asn Lys  Phe Ala Phe Arg Glu  Ala Val Ser
    1010                1015                1020

Lys Leu  Glu Leu Ser Leu Gln  Glu Leu Gln Val Ser  Ser Ala Ala
    1025                1030                1035

Ala Gly  Val Pro Gly Thr Asn  Pro Val Leu Asn Asn  Leu Leu Ser
    1040                1045                1050

Cys Val  Gln Glu Ile Ser Asp  Val Val Gln Arg
    1055                1060


<210> 894
<211> 1161
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 150; "

<220>
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<223> /note="Gene Symbol: ABL2; "

<220>
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<223> /note="Gene Name:
ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="Uniprot ID: P42684; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356595"

<400> 894

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Met Gly Gln Gln Val Gly Arg Val Gly Glu Ala Pro Gly Leu Gln Gln
1               5                   10                  15

Pro Gln Pro Arg Gly Ile Arg Gly Ser Ser Ala Ala Arg Pro Ser Gly
            20                  25                  30

Arg Arg Arg Asp Pro Ala Gly Arg Thr Thr Glu Thr Gly Phe Asn Ile
        35                  40                  45

Phe Thr Gln His Glu Ala Leu His Arg Pro Tyr Gly Cys Asp Val Glu
    50                  55                  60

Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp Ser Ser Lys Glu Asn Leu
65                  70                  75                  80

Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp
                85                  90                  95

Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys Gly Glu Lys
            100                 105                 110

Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly Glu Trp Ser Glu Val Arg
        115                 120                 125

Ser Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr Ile Thr Pro Val
    130                 135                 140

Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Ser
145                 150                 155                 160

Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile Asn Gly Ser Phe Leu Val
```

```
                165                 170                 175

Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu Ser Ile Ser Leu Arg Tyr
            180                 185                 190

Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr Thr Ala Asp Gly Lys
        195                 200                 205

Val Tyr Val Thr Ala Glu Ser Arg Phe Ser Thr Leu Ala Glu Leu Val
    210                 215                 220

His His His Ser Thr Val Ala Asp Gly Leu Val Thr Thr Leu His Tyr
225                 230                 235                 240

Pro Ala Pro Lys Cys Asn Lys Pro Thr Val Tyr Gly Val Ser Pro Ile
                245                 250                 255

His Asp Lys Trp Glu Met Glu Arg Thr Asp Ile Thr Met Lys His Lys
            260                 265                 270

Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr Val Gly Val Trp Lys Lys
        275                 280                 285

Tyr Ser Leu Thr Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met Glu
    290                 295                 300

Val Glu Glu Phe Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys His
305                 310                 315                 320

Pro Asn Leu Val Gln Leu Leu Gly Val Cys Thr Leu Glu Pro Pro Phe
                325                 330                 335

Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly Asn Leu Leu Asp Tyr Leu
            340                 345                 350

Arg Glu Cys Asn Arg Glu Glu Val Thr Ala Val Val Leu Leu Tyr Met
        355                 360                 365

Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe
    370                 375                 380

Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn His
385                 390                 395                 400
```

```
Val Val Lys Val Ala Asp Phe Gly Leu Ser Arg Leu Met Thr Gly Asp
                405                 410                 415

Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala
            420                 425                 430

Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser Ile Lys Ser Asp Val Trp
        435                 440                 445

Ala Phe Gly Val Leu Leu Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro
    450                 455                 460

Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr Asp Leu Leu Glu Lys Gly
465                 470                 475                 480

Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro Pro Lys Val Tyr Glu Leu
                485                 490                 495

Met Arg Ala Cys Trp Lys Trp Ser Pro Ala Asp Arg Pro Ser Phe Ala
            500                 505                 510

Glu Thr His Gln Ala Phe Glu Thr Met Phe His Asp Ser Ser Ile Ser
        515                 520                 525

Glu Glu Val Ala Glu Glu Leu Gly Arg Ala Ala Ser Ser Ser Ser Val
    530                 535                 540

Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu Pro Ser Lys Thr Arg Thr
545                 550                 555                 560

Leu Lys Lys Gln Val Glu Asn Lys Glu Asn Ile Glu Gly Ala Gln Asp
                565                 570                 575

Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala Pro Gly Phe Ile Arg Gly
            580                 585                 590

Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu Pro Arg Lys Gln Arg Asp
        595                 600                 605

Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala Lys Glu Thr Cys Phe Thr
    610                 615                 620
```

```
Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser Phe Met Lys Lys Arg Asn
625                 630                 635                 640

Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe Arg Glu Met Glu Asn
                645                 650                 655

Gln Pro His Lys Lys Tyr Glu Leu Thr Gly Asn Phe Ser Ser Val Ala
            660                 665                 670

Ser Leu Gln His Ala Asp Gly Phe Ser Phe Thr Pro Ala Gln Gln Glu
        675                 680                 685

Ala Asn Leu Val Pro Pro Lys Cys Tyr Gly Gly Ser Phe Ala Gln Arg
    690                 695                 700

Asn Leu Cys Asn Asp Asp Gly Gly Gly Gly Gly Gly Ser Gly Thr Ala
705                 710                 715                 720

Gly Gly Gly Trp Ser Gly Ile Thr Gly Phe Phe Thr Pro Arg Leu Ile
                725                 730                 735

Lys Lys Thr Leu Gly Leu Arg Ala Gly Lys Pro Thr Ala Ser Asp Asp
            740                 745                 750

Thr Ser Lys Pro Phe Pro Arg Ser Asn Ser Thr Ser Ser Met Ser Ser
        755                 760                 765

Gly Leu Pro Glu Gln Asp Arg Met Ala Met Thr Leu Pro Arg Asn Cys
    770                 775                 780

Gln Arg Ser Lys Leu Gln Leu Glu Arg Thr Val Ser Thr Ser Ser Gln
785                 790                 795                 800

Pro Glu Glu Asn Val Asp Arg Ala Asn Asp Met Leu Pro Lys Lys Ser
                805                 810                 815

Glu Glu Ser Ala Ala Pro Ser Arg Glu Arg Pro Lys Ala Lys Leu Leu
            820                 825                 830

Pro Arg Gly Ala Thr Ala Leu Pro Leu Arg Thr Pro Ser Gly Asp Leu
        835                 840                 845
```

```
Ala Ile Thr Glu Lys Asp Pro Pro Gly Val Gly Val Ala Gly Val Ala
    850                 855                 860

Ala Ala Pro Lys Gly Lys Glu Lys Asn Gly Gly Ala Arg Leu Gly Met
865                 870                 875                 880

Ala Gly Val Pro Glu Asp Gly Glu Gln Pro Gly Trp Pro Ser Pro Ala
                885                 890                 895

Lys Ala Ala Pro Val Leu Pro Thr Thr His Asn His Lys Val Pro Val
            900                 905                 910

Leu Ile Ser Pro Thr Leu Lys His Thr Pro Ala Asp Val Gln Leu Ile
        915                 920                 925

Gly Thr Asp Ser Gln Gly Asn Lys Phe Lys Leu Leu Ser Glu His Gln
    930                 935                 940

Val Thr Ser Ser Gly Asp Lys Asp Arg Pro Arg Arg Val Lys Pro Lys
945                 950                 955                 960

Cys Ala Pro Pro Pro Pro Pro Val Met Arg Leu Leu Gln His Pro Ser
                965                 970                 975

Ile Cys Ser Asp Pro Thr Glu Glu Pro Thr Ala Leu Thr Ala Gly Gln
            980                 985                 990

Ser Thr Ser Glu Thr Gln Glu Gly  Gly Lys Lys Ala Ala  Leu Gly
Ala
        995                 1000                1005

Val Pro  Ile Ser Gly Lys Ala  Gly Arg Pro Val Met  Pro Pro Pro
    1010                1015                1020

Gln Val  Pro Leu Pro Thr Ser  Ser Ile Ser Pro Ala  Lys Met Ala
    1025                1030                1035

Asn Gly  Thr Ala Gly Thr Lys  Val Ala Leu Arg Lys  Thr Lys Gln
    1040                1045                1050

Ala Ala  Glu Lys Ile Ser Ala  Asp Lys Ile Ser Lys  Glu Ala Leu
    1055                1060                1065
```

```
Leu Glu  Cys Ala Asp Leu Leu  Ser Ser Ala Leu Thr  Glu Pro Val
    1070                1075                1080

Pro Asn  Ser Gln Leu Val Asp  Thr Gly His Gln Leu  Leu Asp Tyr
    1085                1090                1095

Cys Ser  Gly Tyr Val Asp Cys  Ile Pro Gln Thr Arg  Asn Lys Phe
    1100                1105                1110

Ala Phe  Arg Glu Ala Val Ser  Lys Leu Glu Leu Ser  Leu Gln Glu
    1115                1120                1125

Leu Gln  Val Ser Ser Ala Ala  Ala Gly Val Pro Gly  Thr Asn Pro
    1130                1135                1140

Val Leu  Asn Asn Leu Leu Ser  Cys Val Gln Glu Ile  Ser Asp Val
    1145                1150                1155

Val Gln  Arg
    1160


<210> 895
<211> 542
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 150; "

<220>
<221> source
<223> /note="Gene Symbol: ABL2; "

<220>
<221> source
<223> /note="Gene Name:
      ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="Uniprot ID:  P42684; "

<220>
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<223> /note="ENSP ID: ENSP00000375897"

<400> 895
Met Gly Gln Gln Val Gly Arg Val Gly Glu Ala Pro Gly Leu Gln Gln
1               5                  10                  15
```

```
Pro Gln Pro Arg Gly Ile Arg Gly Ser Ser Ala Ala Arg Pro Ser Gly
            20                  25                  30

Arg Arg Arg Asp Pro Ala Gly Arg Thr Thr Glu Thr Gly Phe Asn Ile
        35                  40                  45

Phe Thr Gln His Glu Ala Leu His Arg Pro Tyr Gly Cys Asp Val Glu
    50                  55                  60

Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp Ser Ser Lys Glu Asn Leu
65                  70                  75                  80

Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp
                85                  90                  95

Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys Gly Glu Lys
            100                 105                 110

Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly Glu Trp Ser Glu Val Arg
        115                 120                 125

Ser Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr Ile Thr Pro Val
    130                 135                 140

Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Ser
145                 150                 155                 160

Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile Asn Gly Ser Phe Leu Val
                165                 170                 175

Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu Ser Ile Ser Leu Arg Tyr
            180                 185                 190

Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr Thr Ala Asp Gly Lys
        195                 200                 205

Val Tyr Val Thr Ala Glu Ser Arg Phe Ser Thr Leu Ala Glu Leu Val
    210                 215                 220

His His His Ser Thr Val Ala Asp Gly Leu Val Thr Thr Leu His Tyr
225                 230                 235                 240
```

```
Pro Ala Pro Lys Cys Asn Lys Pro Thr Val Tyr Gly Val Ser Pro Ile
                245                 250                 255

His Asp Lys Trp Glu Met Glu Arg Thr Asp Ile Thr Met Lys His Lys
            260                 265                 270

Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr Val Gly Val Trp Lys Lys
        275                 280                 285

Tyr Ser Leu Thr Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met Glu
    290                 295                 300

Val Glu Glu Phe Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys His
305                 310                 315                 320

Pro Asn Leu Val Gln Leu Leu Gly Val Cys Thr Leu Glu Pro Pro Phe
                325                 330                 335

Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly Asn Leu Leu Asp Tyr Leu
            340                 345                 350

Arg Glu Cys Asn Arg Glu Glu Val Thr Ala Val Val Leu Leu Tyr Met
        355                 360                 365

Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe
    370                 375                 380

Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn His
385                 390                 395                 400

Val Val Lys Val Ala Asp Phe Gly Leu Ser Arg Leu Met Thr Gly Asp
                405                 410                 415

Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala
            420                 425                 430

Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser Ile Lys Ser Asp Val Trp
        435                 440                 445

Ala Phe Gly Val Leu Leu Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro
    450                 455                 460
```

```
Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr Asp Leu Leu Glu Lys Gly
465                 470                 475                 480


Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro Pro Lys Val Tyr Glu Leu
                485                 490                 495


Met Arg Ala Cys Trp Lys Trp Ser Pro Ala Asp Arg Pro Ser Phe Ala
            500                 505                 510


Glu Thr His Gln Ala Phe Glu Thr Met Phe His Asp Ser Ser Ile Ser
        515                 520                 525


Glu Val Leu Leu His Cys Ala Asn Gln Thr Cys Ile Thr Leu
    530                 535                 540


<210> 896
<211> 1058
<212> PRT
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<220>
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<220>
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<220>
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<223> /note="Gene Name:
      ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
<221> source
<223> /note="Uniprot ID:  P42684; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423413"

<400> 896
Met Gly Gln Gln Val Gly Arg Val Gly Glu Ala Pro Gly Leu Gln Gln
1               5                   10                  15


Pro Gln Pro Arg Gly Ile Arg Gly Ser Ser Ala Ala Arg Pro Ser Gly
            20                  25                  30


Arg Arg Arg Asp Pro Ala Gly Arg Thr Thr Glu Thr Gly Phe Asn Ile
        35                  40                  45
```

```
Phe Thr Gln His Glu Ala Leu His Arg Pro Tyr Gly Cys Asp Val Glu
    50                  55                  60

Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp Ser Ser Lys Glu Asn Leu
65                  70                  75                  80

Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp
                85                  90                  95

Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys Gly Glu Lys
            100                 105                 110

Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly Glu Trp Ser Glu Val Arg
        115                 120                 125

Ser Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr Ile Thr Pro Val
    130                 135                 140

Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Ser
145                 150                 155                 160

Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile Asn Gly Ser Phe Leu Val
                165                 170                 175

Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu Ser Ile Ser Leu Arg Tyr
            180                 185                 190

Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr Thr Ala Asp Gly Lys
        195                 200                 205

Val Tyr Val Thr Ala Glu Ser Arg Phe Ser Thr Leu Ala Glu Leu Val
    210                 215                 220

His His His Ser Thr Val Ala Asp Gly Leu Val Thr Thr Leu His Tyr
225                 230                 235                 240

Pro Ala Pro Lys Cys Asn Lys Pro Thr Val Tyr Gly Val Ser Pro Ile
                245                 250                 255

His Asp Lys Trp Glu Met Glu Arg Thr Asp Ile Thr Met Lys His Lys
            260                 265                 270
```

```
Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr Val Gly Val Trp Lys Lys
        275                 280                 285

Tyr Ser Leu Thr Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met Glu
    290                 295                 300

Val Glu Glu Phe Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys His
305                 310                 315                 320

Pro Asn Leu Val Gln Leu Leu Gly Val Cys Thr Leu Glu Pro Pro Phe
                325                 330                 335

Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly Asn Leu Leu Asp Tyr Leu
            340                 345                 350

Arg Glu Cys Asn Arg Glu Glu Val Thr Ala Val Val Leu Leu Tyr Met
        355                 360                 365

Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe
    370                 375                 380

Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn His
385                 390                 395                 400

Val Val Lys Val Ala Asp Phe Gly Leu Ser Arg Leu Met Thr Gly Asp
                405                 410                 415

Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala
            420                 425                 430

Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser Ile Lys Ser Asp Val Trp
        435                 440                 445

Ala Phe Gly Val Leu Leu Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro
    450                 455                 460

Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr Asp Leu Leu Glu Lys Gly
465                 470                 475                 480

Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro Pro Lys Val Tyr Glu Leu
                485                 490                 495
```

```
Met Arg Ala Cys Trp Lys Trp Ser Pro Ala Asp Arg Pro Ser Phe Ala
            500                 505                 510

Glu Thr His Gln Ala Phe Glu Thr Met Phe His Asp Ser Ser Ile Ser
        515                 520                 525

Glu Glu Val Ala Glu Glu Leu Gly Arg Ala Ala Ser Ser Ser Ser Val
    530                 535                 540

Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu Pro Ser Lys Thr Arg Thr
545                 550                 555                 560

Leu Lys Lys Gln Val Glu Asn Lys Glu Asn Ile Glu Gly Ala Gln Asp
                565                 570                 575

Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala Pro Gly Phe Ile Arg Gly
            580                 585                 590

Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu Pro Arg Lys Gln Arg Asp
        595                 600                 605

Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala Lys Glu Thr Cys Phe Thr
    610                 615                 620

Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser Phe Met Lys Lys Arg Asn
625                 630                 635                 640

Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe Arg Glu Met Glu Asn
                645                 650                 655

Gln Pro His Lys Lys Tyr Glu Leu Thr Gly Leu Pro Glu Gln Asp Arg
            660                 665                 670

Met Ala Met Thr Leu Pro Arg Asn Cys Gln Arg Ser Lys Leu Gln Leu
        675                 680                 685

Glu Arg Thr Val Ser Thr Ser Ser Gln Pro Glu Glu Asn Val Asp Arg
    690                 695                 700

Ala Asn Asp Met Leu Pro Lys Lys Ser Glu Glu Ser Ala Ala Pro Ser
705                 710                 715                 720

Arg Glu Arg Pro Lys Ala Lys Leu Leu Pro Arg Gly Ala Thr Ala Leu
```

```
                725                 730                 735

Pro Leu Arg Thr Pro Ser Gly Asp Leu Ala Ile Thr Glu Lys Asp Pro
            740                 745                 750

Pro Gly Val Gly Val Ala Gly Val Ala Ala Ala Pro Lys Gly Lys Glu
        755                 760                 765

Lys Asn Gly Gly Ala Arg Leu Gly Met Ala Gly Val Pro Glu Asp Gly
    770                 775                 780

Glu Gln Pro Gly Trp Pro Ser Pro Ala Lys Ala Ala Pro Val Leu Pro
785                 790                 795                 800

Thr Thr His Asn His Lys Val Pro Val Leu Ile Ser Pro Thr Leu Lys
                805                 810                 815

His Thr Pro Ala Asp Val Gln Leu Ile Gly Thr Asp Ser Gln Gly Asn
            820                 825                 830

Lys Phe Lys Leu Leu Ser Glu His Gln Val Thr Ser Ser Gly Asp Lys
        835                 840                 845

Asp Arg Pro Arg Arg Val Lys Pro Lys Cys Ala Pro Pro Pro Pro Pro
    850                 855                 860

Val Met Arg Leu Leu Gln His Pro Ser Ile Cys Ser Asp Pro Thr Glu
865                 870                 875                 880

Glu Pro Thr Ala Leu Thr Ala Gly Gln Ser Thr Ser Glu Thr Gln Glu
                885                 890                 895

Gly Gly Lys Lys Ala Ala Leu Gly Ala Val Pro Ile Ser Gly Lys Ala
            900                 905                 910

Gly Arg Pro Val Met Pro Pro Pro Gln Val Pro Leu Pro Thr Ser Ser
        915                 920                 925

Ile Ser Pro Ala Lys Met Ala Asn Gly Thr Ala Gly Thr Lys Val Ala
    930                 935                 940

Leu Arg Lys Thr Lys Gln Ala Ala Glu Lys Ile Ser Ala Asp Lys Ile
945                 950                 955                 960
```

```
Ser Lys Glu Ala Leu Leu Glu Cys Ala Asp Leu Leu Ser Ser Ala Leu
                965                 970                 975

Thr Glu Pro Val Pro Asn Ser Gln Leu Val Asp Thr Gly His Gln Leu
            980                 985                 990

Leu Asp Tyr Cys Ser Gly Tyr Val  Asp Cys Ile Pro Gln  Thr Arg
Asn
        995                 1000                1005

Lys Phe  Ala Phe Arg Glu Ala  Val Ser Lys Leu Glu  Leu Ser Leu
    1010                1015                1020

Gln Glu  Leu Gln Val Ser Ser  Ala Ala Ala Gly Val  Pro Gly Thr
    1025                1030                1035

Asn Pro  Val Leu Asn Asn Leu  Leu Ser Cys Val Gln  Glu Ile Ser
    1040                1045                1050

Asp Val  Val Gln Arg
    1055


<210> 897
<211> 1167
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 150; "

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<221> source
<223> /note="Gene Symbol: ABL2; "

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<223> /note="Gene Name:
      ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
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<223> /note="Uniprot ID:  P42684; "

<220>
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<400> 897
Met Val Leu Gly Thr Val Leu Leu Pro Pro Asn Ser Tyr Gly Arg Asp
1 5 10 15

Gln Asp Thr Ser Leu Cys Cys Leu Cys Thr Glu Ala Ser Glu Ser Ala
20 25 30

Leu Pro Asp Leu Thr Asp His Phe Ala Ser Cys Val Glu Asp Gly Phe
35 40 45

Glu Gly Asp Lys Thr Gly Gly Ser Ser Pro Glu Ala Leu His Arg Pro
50 55 60

Tyr Gly Cys Asp Val Glu Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp
65 70 75 80

Ser Ser Lys Glu Asn Leu Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu
85 90 95

Phe Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser
100 105 110

Ile Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly
115 120 125

Glu Trp Ser Glu Val Arg Ser Lys Asn Gly Gln Gly Trp Val Pro Ser
130 135 140

Asn Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr His
145 150 155 160

Gly Pro Val Ser Arg Ser Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile
165 170 175

Asn Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu
180 185 190

Ser Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile Asn
195 200 205

Thr Thr Ala Asp Gly Lys Val Tyr Val Thr Ala Glu Ser Arg Phe Ser
210 215 220

```
Thr Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp Gly Leu
225                 230                 235                 240

Val Thr Thr Leu His Tyr Pro Ala Pro Lys Cys Asn Lys Pro Thr Val
                245                 250                 255

Tyr Gly Val Ser Pro Ile His Asp Lys Trp Glu Met Glu Arg Thr Asp
            260                 265                 270

Ile Thr Met Lys His Lys Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr
        275                 280                 285

Val Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala Val Lys Thr Leu
    290                 295                 300

Lys Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys Glu Ala Ala Val
305                 310                 315                 320

Met Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu Leu Gly Val Cys
                325                 330                 335

Thr Leu Glu Pro Pro Phe Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly
            340                 345                 350

Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Glu Glu Val Thr Ala
        355                 360                 365

Val Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr
    370                 375                 380

Leu Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys
385                 390                 395                 400

Leu Val Gly Glu Asn His Val Val Lys Val Ala Asp Phe Gly Leu Ser
                405                 410                 415

Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala Gly Ala Lys Phe
            420                 425                 430

Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser
        435                 440                 445

Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu Trp Glu Ile Ala
```

```
    450                 455                 460

Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr
465                 470                 475                 480

Asp Leu Leu Glu Lys Gly Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro
                485                 490                 495

Pro Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Lys Trp Ser Pro Ala
            500                 505                 510

Asp Arg Pro Ser Phe Ala Glu Thr His Gln Ala Phe Glu Thr Met Phe
        515                 520                 525

His Asp Ser Ser Ile Ser Glu Glu Val Ala Glu Glu Leu Gly Arg Ala
    530                 535                 540

Ala Ser Ser Ser Ser Val Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu
545                 550                 555                 560

Pro Ser Lys Thr Arg Thr Leu Lys Lys Gln Val Glu Asn Lys Glu Asn
                565                 570                 575

Ile Glu Gly Ala Gln Asp Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala
            580                 585                 590

Pro Gly Phe Ile Arg Gly Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu
        595                 600                 605

Pro Arg Lys Gln Arg Asp Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala
    610                 615                 620

Lys Glu Thr Cys Phe Thr Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser
625                 630                 635                 640

Phe Met Lys Lys Arg Asn Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser
                645                 650                 655

Phe Arg Glu Met Glu Asn Gln Pro His Lys Lys Tyr Glu Leu Thr Gly
            660                 665                 670

Asn Phe Ser Ser Val Ala Ser Leu Gln His Ala Asp Gly Phe Ser Phe
        675                 680                 685
```

```
Thr Pro Ala Gln Gln Glu Ala Asn Leu Val Pro Pro Lys Cys Tyr Gly
    690                 695                 700

Gly Ser Phe Ala Gln Arg Asn Leu Cys Asn Asp Asp Gly Gly Gly Gly
705                 710                 715                 720

Gly Gly Ser Gly Thr Ala Gly Gly Gly Trp Ser Gly Ile Thr Gly Phe
                725                 730                 735

Phe Thr Pro Arg Leu Ile Lys Lys Thr Leu Gly Leu Arg Ala Gly Lys
            740                 745                 750

Pro Thr Ala Ser Asp Asp Thr Ser Lys Pro Phe Pro Arg Ser Asn Ser
        755                 760                 765

Thr Ser Ser Met Ser Ser Gly Leu Pro Glu Gln Asp Arg Met Ala Met
    770                 775                 780

Thr Leu Pro Arg Asn Cys Gln Arg Ser Lys Leu Gln Leu Glu Arg Thr
785                 790                 795                 800

Val Ser Thr Ser Ser Gln Pro Glu Glu Asn Val Asp Arg Ala Asn Asp
                805                 810                 815

Met Leu Pro Lys Lys Ser Glu Glu Ser Ala Ala Pro Ser Arg Glu Arg
            820                 825                 830

Pro Lys Ala Lys Leu Leu Pro Arg Gly Ala Thr Ala Leu Pro Leu Arg
        835                 840                 845

Thr Pro Ser Gly Asp Leu Ala Ile Thr Glu Lys Asp Pro Pro Gly Val
    850                 855                 860

Gly Val Ala Gly Val Ala Ala Ala Pro Lys Gly Lys Glu Lys Asn Gly
865                 870                 875                 880

Gly Ala Arg Leu Gly Met Ala Gly Val Pro Glu Asp Gly Glu Gln Pro
                885                 890                 895

Gly Trp Pro Ser Pro Ala Lys Ala Ala Pro Val Leu Pro Thr Thr His
            900                 905                 910
```

```
Asn His Lys Val Pro Val Leu Ile Ser Pro Thr Leu Lys His Thr Pro
        915                 920                 925

Ala Asp Val Gln Leu Ile Gly Thr Asp Ser Gln Gly Asn Lys Phe Lys
    930                 935                 940

Leu Leu Ser Glu His Gln Val Thr Ser Ser Gly Asp Lys Asp Arg Pro
945                 950                 955                 960

Arg Arg Val Lys Pro Lys Cys Ala Pro Pro Pro Pro Pro Val Met Arg
                965                 970                 975

Leu Leu Gln His Pro Ser Ile Cys Ser Asp Pro Thr Glu Glu Pro Thr
            980                 985                 990

Ala Leu Thr Ala Gly Gln Ser Thr  Ser Glu Thr Gln Glu  Gly Gly
Lys
        995                 1000                1005

Lys Ala  Ala Leu Gly Ala Val  Pro Ile Ser Gly Lys  Ala Gly Arg
    1010                1015                1020

Pro Val  Met Pro Pro Pro Gln  Val Pro Leu Pro Thr  Ser Ser Ile
    1025                1030                1035

Ser Pro  Ala Lys Met Ala Asn  Gly Thr Ala Gly Thr  Lys Val Ala
    1040                1045                1050

Leu Arg  Lys Thr Lys Gln Ala  Ala Glu Lys Ile Ser  Ala Asp Lys
    1055                1060                1065

Ile Ser  Lys Glu Ala Leu Leu  Glu Cys Ala Asp Leu  Leu Ser Ser
    1070                1075                1080

Ala Leu  Thr Glu Pro Val Pro  Asn Ser Gln Leu Val  Asp Thr Gly
    1085                1090                1095

His Gln  Leu Leu Asp Tyr Cys  Ser Gly Tyr Val Asp  Cys Ile Pro
    1100                1105                1110

Gln Thr  Arg Asn Lys Phe Ala  Phe Arg Glu Ala Val  Ser Lys Leu
    1115                1120                1125
```

Glu Leu Ser Leu Gln Glu Leu Gln Val Ser Ser Ala Ala Ala Gly
    1130   1135   1140

Val Pro Gly Thr Asn Pro Val Leu Asn Asn Leu Leu Ser Cys Val
    1145   1150   1155

Gln Glu Ile Ser Asp Val Val Gln Arg
    1160   1165

<210> 898
<211> 1079
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ABL2; "

<220>
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<223> /note="Gene Name:
      ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
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<223> /note="Uniprot ID: P42684; "

<220>
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<223> /note="ENSP ID: ENSP00000424697"

<400> 898
Met Gly Gln Gln Val Gly Arg Val Gly Glu Ala Pro Gly Leu Gln Gln
1   5   10   15

Pro Gln Pro Arg Gly Ile Arg Gly Ser Ser Ala Ala Arg Pro Ser Gly
            20   25   30

Arg Arg Arg Asp Pro Ala Gly Arg Thr Thr Glu Thr Gly Phe Asn Ile
        35   40   45

Phe Thr Gln His Asp His Phe Ala Ser Cys Val Glu Asp Gly Phe Glu
    50   55   60

Gly Asp Lys Thr Gly Gly Ser Ser Pro Glu Ala Leu His Arg Pro Tyr

65 70 75 80

Gly Cys Asp Val Glu Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp Ser
85 90 95

Ser Lys Glu Asn Leu Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu Phe
100 105 110

Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile
115 120 125

Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly Glu
130 135 140

Trp Ser Glu Val Arg Ser Lys Asn Gly Gln Gly Trp Val Pro Ser Asn
145 150 155 160

Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly
165 170 175

Pro Val Ser Arg Ser Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile Asn
180 185 190

Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu Ser
195 200 205

Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr
210 215 220

Thr Ala Asp Gly Lys Val Tyr Val Thr Ala Glu Ser Arg Phe Ser Thr
225 230 235 240

Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp Gly Leu Val
245 250 255

Thr Thr Leu His Tyr Pro Ala Pro Lys Cys Asn Lys Pro Thr Val Tyr
260 265 270

Gly Val Ser Pro Ile His Asp Lys Trp Glu Met Glu Arg Thr Asp Ile
275 280 285

Thr Met Lys His Lys Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr Val
290 295 300

```
Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala Val Lys Thr Leu Lys
305                 310                 315                 320

Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys Glu Ala Ala Val Met
                325                 330                 335

Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu Leu Gly Val Cys Thr
            340                 345                 350

Leu Glu Pro Pro Phe Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly Asn
        355                 360                 365

Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Glu Glu Val Thr Ala Val
    370                 375                 380

Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu
385                 390                 395                 400

Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu
                405                 410                 415

Val Gly Glu Asn His Val Val Lys Val Ala Asp Phe Gly Leu Ser Arg
            420                 425                 430

Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro
        435                 440                 445

Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser Ile
    450                 455                 460

Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu Trp Glu Ile Ala Thr
465                 470                 475                 480

Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr Asp
                485                 490                 495

Leu Leu Glu Lys Gly Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro Pro
            500                 505                 510

Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Lys Trp Ser Pro Ala Asp
        515                 520                 525
```

Arg Pro Ser Phe Ala Glu Thr His Gln Ala Phe Glu Thr Met Phe His
530 535 540

Asp Ser Ser Ile Ser Glu Glu Val Ala Glu Glu Leu Gly Arg Ala Ala
545 550 555 560

Ser Ser Ser Ser Val Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu Pro
565 570 575

Ser Lys Thr Arg Thr Leu Lys Lys Gln Val Glu Asn Lys Glu Asn Ile
580 585 590

Glu Gly Ala Gln Asp Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala Pro
595 600 605

Gly Phe Ile Arg Gly Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu Pro
610 615 620

Arg Lys Gln Arg Asp Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala Lys
625 630 635 640

Glu Thr Cys Phe Thr Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser Phe
645 650 655

Met Lys Lys Arg Asn Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe
660 665 670

Arg Glu Met Glu Asn Gln Pro His Lys Lys Tyr Glu Leu Thr Gly Leu
675 680 685

Pro Glu Gln Asp Arg Met Ala Met Thr Leu Pro Arg Asn Cys Gln Arg
690 695 700

Ser Lys Leu Gln Leu Glu Arg Thr Val Ser Thr Ser Ser Gln Pro Glu
705 710 715 720

Glu Asn Val Asp Arg Ala Asn Asp Met Leu Pro Lys Lys Ser Glu Glu
725 730 735

Ser Ala Ala Pro Ser Arg Glu Arg Pro Lys Ala Lys Leu Leu Pro Arg
740 745 750

```
Gly Ala Thr Ala Leu Pro Leu Arg Thr Pro Ser Gly Asp Leu Ala Ile
        755                 760                 765

Thr Glu Lys Asp Pro Pro Gly Val Gly Val Ala Gly Val Ala Ala Ala
    770                 775                 780

Pro Lys Gly Lys Glu Lys Asn Gly Gly Ala Arg Leu Gly Met Ala Gly
785                 790                 795                 800

Val Pro Glu Asp Gly Glu Gln Pro Gly Trp Pro Ser Pro Ala Lys Ala
                805                 810                 815

Ala Pro Val Leu Pro Thr Thr His Asn His Lys Val Pro Val Leu Ile
            820                 825                 830

Ser Pro Thr Leu Lys His Thr Pro Ala Asp Val Gln Leu Ile Gly Thr
        835                 840                 845

Asp Ser Gln Gly Asn Lys Phe Lys Leu Leu Ser Glu His Gln Val Thr
    850                 855                 860

Ser Ser Gly Asp Lys Asp Arg Pro Arg Arg Val Lys Pro Lys Cys Ala
865                 870                 875                 880

Pro Pro Pro Pro Pro Val Met Arg Leu Leu Gln His Pro Ser Ile Cys
                885                 890                 895

Ser Asp Pro Thr Glu Glu Pro Thr Ala Leu Thr Ala Gly Gln Ser Thr
            900                 905                 910

Ser Glu Thr Gln Glu Gly Gly Lys Lys Ala Ala Leu Gly Ala Val Pro
        915                 920                 925

Ile Ser Gly Lys Ala Gly Arg Pro Val Met Pro Pro Pro Gln Val Pro
    930                 935                 940

Leu Pro Thr Ser Ser Ile Ser Pro Ala Lys Met Ala Asn Gly Thr Ala
945                 950                 955                 960

Gly Thr Lys Val Ala Leu Arg Lys Thr Lys Gln Ala Ala Glu Lys Ile
                965                 970                 975

Ser Ala Asp Lys Ile Ser Lys Glu Ala Leu Leu Glu Cys Ala Asp Leu
```

980 985 990

Leu Ser Ser Ala Leu Thr Glu Pro Val Pro Asn Ser Gln Leu Val Asp
995 1000 1005

Thr Gly His Gln Leu Leu Asp Tyr Cys Ser Gly Tyr Val Asp Cys
1010 1015 1020

Ile Pro Gln Thr Arg Asn Lys Phe Ala Phe Arg Glu Ala Val Ser
1025 1030 1035

Lys Leu Glu Leu Ser Leu Gln Glu Leu Gln Val Ser Ser Ala Ala
1040 1045 1050

Ala Gly Val Pro Gly Thr Asn Pro Val Leu Asn Asn Leu Leu Ser
1055 1060 1065

Cys Val Gln Glu Ile Ser Asp Val Val Gln Arg
1070 1075

<210> 899
<211> 1043
<212> PRT
<213> Homo sapiens

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<220>
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<223> /note="Gene Symbol: ABL2; "

<220>
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<223> /note="Gene Name:
ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
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<223> /note="Uniprot ID: P42684; "

<220>
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<223> /note="ENSP ID: ENSP00000426831"

<400> 899
Met Val Leu Gly Thr Val Leu Leu Pro Pro Asn Ser Tyr Gly Arg Asp
1 5 10 15

```
Gln Asp Thr Ser Leu Cys Cys Leu Cys Thr Glu Ala Ser Glu Ser Ala
            20                  25                  30

Leu Pro Asp Leu Thr Glu Ala Leu His Arg Pro Tyr Gly Cys Asp Val
        35                  40                  45

Glu Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp Ser Ser Lys Glu Asn
    50                  55                  60

Leu Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu Phe Val Ala Leu Tyr
65                  70                  75                  80

Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys Gly Glu
                85                  90                  95

Lys Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly Glu Trp Ser Glu Val
            100                 105                 110

Arg Ser Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr Ile Thr Pro
        115                 120                 125

Val Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg
    130                 135                 140

Ser Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile Asn Gly Ser Phe Leu
145                 150                 155                 160

Val Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu Ser Ile Ser Leu Arg
                165                 170                 175

Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr Thr Ala Asp Gly
            180                 185                 190

Lys Val Tyr Val Thr Ala Glu Ser Arg Phe Ser Thr Leu Ala Glu Leu
        195                 200                 205

Val His His His Ser Thr Val Ala Asp Gly Leu Val Thr Thr Leu His
    210                 215                 220

Tyr Pro Ala Pro Lys Cys Asn Lys Pro Thr Val Tyr Gly Val Ser Pro
225                 230                 235                 240
```

```
Ile His Asp Lys Trp Glu Met Glu Arg Thr Asp Ile Thr Met Lys His
                245                 250                 255

Lys Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr Val Gly Val Trp Lys
            260                 265                 270

Lys Tyr Ser Leu Thr Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met
        275                 280                 285

Glu Val Glu Glu Phe Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys
    290                 295                 300

His Pro Asn Leu Val Gln Leu Leu Gly Val Cys Thr Leu Glu Pro Pro
305                 310                 315                 320

Phe Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly Asn Leu Leu Asp Tyr
                325                 330                 335

Leu Arg Glu Cys Asn Arg Glu Glu Val Thr Ala Val Val Leu Leu Tyr
            340                 345                 350

Met Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu Glu Lys Lys Asn
        355                 360                 365

Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn
    370                 375                 380

His Val Val Lys Val Ala Asp Phe Gly Leu Ser Arg Leu Met Thr Gly
385                 390                 395                 400

Asp Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro Ile Lys Trp Thr
                405                 410                 415

Ala Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser Ile Lys Ser Asp Val
            420                 425                 430

Trp Ala Phe Gly Val Leu Leu Trp Glu Ile Ala Thr Tyr Gly Met Ser
        435                 440                 445

Pro Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr Asp Leu Leu Glu Lys
    450                 455                 460
```

```
Gly Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro Pro Lys Val Tyr Glu
465                 470                 475                 480

Leu Met Arg Ala Cys Trp Lys Trp Ser Pro Ala Asp Arg Pro Ser Phe
                485                 490                 495

Ala Glu Thr His Gln Ala Phe Glu Thr Met Phe His Asp Ser Ser Ile
            500                 505                 510

Ser Glu Glu Val Ala Glu Glu Leu Gly Arg Ala Ala Ser Ser Ser Ser
        515                 520                 525

Val Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu Pro Ser Lys Thr Arg
    530                 535                 540

Thr Leu Lys Lys Gln Val Glu Asn Lys Glu Asn Ile Glu Gly Ala Gln
545                 550                 555                 560

Asp Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala Pro Gly Phe Ile Arg
                565                 570                 575

Gly Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu Pro Arg Lys Gln Arg
            580                 585                 590

Asp Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala Lys Glu Thr Cys Phe
        595                 600                 605

Thr Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser Phe Met Lys Lys Arg
    610                 615                 620

Asn Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe Arg Glu Met Glu
625                 630                 635                 640

Asn Gln Pro His Lys Lys Tyr Glu Leu Thr Gly Leu Pro Glu Gln Asp
                645                 650                 655

Arg Met Ala Met Thr Leu Pro Arg Asn Cys Gln Arg Ser Lys Leu Gln
            660                 665                 670

Leu Glu Arg Thr Val Ser Thr Ser Ser Gln Pro Glu Glu Asn Val Asp
        675                 680                 685

Arg Ala Asn Asp Met Leu Pro Lys Lys Ser Glu Glu Ser Ala Ala Pro
```

690 695 700

Ser Arg Glu Arg Pro Lys Ala Lys Leu Leu Pro Arg Gly Ala Thr Ala
705 710 715 720

Leu Pro Leu Arg Thr Pro Ser Gly Asp Leu Ala Ile Thr Glu Lys Asp
725 730 735

Pro Pro Gly Val Gly Val Ala Gly Val Ala Ala Ala Pro Lys Gly Lys
740 745 750

Glu Lys Asn Gly Gly Ala Arg Leu Gly Met Ala Gly Val Pro Glu Asp
755 760 765

Gly Glu Gln Pro Gly Trp Pro Ser Pro Ala Lys Ala Ala Pro Val Leu
770 775 780

Pro Thr Thr His Asn His Lys Val Pro Val Leu Ile Ser Pro Thr Leu
785 790 795 800

Lys His Thr Pro Ala Asp Val Gln Leu Ile Gly Thr Asp Ser Gln Gly
805 810 815

Asn Lys Phe Lys Leu Leu Ser Glu His Gln Val Thr Ser Ser Gly Asp
820 825 830

Lys Asp Arg Pro Arg Arg Val Lys Pro Lys Cys Ala Pro Pro Pro Pro
835 840 845

Pro Val Met Arg Leu Leu Gln His Pro Ser Ile Cys Ser Asp Pro Thr
850 855 860

Glu Glu Pro Thr Ala Leu Thr Ala Gly Gln Ser Thr Ser Glu Thr Gln
865 870 875 880

Glu Gly Gly Lys Lys Ala Ala Leu Gly Ala Val Pro Ile Ser Gly Lys
885 890 895

Ala Gly Arg Pro Val Met Pro Pro Pro Gln Val Pro Leu Pro Thr Ser
900 905 910

Ser Ile Ser Pro Ala Lys Met Ala Asn Gly Thr Ala Gly Thr Lys Val
915 920 925

```
Ala Leu Arg Lys Thr Lys Gln Ala Ala Glu Lys Ile Ser Ala Asp Lys
    930                 935                 940

Ile Ser Lys Glu Ala Leu Leu Glu Cys Ala Asp Leu Leu Ser Ser Ala
945                 950                 955                 960

Leu Thr Glu Pro Val Pro Asn Ser Gln Leu Val Asp Thr Gly His Gln
                965                 970                 975

Leu Leu Asp Tyr Cys Ser Gly Tyr Val Asp Cys Ile Pro Gln Thr Arg
            980                 985                 990

Asn Lys Phe Ala Phe Arg Glu Ala  Val Ser Lys Leu Glu  Leu Ser
Leu
        995                 1000                1005

Gln Glu  Leu Gln Val Ser Ser  Ala Ala Ala Gly Val  Pro Gly Thr
    1010                1015                1020

Asn Pro  Val Leu Asn Asn Leu  Leu Ser Cys Val Gln  Glu Ile Ser
    1025                1030                1035

Asp Val  Val Gln Arg
    1040


<210> 900
<211> 1182
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<223> /note="Gene Name:
      ABL proto-oncogene 2, non-receptor tyr kinase; "

<220>
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<223> /note="Uniprot ID:  P42684; "
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<220>
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<400> 900
Met Gly Gln Gln Val Gly Arg Val Gly Glu Ala Pro Gly Leu Gln Gln
1   5   10   15

Pro Gln Pro Arg Gly Ile Arg Gly Ser Ser Ala Ala Arg Pro Ser Gly
            20   25   30

Arg Arg Arg Asp Pro Ala Gly Arg Thr Thr Glu Thr Gly Phe Asn Ile
        35   40   45

Phe Thr Gln His Asp His Phe Ala Ser Cys Val Glu Asp Gly Phe Glu
    50   55   60

Gly Asp Lys Thr Gly Gly Ser Ser Pro Glu Ala Leu His Arg Pro Tyr
65   70   75   80

Gly Cys Asp Val Glu Pro Gln Ala Leu Asn Glu Ala Ile Arg Trp Ser
                85   90   95

Ser Lys Glu Asn Leu Leu Gly Ala Thr Glu Ser Asp Pro Asn Leu Phe
            100   105   110

Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile
        115   120   125

Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn Gln Asn Gly Glu
    130   135   140

Trp Ser Glu Val Arg Ser Lys Asn Gly Gln Gly Trp Val Pro Ser Asn
145   150   155   160

Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly
                165   170   175

Pro Val Ser Arg Ser Ala Ala Glu Tyr Leu Leu Ser Ser Leu Ile Asn
            180   185   190

Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Gly Gln Leu Ser
        195   200   205

```
Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr
    210                 215                 220

Thr Ala Asp Gly Lys Val Tyr Val Thr Ala Glu Ser Arg Phe Ser Thr
225                 230                 235                 240

Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp Gly Leu Val
                245                 250                 255

Thr Thr Leu His Tyr Pro Ala Pro Lys Cys Asn Lys Pro Thr Val Tyr
            260                 265                 270

Gly Val Ser Pro Ile His Asp Lys Trp Glu Met Glu Arg Thr Asp Ile
        275                 280                 285

Thr Met Lys His Lys Leu Gly Gly Gly Gln Tyr Gly Glu Val Tyr Val
    290                 295                 300

Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala Val Lys Thr Leu Lys
305                 310                 315                 320

Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys Glu Ala Ala Val Met
                325                 330                 335

Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu Leu Gly Val Cys Thr
            340                 345                 350

Leu Glu Pro Pro Phe Tyr Ile Val Thr Glu Tyr Met Pro Tyr Gly Asn
        355                 360                 365

Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Glu Glu Val Thr Ala Val
    370                 375                 380

Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu
385                 390                 395                 400

Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu
                405                 410                 415

Val Gly Glu Asn His Val Val Lys Val Ala Asp Phe Gly Leu Ser Arg
            420                 425                 430

Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro
```

```
        435                 440                 445

Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr Asn Thr Phe Ser Ile
    450                 455                 460

Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu Trp Glu Ile Ala Thr
465                 470                 475                 480

Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu Ser Gln Val Tyr Asp
                485                 490                 495

Leu Leu Glu Lys Gly Tyr Arg Met Glu Gln Pro Glu Gly Cys Pro Pro
            500                 505                 510

Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Lys Trp Ser Pro Ala Asp
        515                 520                 525

Arg Pro Ser Phe Ala Glu Thr His Gln Ala Phe Glu Thr Met Phe His
    530                 535                 540

Asp Ser Ser Ile Ser Glu Glu Val Ala Glu Glu Leu Gly Arg Ala Ala
545                 550                 555                 560

Ser Ser Ser Ser Val Val Pro Tyr Leu Pro Arg Leu Pro Ile Leu Pro
                565                 570                 575

Ser Lys Thr Arg Thr Leu Lys Lys Gln Val Glu Asn Lys Glu Asn Ile
            580                 585                 590

Glu Gly Ala Gln Asp Ala Thr Glu Asn Ser Ala Ser Ser Leu Ala Pro
        595                 600                 605

Gly Phe Ile Arg Gly Ala Gln Ala Ser Ser Gly Ser Pro Ala Leu Pro
    610                 615                 620

Arg Lys Gln Arg Asp Lys Ser Pro Ser Ser Leu Leu Glu Asp Ala Lys
625                 630                 635                 640

Glu Thr Cys Phe Thr Arg Asp Arg Lys Gly Gly Phe Phe Ser Ser Phe
                645                 650                 655

Met Lys Lys Arg Asn Ala Pro Thr Pro Pro Lys Arg Ser Ser Ser Phe
            660                 665                 670
```

```
Arg Glu Met Glu Asn Gln Pro His Lys Lys Tyr Glu Leu Thr Gly Asn
        675                 680                 685

Phe Ser Ser Val Ala Ser Leu Gln His Ala Asp Gly Phe Ser Phe Thr
    690                 695                 700

Pro Ala Gln Gln Glu Ala Asn Leu Val Pro Pro Lys Cys Tyr Gly Gly
705                 710                 715                 720

Ser Phe Ala Gln Arg Asn Leu Cys Asn Asp Asp Gly Gly Gly Gly Gly
                725                 730                 735

Gly Ser Gly Thr Ala Gly Gly Gly Trp Ser Gly Ile Thr Gly Phe Phe
            740                 745                 750

Thr Pro Arg Leu Ile Lys Lys Thr Leu Gly Leu Arg Ala Gly Lys Pro
        755                 760                 765

Thr Ala Ser Asp Asp Thr Ser Lys Pro Phe Pro Arg Ser Asn Ser Thr
    770                 775                 780

Ser Ser Met Ser Ser Gly Leu Pro Glu Gln Asp Arg Met Ala Met Thr
785                 790                 795                 800

Leu Pro Arg Asn Cys Gln Arg Ser Lys Leu Gln Leu Glu Arg Thr Val
                805                 810                 815

Ser Thr Ser Ser Gln Pro Glu Glu Asn Val Asp Arg Ala Asn Asp Met
            820                 825                 830

Leu Pro Lys Lys Ser Glu Glu Ser Ala Ala Pro Ser Arg Glu Arg Pro
        835                 840                 845

Lys Ala Lys Leu Leu Pro Arg Gly Ala Thr Ala Leu Pro Leu Arg Thr
    850                 855                 860

Pro Ser Gly Asp Leu Ala Ile Thr Glu Lys Asp Pro Pro Gly Val Gly
865                 870                 875                 880

Val Ala Gly Val Ala Ala Ala Pro Lys Gly Lys Glu Lys Asn Gly Gly
                885                 890                 895
```

```
Ala Arg Leu Gly Met Ala Gly Val Pro Glu Asp Gly Glu Gln Pro Gly
            900                 905                 910

Trp Pro Ser Pro Ala Lys Ala Ala Pro Val Leu Pro Thr Thr His Asn
        915                 920                 925

His Lys Val Pro Val Leu Ile Ser Pro Thr Leu Lys His Thr Pro Ala
    930                 935                 940

Asp Val Gln Leu Ile Gly Thr Asp Ser Gln Gly Asn Lys Phe Lys Leu
945                 950                 955                 960

Leu Ser Glu His Gln Val Thr Ser Ser Gly Asp Lys Asp Arg Pro Arg
                965                 970                 975

Arg Val Lys Pro Lys Cys Ala Pro Pro Pro Pro Pro Val Met Arg Leu
            980                 985                 990

Leu Gln His Pro Ser Ile Cys Ser  Asp Pro Thr Glu Glu  Pro Thr
Ala
        995                 1000                1005

Leu Thr  Ala Gly Gln Ser Thr  Ser Glu Thr Gln Glu  Gly Gly Lys
    1010                1015                1020

Lys Ala  Ala Leu Gly Ala Val  Pro Ile Ser Gly Lys  Ala Gly Arg
    1025                1030                1035

Pro Val  Met Pro Pro Pro Gln  Val Pro Leu Pro Thr  Ser Ser Ile
    1040                1045                1050

Ser Pro  Ala Lys Met Ala Asn  Gly Thr Ala Gly Thr  Lys Val Ala
    1055                1060                1065

Leu Arg  Lys Thr Lys Gln Ala  Ala Glu Lys Ile Ser  Ala Asp Lys
    1070                1075                1080

Ile Ser  Lys Glu Ala Leu Leu  Glu Cys Ala Asp Leu  Leu Ser Ser
    1085                1090                1095

Ala Leu  Thr Glu Pro Val Pro  Asn Ser Gln Leu Val  Asp Thr Gly
    1100                1105                1110
```

```
His Gln  Leu Leu Asp Tyr Cys  Ser Gly Tyr Val Asp  Cys Ile Pro
    1115                1120                1125

Gln Thr  Arg Asn Lys Phe Ala  Phe Arg Glu Ala Val  Ser Lys Leu
    1130                1135                1140

Glu Leu  Ser Leu Gln Glu Leu  Gln Val Ser Ser Ala  Ala Ala Gly
    1145                1150                1155

Val Pro  Gly Thr Asn Pro Val  Leu Asn Asn Leu Leu  Ser Cys Val
    1160                1165                1170

Gln Glu  Ile Ser Asp Val Val  Gln Arg
    1175                1180
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<210> 901
<211> 496
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
abl-interactor 1; "

<220>
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<223> /note="Uniprot ID: Q8IZP0; "

<220>
<221> source
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<400> 901

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Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1               5                  10                  15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Arg His Gly Phe Ala Val Leu Leu Cys
```

35 40 45

Leu Leu Ser Asn Ser Trp Pro Gln Ala Thr Asp Lys Arg Lys Ala Leu
50 55 60

Glu Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr
65 70 75 80

Gln Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln
85 90 95

Ala Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln
100 105 110

Thr Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile
115 120 125

Leu Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro
130 135 140

Ala Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr
145 150 155 160

Thr Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys
165 170 175

His Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn
180 185 190

Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr
195 200 205

Leu Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro
210 215 220

Thr Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln
225 230 235 240

His Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His
245 250 255

Ser Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser
260 265 270

```
Ser Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile
        275                 280                 285

Gly Pro Glu Asn Ile Ser Val Pro Pro Pro Ser Gly Ala Pro Pro Ala
    290                 295                 300

Pro Pro Leu Ala Pro Leu Leu Pro Val Ser Thr Val Ile Ala Ala Pro
305                 310                 315                 320

Gly Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser
                325                 330                 335

Arg His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg
            340                 345                 350

Thr Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly
        355                 360                 365

Gly Pro Leu Tyr Ser Gln Asn Ser Ile Ala Asp Ser Pro Thr Pro Pro
    370                 375                 380

Pro Pro Pro Pro Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro
385                 390                 395                 400

Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val
                405                 410                 415

Val Gln Tyr Asn Asp Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala Pro
            420                 425                 430

Lys Asn Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp
        435                 440                 445

Lys Asp Asp Glu Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile
    450                 455                 460

Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr
465                 470                 475                 480

Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
                485                 490                 495
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<210> 902
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
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<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZP0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000352114"

<400> 902
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1   5   10   15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35   40   45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50   55   60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65   70   75   80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85   90   95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100   105   110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala

```
        115                 120                 125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145                 150                 155                 160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180                 185                 190

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195                 200                 205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270

Pro Ala Pro Gly Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg
        275                 280                 285

Gln Ile Ser Arg His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly
    290                 295                 300

Tyr Arg Arg Thr Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His
305                 310                 315                 320

Val Asn Gly Gly Pro Leu Tyr Ser Gln Asn Ser Ile Ser Ile Ala Pro
                325                 330                 335

Pro Pro Pro Pro Met Pro Gln Leu Thr Pro Gln Ile Pro Leu Thr Gly
            340                 345                 350
```

```
Phe Val Ala Arg Val Gln Glu Asn Ile Ala Asp Ser Pro Thr Pro Pro
        355                 360                 365

Pro Pro Pro Pro Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro
    370                 375                 380

Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val
385                 390                 395                 400

Val Gln Tyr Asn Asp Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala Pro
                405                 410                 415

Lys Asn Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp
            420                 425                 430

Lys Asp Asp Glu Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile
        435                 440                 445

Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr
    450                 455                 460

Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
465                 470                 475                 480


<210> 903
<211> 422
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8IZP0; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000365307"

<400> 903
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1   5   10   15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35   40   45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50   55   60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65   70   75   80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85   90   95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100   105   110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115   120   125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130   135   140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145   150   155   160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
                165   170   175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180   185   190

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195   200   205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His

```
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270

Pro Val Ser Ile Ala Pro Pro Pro Pro Pro Met Pro Gln Leu Thr Pro
        275                 280                 285

Gln Ile Pro Leu Thr Gly Phe Val Ala Arg Val Gln Glu Asn Ile Ala
    290                 295                 300

Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile Pro Met
305                 310                 315                 320

Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu
                325                 330                 335

Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr Ala Asp Gly
            340                 345                 350

Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val Val Ala Ile
        355                 360                 365

Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe Met Glu Gly
    370                 375                 380

Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly
385                 390                 395                 400

Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser
                405                 410                 415

Ile Met His Tyr Thr Asp
            420

<210> 904
<211> 452
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<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
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<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZP0; "

<220>
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<223> /note="ENSP ID: ENSP00000365308"

<400> 904

Met	Ala	Glu	Leu	Gln	Met	Leu	Leu	Glu	Glu	Glu	Ile	Pro	Ser	Gly	Lys
1				5				10					15		
Arg	Ala	Leu	Ile	Glu	Ser	Tyr	Gln	Asn	Leu	Thr	Arg	Val	Ala	Asp	Tyr
			20					25					30		
Cys	Glu	Asn	Asn	Tyr	Ile	Gln	Ala	Thr	Asp	Lys	Arg	Lys	Ala	Leu	Glu
		35					40					45			
Glu	Thr	Lys	Ala	Tyr	Thr	Thr	Gln	Ser	Leu	Ala	Ser	Val	Ala	Tyr	Gln
	50					55					60				
Ile	Asn	Ala	Leu	Ala	Asn	Asn	Val	Leu	Gln	Leu	Leu	Asp	Ile	Gln	Ala
65					70					75					80
Ser	Gln	Leu	Arg	Arg	Met	Glu	Ser	Ser	Ile	Asn	His	Ile	Ser	Gln	Thr
				85					90					95	
Val	Asp	Ile	His	Lys	Glu	Lys	Val	Ala	Arg	Arg	Glu	Ile	Gly	Ile	Leu
			100					105					110		
Thr	Thr	Asn	Lys	Asn	Thr	Ser	Arg	Thr	His	Lys	Ile	Ile	Ala	Pro	Ala
		115					120					125			

```
Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145                 150                 155                 160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180                 185                 190

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195                 200                 205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270

Pro Ala Ala Pro Gly Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr
        275                 280                 285

Arg Gln Ile Ser Arg His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly
    290                 295                 300

Gly Tyr Arg Arg Thr Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro
305                 310                 315                 320

His Val Asn Gly Gly Pro Leu Tyr Ser Gln Asn Ser Ile Ala Asp Ser
                325                 330                 335

Pro Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile Pro Met Phe Asp
            340                 345                 350

Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu
```

```
        355                 360                 365

Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr Ala Asp Gly Asp Pro
    370                 375                 380

Ala Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp
385                 390                 395                 400

Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe Met Glu Gly Ala Ile
                405                 410                 415

Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys
            420                 425                 430

Asn Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met
        435                 440                 445

His Tyr Thr Asp
    450


<210> 905
<211> 476
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8IZP0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000365309"

<400> 905
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1               5                   10                  15
```

```
Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35                  40                  45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50                  55                  60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Val Leu Asp Asp Val Gly His Gly Val Lys His Gly Asn Asn Gln Pro
145                 150                 155                 160

Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro Pro Thr Gln Lys Pro
                165                 170                 175

Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro
            180                 185                 190

Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr
        195                 200                 205

Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr
    210                 215                 220

Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser Gly Ser Ser Gly Gly
225                 230                 235                 240
```

```
Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile
                245                 250                 255

Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly Pro Ala Ala Pro Gly
            260                 265                 270

Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg
        275                 280                 285

His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr
    290                 295                 300

Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly Gly
305                 310                 315                 320

Pro Leu Tyr Ser Gln Asn Ser Ile Ser Ile Ala Pro Pro Pro Pro Pro
                325                 330                 335

Met Pro Gln Leu Thr Pro Gln Ile Pro Leu Thr Gly Phe Val Ala Arg
            340                 345                 350

Val Gln Glu Asn Ile Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro
        355                 360                 365

Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro
    370                 375                 380

Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn
385                 390                 395                 400

Asp Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile
                405                 410                 415

Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu
            420                 425                 430

Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp
        435                 440                 445

Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro
    450                 455                 460

Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
```

465 470 475

<210> 906
<211> 481
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
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<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZP0; "

<220>
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<223> /note="ENSP ID: ENSP00000365310"

<400> 906
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1 5 10 15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
20 25 30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
35 40 45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
50 55 60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65 70 75 80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
85 90 95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
100 105 110

```
Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145                 150                 155                 160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180                 185                 190

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195                 200                 205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270

Pro Ala Ala Pro Gly Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr
        275                 280                 285

Arg Gln Ile Ser Arg His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly
    290                 295                 300

Gly Tyr Arg Arg Thr Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro
305                 310                 315                 320

His Val Asn Gly Gly Pro Leu Tyr Ser Gln Asn Ser Ile Ser Ile Ala
                325                 330                 335
```

```
Pro Pro Pro Pro Pro Met Pro Gln Leu Thr Pro Gln Ile Pro Leu Thr
            340                 345                 350

Gly Phe Val Ala Arg Val Gln Glu Asn Ile Ala Asp Ser Pro Thr Pro
        355                 360                 365

Pro Pro Pro Pro Pro Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro
    370                 375                 380

Pro Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala
385                 390                 395                 400

Val Val Gln Tyr Asn Asp Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala
                405                 410                 415

Pro Lys Asn Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys
            420                 425                 430

Asp Lys Asp Asp Glu Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val
        435                 440                 445

Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val
    450                 455                 460

Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr
465                 470                 475                 480

Asp
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<210> 907
<211> 508
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZP0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000365312"

<400> 907
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1   5   10   15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35   40   45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50   55   60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65   70   75   80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85   90   95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100   105   110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115   120   125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130   135   140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145   150   155   160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
                165   170   175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180   185   190

```
Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195                 200                 205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270

Pro Glu Asn Ile Ser Val Pro Pro Pro Ser Gly Ala Pro Pro Ala Pro
        275                 280                 285

Pro Leu Ala Pro Leu Leu Pro Val Ser Thr Val Ile Ala Ala Pro Gly
    290                 295                 300

Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg
305                 310                 315                 320

His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr
                325                 330                 335

Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly Gly
            340                 345                 350

Pro Leu Tyr Ser Gln Asn Ser Ile Ser Ile Ala Pro Pro Pro Pro Pro
        355                 360                 365

Met Pro Gln Leu Thr Pro Gln Ile Pro Leu Thr Gly Phe Val Ala Arg
    370                 375                 380

Val Gln Glu Asn Ile Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro
385                 390                 395                 400

Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro
                405                 410                 415
```

```
Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn
            420                 425                 430

Asp Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile
        435                 440                 445

Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu
    450                 455                 460

Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp
465                 470                 475                 480

Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro
                485                 490                 495

Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
            500                 505


<210> 908
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 1; "

<220>
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<223> /note="ENSP ID: ENSP00000365330"

<400> 908
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1               5                   10                  15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35                  40                  45
```

```
Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50                  55                  60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Val Leu Asp Asp Val Gly His Gly Val Lys His Gly Asn Asn Gln Pro
145                 150                 155                 160

Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro Pro Thr Gln Lys Pro
                165                 170                 175

Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro
            180                 185                 190

Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr
        195                 200                 205

Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr
    210                 215                 220

Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser Gly Ser Ser Gly Gly
225                 230                 235                 240

Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile
                245                 250                 255

Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly Pro Ala Pro Gly Ser
            260                 265                 270
```

```
Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg His
        275                 280                 285

Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr Pro
    290                 295                 300

Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly Gly Pro
305                 310                 315                 320

Leu Tyr Ser Gln Asn Ser Ile Ser Ile Ala Pro Pro Pro Pro Pro Met
                325                 330                 335

Pro Gln Leu Thr Pro Gln Ile Pro Leu Thr Gly Phe Val Ala Arg Val
            340                 345                 350

Gln Glu Asn Ile Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro
        355                 360                 365

Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro
    370                 375                 380

Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp
385                 390                 395                 400

Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile Glu
                405                 410                 415

Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu
            420                 425                 430

Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp
        435                 440                 445

Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly
    450                 455                 460

Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
465                 470                 475
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<210> 909
<211> 446
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
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<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZP0; "

<220>
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<400> 909
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1   5   10   15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35   40   45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50   55   60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65   70   75   80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85   90   95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100   105   110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115   120   125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130   135   140

```
Val Leu Asp Asp Val Gly His Gly Val Lys His Gly Asn Asn Gln Pro
145                 150                 155                 160

Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro Pro Thr Gln Lys Pro
                165                 170                 175

Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro
            180                 185                 190

Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr
        195                 200                 205

Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr
    210                 215                 220

Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser Gly Ser Ser Gly Gly
225                 230                 235                 240

Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile
                245                 250                 255

Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly Pro Ala Pro Gly Ser
            260                 265                 270

Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg His
        275                 280                 285

Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr Pro
    290                 295                 300

Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly Gly Pro
305                 310                 315                 320

Leu Tyr Ser Gln Asn Ser Ile Ala Asp Ser Pro Thr Pro Pro Pro Pro
                325                 330                 335

Pro Pro Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro Pro Pro
            340                 345                 350

Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln
        355                 360                 365
```

```
Tyr Asn Asp Pro Tyr Ala Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn
    370                 375                 380

Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp
385                 390                 395                 400

Asp Glu Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys
                405                 410                 415

Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr Gly Leu
            420                 425                 430

Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
        435                 440                 445


<210> 910
<211> 451
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID:  Q8IZP0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000365340"

<400> 910
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1               5                   10                  15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
```

```
        35                  40                  45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50                  55                  60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145                 150                 155                 160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180                 185                 190

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195                 200                 205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270
```

```
Pro Ala Pro Gly Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg
        275                 280                 285

Gln Ile Ser Arg His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly
    290                 295                 300

Tyr Arg Arg Thr Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His
305                 310                 315                 320

Val Asn Gly Gly Pro Leu Tyr Ser Gln Asn Ser Ile Ala Asp Ser Pro
                325                 330                 335

Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile Pro Met Phe Asp Asp
            340                 345                 350

Ser Pro Pro Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu Glu
        355                 360                 365

Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr Ala Asp Gly Asp Pro Ala
    370                 375                 380

Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp Tyr
385                 390                 395                 400

Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe Met Glu Gly Ala Ile Ile
                405                 410                 415

Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys Asn
            420                 425                 430

Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His
        435                 440                 445

Tyr Thr Asp
    450


<210> 911
<211> 393
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439646"

<400> 911
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1 5 10 15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
20 25 30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
35 40 45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
50 55 60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65 70 75 80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
85 90 95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
100 105 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
115 120 125

Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
130 135 140

Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys His
145 150 155 160

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro

```
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
            180                 185                 190

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
        195                 200                 205

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
    210                 215                 220

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
225                 230                 235                 240

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
                245                 250                 255

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
            260                 265                 270

Pro Val Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp
        275                 280                 285

Ile Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val
    290                 295                 300

Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr
305                 310                 315                 320

Ala Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val
                325                 330                 335

Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe
            340                 345                 350

Met Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp
        355                 360                 365

Tyr Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr
    370                 375                 380

Val Glu Ser Ile Met His Tyr Thr Asp
385                 390
```

<210> 912
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 151; "

<220>
<221> source
<223> /note="Gene Symbol: ABI1; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZP0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000440101"

<400> 912
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Ser Gly Lys
1   5   10   15

Arg Ala Leu Ile Glu Ser Tyr Gln Asn Leu Thr Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu
        35   40   45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Gln
    50   55   60

Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln Ala
65   70   75   80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln His
                85   90   95

Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn Pro
            100   105   110

```
Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr Leu
        115                 120                 125

Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro Thr
    130                 135                 140

Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln His
145                 150                 155                 160

Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His Ser
                165                 170                 175

Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser Ser
            180                 185                 190

Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile Gly
        195                 200                 205

Pro Val Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp
    210                 215                 220

Ile Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val
225                 230                 235                 240

Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr
                245                 250                 255

Ala Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val
            260                 265                 270

Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe
        275                 280                 285

Met Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp
    290                 295                 300

Tyr Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr
305                 310                 315                 320

Val Glu Ser Ile Met His Tyr Thr Asp
                325
```

<210> 913

<211> 390
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000261016"

<400> 913

```
Met Phe Phe Lys Ser Tyr Leu Leu Lys Ile Ser Ile Leu Arg Gln Ile
1               5                  10                  15

Arg Gly Val Asp Leu Glu Ser Thr Phe Val Thr Lys Phe Gly Asn Asn
            20                  25                  30

Cys Ser Leu Arg Leu Asn Glu Thr Val Asp Ile His Lys Glu Lys Val
        35                  40                  45

Ala Arg Arg Glu Ile Gly Ile Leu Thr Thr Asn Lys Asn Thr Ser Arg
    50                  55                  60

Thr His Lys Ile Ile Ala Pro Ala Asn Leu Glu Arg Pro Val Arg Tyr
65                  70                  75                  80

Ile Arg Lys Pro Ile Asp Tyr Thr Ile Leu Asp Asp Ile Gly His Gly
                85                  90                  95

Val Lys Val Ser Thr Gln Asn Met Lys Met Gly Gly Leu Pro Arg Thr
            100                 105                 110

Thr Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Lys Gly
        115                 120                 125

Thr Leu Gly Arg His Ser Pro Tyr Arg Thr Leu Glu Pro Val Arg Pro
    130                 135                 140
```

```
Pro Val Val Pro Asn Asp Tyr Val Pro Ser Pro Thr Arg Asn Met Ala
145                 150                 155                 160

Pro Ser Gln Gln Ser Pro Val Arg Thr Ala Ser Val Asn Gln Arg Asn
                165                 170                 175

Arg Thr Tyr Ser Ser Ser Gly Ser Ser Gly Gly Ser His Pro Ser Ser
            180                 185                 190

Arg Ser Ser Ser Arg Glu Asn Ser Gly Ser Gly Ser Val Gly Val Pro
        195                 200                 205

Ile Ala Val Pro Thr Pro Ser Pro Pro Ser Val Phe Pro Gly His Pro
    210                 215                 220

Val Gln Phe Tyr Ser Met Asn Arg Pro Ala Ser Arg His Thr Pro Pro
225                 230                 235                 240

Thr Ile Gly Gly Ser Leu Pro Tyr Arg Arg Pro Pro Ser Ile Thr Ser
                245                 250                 255

Gln Thr Ser Leu Gln Asn Gln Met Asn Gly Gly Pro Phe Tyr Ser Gln
            260                 265                 270

Asn Pro Val Ser Asp Thr Pro Pro Pro Pro Pro Pro Val Glu Glu Pro
        275                 280                 285

Val Phe Asp Glu Ser Pro Pro Pro Pro Pro Pro Pro Glu Asp Tyr Glu
    290                 295                 300

Glu Glu Glu Ala Ala Val Val Glu Tyr Ser Asp Pro Tyr Ala Glu Glu
305                 310                 315                 320

Asp Pro Pro Trp Ala Pro Arg Ser Tyr Leu Glu Lys Val Val Ala Ile
                325                 330                 335

Tyr Asp Tyr Thr Lys Asp Lys Glu Asp Glu Leu Ser Phe Gln Glu Gly
            340                 345                 350

Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly
        355                 360                 365
```

```
Val Met Asn Gly Val Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser
    370                 375                 380


Ile Met His Tyr Ser Glu
385                 390


<210> 914
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID:  Q9NYB9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000261017"

<400> 914
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                   10                  15


Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30


Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
        35                  40                  45


Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
    50                  55                  60


Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65                  70                  75                  80


Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95
```

```
Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Val Ser Thr Gln Asn Met
145                 150                 155                 160

Lys Met Gly Gly Leu Pro Arg Thr Thr Pro Pro Thr Gln Lys Pro Pro
                165                 170                 175

Ser Pro Pro Met Ser Gly Lys Gly Thr Leu Gly Arg His Ser Pro Tyr
            180                 185                 190

Arg Thr Leu Glu Pro Val Arg Pro Pro Val Val Pro Asn Asp Tyr Val
        195                 200                 205

Pro Ser Pro Thr Arg Asn Met Ala Pro Ser Gln Gln Ser Pro Val Arg
    210                 215                 220

Thr Ala Ser Val Asn Gln Arg Asn Arg Thr Tyr Ser Ser Ser Gly Ser
225                 230                 235                 240

Ser Gly Gly Ser His Pro Ser Ser Arg Ser Ser Ser Arg Glu Asn Ser
                245                 250                 255

Gly Ser Gly Ser Val Gly Val Pro Ile Ala Val Pro Thr Pro Ser Pro
            260                 265                 270

Pro Ser Val Phe Pro Gly His Pro Val Gln Phe Tyr Ser Met Asn Arg
        275                 280                 285

Pro Ala Ser Arg His Thr Pro Pro Thr Ile Gly Gly Ser Leu Pro Tyr
    290                 295                 300

Arg Arg Pro Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln Asn Gln Met
305                 310                 315                 320
```

```
Asn Gly Gly Pro Phe Tyr Ser Gln Asn Pro Val Ser Leu Ala Pro Pro
                325                 330                 335

Pro Pro Ser Ile Leu Gln Val Thr Pro Gln Leu Pro Leu Met Gly Phe
            340                 345                 350

Val Ala Arg Val Gln Glu Asn Ile Ser Asp Thr Pro Pro Pro Pro Pro
        355                 360                 365

Pro Val Glu Glu Pro Val Phe Asp Glu Ser Pro Pro Pro Pro Pro Pro
    370                 375                 380

Pro Glu Asp Tyr Glu Glu Glu Glu Ala Ala Val Val Glu Tyr Ser Asp
385                 390                 395                 400

Pro Tyr Ala Glu Glu Asp Pro Pro Trp Ala Pro Arg Ser Tyr Leu Glu
                405                 410                 415

Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Glu Asp Glu Leu
            420                 425                 430

Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp
        435                 440                 445

Gly Trp Tyr Glu Gly Val Met Asn Gly Val Thr Gly Leu Phe Pro Gly
    450                 455                 460

Asn Tyr Val Glu Ser Ile Met His Tyr Ser Glu
465                 470                 475


<210> 915
<211> 513
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
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abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000261018"

<400> 915

```
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                  10                  15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
        35                  40                  45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
    50                  55                  60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Trp Leu Leu Arg Phe Lys
145                 150                 155                 160

Val Ser Thr Gln Asn Met Lys Met Gly Gly Leu Pro Arg Thr Thr Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Lys Gly Thr Leu
            180                 185                 190

Gly Arg His Ser Pro Tyr Arg Thr Leu Glu Pro Val Arg Pro Pro Val
        195                 200                 205
```

```
Val Pro Asn Asp Tyr Val Pro Ser Pro Thr Arg Asn Met Ala Pro Ser
    210                 215                 220

Gln Gln Ser Pro Val Arg Thr Ala Ser Val Asn Gln Arg Asn Arg Thr
225                 230                 235                 240

Tyr Ser Ser Ser Gly Ser Ser Gly Gly Ser His Pro Ser Ser Arg Ser
                245                 250                 255

Ser Ser Arg Glu Asn Ser Gly Ser Gly Ser Val Gly Val Pro Ile Ala
            260                 265                 270

Val Pro Thr Pro Ser Pro Pro Ser Val Phe Pro Ala Pro Ala Gly Ser
        275                 280                 285

Ala Gly Thr Pro Pro Leu Pro Ala Thr Ser Ala Ser Ala Pro Ala Pro
    290                 295                 300

Leu Val Pro Ala Thr Val Pro Ser Ser Thr Ala Pro Asp Ala Ala Ala
305                 310                 315                 320

Gly Gly Ala Gln Thr Leu Ala Asp Gly Phe Thr Ser Pro Thr Pro Pro
                325                 330                 335

Val Val Ser Ser Thr Pro Pro Thr Gly His Pro Val Gln Phe Tyr Ser
            340                 345                 350

Met Asn Arg Pro Ala Ser Arg His Thr Pro Pro Thr Ile Gly Gly Ser
        355                 360                 365

Leu Pro Tyr Arg Arg Pro Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln
    370                 375                 380

Asn Gln Met Asn Gly Gly Pro Phe Tyr Ser Gln Asn Pro Val Ser Asp
385                 390                 395                 400

Thr Pro Pro Pro Pro Pro Pro Val Glu Glu Pro Val Phe Asp Glu Ser
                405                 410                 415

Pro Pro Pro Pro Pro Pro Pro Glu Asp Tyr Glu Glu Glu Glu Ala Ala
            420                 425                 430
```

```
Val Val Glu Tyr Ser Asp Pro Tyr Ala Glu Glu Asp Pro Pro Trp Ala
        435                 440                 445

Pro Arg Ser Tyr Leu Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys
    450                 455                 460

Asp Lys Glu Asp Glu Leu Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val
465                 470                 475                 480

Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Met Asn Gly Val
                485                 490                 495

Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Ser
            500                 505                 510

Glu
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<210> 916
<211> 513
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000295851"

<400> 916

```
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                   10                  15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
```

```
        35                  40                  45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
    50                  55                  60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Trp Leu Leu Arg Phe Lys
145                 150                 155                 160

Val Ser Thr Gln Asn Met Lys Met Gly Gly Leu Pro Arg Thr Thr Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Lys Gly Thr Leu
            180                 185                 190

Gly Arg His Ser Pro Tyr Arg Thr Leu Glu Pro Val Arg Pro Pro Val
        195                 200                 205

Val Pro Asn Asp Tyr Val Pro Ser Pro Thr Arg Asn Met Ala Pro Ser
    210                 215                 220

Gln Gln Ser Pro Val Arg Thr Ala Ser Val Asn Gln Arg Asn Arg Thr
225                 230                 235                 240

Tyr Ser Ser Ser Gly Ser Ser Gly Gly Ser His Pro Ser Ser Arg Ser
                245                 250                 255

Ser Ser Arg Glu Asn Ser Gly Ser Gly Ser Val Gly Val Pro Ile Ala
            260                 265                 270
```

```
Val Pro Thr Pro Ser Pro Pro Ser Val Phe Pro Ala Pro Ala Gly Ser
        275                 280                 285

Ala Gly Thr Pro Pro Leu Pro Ala Thr Ser Ala Ser Ala Pro Ala Pro
    290                 295                 300

Leu Val Pro Ala Thr Val Pro Ser Ser Thr Ala Pro Asp Ala Ala Ala
305                 310                 315                 320

Gly Gly Ala Gln Thr Leu Ala Asp Gly Phe Thr Ser Pro Thr Pro Pro
                325                 330                 335

Val Val Ser Ser Thr Pro Pro Thr Gly His Pro Val Gln Phe Tyr Ser
            340                 345                 350

Met Asn Arg Pro Ala Ser Arg His Thr Pro Pro Thr Ile Gly Gly Ser
        355                 360                 365

Leu Pro Tyr Arg Arg Pro Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln
    370                 375                 380

Asn Gln Met Asn Gly Gly Pro Phe Tyr Ser Gln Asn Pro Val Ser Asp
385                 390                 395                 400

Thr Pro Pro Pro Pro Pro Pro Val Glu Glu Pro Val Phe Asp Glu Ser
                405                 410                 415

Pro Pro Pro Pro Pro Pro Pro Glu Asp Tyr Glu Glu Glu Glu Ala Ala
            420                 425                 430

Val Val Glu Tyr Ser Asp Pro Tyr Ala Glu Glu Asp Pro Pro Trp Ala
        435                 440                 445

Pro Arg Ser Tyr Leu Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys
    450                 455                 460

Asp Lys Glu Asp Glu Leu Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val
465                 470                 475                 480

Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Met Asn Gly Val
                485                 490                 495
```

Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Ser
500 505 510

Glu

<210> 917
<211> 507
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391433"

<400> 917
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1 5 10 15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
20 25 30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
35 40 45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
50 55 60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65 70 75 80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
85 90 95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu

```
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Val Ser Thr Gln Asn Met
145                 150                 155                 160

Lys Met Gly Gly Leu Pro Arg Thr Thr Pro Pro Thr Gln Lys Pro Pro
                165                 170                 175

Ser Pro Pro Met Ser Gly Lys Gly Thr Leu Gly Arg His Ser Pro Tyr
            180                 185                 190

Arg Thr Leu Glu Pro Val Arg Pro Pro Val Val Pro Asn Asp Tyr Val
        195                 200                 205

Pro Ser Pro Thr Arg Asn Met Ala Pro Ser Gln Gln Ser Pro Val Arg
    210                 215                 220

Thr Ala Ser Val Asn Gln Arg Asn Arg Thr Tyr Ser Ser Ser Gly Ser
225                 230                 235                 240

Ser Gly Gly Ser His Pro Ser Ser Arg Ser Ser Ser Arg Glu Asn Ser
                245                 250                 255

Gly Ser Gly Ser Val Gly Val Pro Ile Ala Val Pro Thr Pro Ser Pro
            260                 265                 270

Pro Ser Val Phe Pro Ala Pro Ala Gly Ser Ala Gly Thr Pro Pro Leu
        275                 280                 285

Pro Ala Thr Ser Ala Ser Ala Pro Ala Pro Leu Val Pro Ala Thr Val
    290                 295                 300

Pro Ser Ser Thr Ala Pro Asp Ala Ala Ala Gly Gly Ala Gln Thr Leu
305                 310                 315                 320

Ala Asp Gly Phe Thr Ser Pro Thr Pro Pro Val Val Ser Ser Thr Pro
                325                 330                 335
```

```
Pro Thr Gly His Pro Val Gln Phe Tyr Ser Met Asn Arg Pro Ala Ser
            340                 345                 350

Arg His Thr Pro Pro Thr Ile Gly Gly Ser Leu Pro Tyr Arg Arg Pro
        355                 360                 365

Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln Asn Gln Met Asn Gly Gly
    370                 375                 380

Pro Phe Tyr Ser Gln Asn Pro Val Ser Asp Thr Pro Pro Pro Pro Pro
385                 390                 395                 400

Pro Val Glu Glu Pro Val Phe Asp Glu Ser Pro Pro Pro Pro Pro Pro
                405                 410                 415

Pro Glu Asp Tyr Glu Glu Glu Glu Ala Ala Val Val Glu Tyr Ser Asp
            420                 425                 430

Pro Tyr Ala Glu Glu Asp Pro Pro Trp Ala Pro Arg Ser Tyr Leu Glu
        435                 440                 445

Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Glu Asp Glu Leu
    450                 455                 460

Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp
465                 470                 475                 480

Gly Trp Tyr Glu Gly Val Met Asn Gly Val Thr Gly Leu Phe Pro Gly
                485                 490                 495

Asn Tyr Val Glu Ser Ile Met His Tyr Ser Glu
            500                 505


<210> 918
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
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<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396249"

<400> 918

```
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                  10                  15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
        35                  40                  45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
    50                  55                  60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Trp Leu Leu Arg Phe Lys
145                 150                 155                 160

Val Ser Thr Gln Asn Met Lys Met Gly Gly Leu Pro Arg Thr Thr Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Lys Gly Thr Leu
```

```
            180                 185                 190

Gly Arg His Ser Pro Tyr Arg Thr Leu Glu Pro Val Arg Pro Pro Val
        195                 200                 205

Val Pro Asn Asp Tyr Val Pro Ser Pro Thr Arg Asn Met Ala Pro Ser
    210                 215                 220

Gln Gln Ser Pro Val Arg Thr Ala Ser Val Asn Gln Arg Asn Arg Thr
225                 230                 235                 240

Tyr Ser Ser Ser Gly Ser Ser Gly Gly Ser His Pro Ser Ser Arg Ser
                245                 250                 255

Ser Ser Arg Glu Asn Ser Gly Ser Gly Ser Val Gly Val Pro Ile Ala
            260                 265                 270

Val Pro Thr Pro Ser Pro Pro Ser Val Phe Pro Asp Ala Ala Ala Gly
        275                 280                 285

Gly Ala Gln Thr Leu Ala Asp Gly Phe Thr Ser Pro Thr Pro Pro Val
    290                 295                 300

Val Ser Ser Thr Pro Pro Thr Gly His Pro Val Gln Phe Tyr Ser Met
305                 310                 315                 320

Asn Arg Pro Ala Ser Arg His Thr Pro Pro Thr Ile Gly Gly Ser Leu
                325                 330                 335

Pro Tyr Arg Arg Pro Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln Asn
            340                 345                 350

Gln Met Asn Gly Gly Pro Phe Tyr Ser Gln Asn Pro Val Ser Asp Thr
        355                 360                 365

Pro Pro Pro Pro Pro Pro Val Glu Glu Pro Val Phe Asp Glu Ser Pro
    370                 375                 380

Pro Pro Pro Pro Pro Pro Glu Asp Tyr Glu Glu Glu Glu Ala Ala Val
385                 390                 395                 400

Val Glu Tyr Ser Asp Pro Tyr Ala Glu Glu Asp Pro Pro Trp Ala Pro
                405                 410                 415
```

```
Arg Ser Tyr Leu Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp
            420                 425                 430

Lys Glu Asp Glu Leu Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val Ile
        435                 440                 445

Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Met Asn Gly Val Thr
    450                 455                 460

Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Ser Glu
465                 470                 475                 480


<210> 919
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397850"

<400> 919
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                   10                  15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Arg Trp Gly Leu Gly Met Ser Cys Arg
        35                  40                  45

Leu Glu Cys Ser Gly Val Ile Ile Ala His Cys Ser Leu Glu Leu Leu
    50                  55                  60
```

```
Cys Ser Ser Asp His Pro Ala Ser Val Ser Gln
65                  70                  75


<210> 920
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398487"

<400> 920
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                   10                  15


Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30


Cys Glu Asn Asn Tyr Ile Gln Ile Ser Arg Glu Pro
        35                  40


<210> 921
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 2; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000399040"

<400> 921
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1   5   10   15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ala Phe Arg Phe Asp Ser Ala Tyr Pro
        35   40   45

Leu Val Leu Pro Asp Lys Glu Tyr Met Glu Ser
    50   55

<210> 922
<211> 293
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404352"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 922
Xaa Val Ser Thr Gln Asn Met Lys Met Gly Gly Leu Pro Arg Thr Thr
1   5   10   15

Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Lys Gly Thr
            20   25   30

```
Leu Gly Arg His Ser Pro Tyr Arg Thr Leu Glu Pro Val Arg Pro Pro
        35                  40                  45

Val Val Pro Asn Asp Tyr Val Pro Ser Pro Thr Arg Asn Met Ala Pro
    50                  55                  60

Ser Gln Gln Ser Pro Val Arg Thr Ala Ser Val Asn Gln Arg Asn Arg
65                  70                  75                  80

Thr Tyr Ser Ser Ser Gly Ser Ser Gly Gly Ser His Pro Ser Ser Arg
                85                  90                  95

Ser Ser Ser Arg Glu Asn Ser Gly Ser Gly Ser Val Gly Val Pro Ile
            100                 105                 110

Ala Val Pro Thr Pro Ser Pro Pro Ser Val Phe Pro Gly His Pro Val
        115                 120                 125

Gln Phe Tyr Ser Met Asn Arg Pro Ala Ser Arg His Thr Pro Pro Thr
    130                 135                 140

Ile Gly Gly Ser Leu Pro Tyr Arg Arg Pro Pro Ser Ile Thr Ser Gln
145                 150                 155                 160

Thr Ser Leu Gln Asn Gln Met Asn Gly Gly Pro Phe Tyr Ser Gln Asn
                165                 170                 175

Pro Val Ser Asp Thr Pro Pro Pro Pro Pro Pro Val Glu Glu Pro Val
            180                 185                 190

Phe Asp Glu Ser Pro Pro Pro Pro Pro Pro Pro Glu Asp Tyr Glu Glu
        195                 200                 205

Glu Glu Ala Ala Val Val Glu Tyr Ser Asp Pro Tyr Ala Glu Glu Asp
    210                 215                 220

Pro Pro Trp Ala Pro Arg Ser Tyr Leu Glu Lys Val Val Ala Ile Tyr
225                 230                 235                 240

Asp Tyr Thr Lys Asp Lys Glu Asp Glu Leu Ser Phe Gln Glu Gly Ala
                245                 250                 255
```

```
Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val
            260                 265                 270

Met Asn Gly Val Thr Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile
        275                 280                 285

Met His Tyr Ser Glu
    290
```

<210> 923
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405255"

<400> 923

```
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                  10                  15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Leu Leu Ser Ile Phe Pro Phe Cys Glu
        35                  40                  45

Val Ser Val Ser Arg
    50
```

<210> 924
<211> 87
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405801"

<400> 924
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1 5 10 15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
20 25 30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
35 40 45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
50 55 60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Val
65 70 75 80

Ile Leu Tyr Ser Ser Thr Ala
85

<210> 925
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:

abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408334"

<400> 925
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1   5   10   15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20   25   30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
        35   40   45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
    50   55   60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65   70   75   80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Met
                85   90   95

Phe Ser His Thr Asp Gly Gln Leu Thr Glu Ala Asn
            100   105

<210> 926
<211> 458
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408898"

<400> 926
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1 5 10 15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
20 25 30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
35 40 45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
50 55 60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65 70 75 80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
85 90 95

Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
100 105 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
115 120 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
130 135 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Val Ser Thr Gln Asn Met
145 150 155 160

Lys Met Gly Gly Leu Pro Arg Thr Thr Pro Pro Thr Gln Lys Pro Pro
165 170 175

Ser Pro Pro Met Ser Gly Lys Gly Thr Leu Gly Ser Ser Gly Ser Ser
180 185 190

Gly Gly Ser His Pro Ser Ser Arg Ser Ser Ser Arg Glu Asn Ser Gly
195 200 205

Ser Gly Ser Val Gly Val Pro Ile Ala Val Pro Thr Pro Ser Pro Pro
210 215 220

```
Ser Val Phe Pro Ala Pro Ala Gly Ser Ala Gly Thr Pro Pro Leu Pro
225                 230                 235                 240

Ala Thr Ser Ala Ser Ala Pro Ala Pro Leu Val Pro Ala Thr Val Pro
                245                 250                 255

Ser Ser Thr Ala Pro Asp Ala Ala Ala Gly Gly Ala Gln Thr Leu Ala
            260                 265                 270

Asp Gly Phe Thr Ser Pro Thr Pro Pro Val Val Ser Ser Thr Pro Pro
        275                 280                 285

Thr Gly His Pro Val Gln Phe Tyr Ser Met Asn Arg Pro Ala Ser Arg
    290                 295                 300

His Thr Pro Pro Thr Ile Gly Gly Ser Leu Pro Tyr Arg Arg Pro Pro
305                 310                 315                 320

Ser Ile Thr Ser Gln Thr Ser Leu Gln Asn Gln Met Asn Gly Gly Pro
                325                 330                 335

Phe Tyr Ser Gln Asn Pro Val Ser Asp Thr Pro Pro Pro Pro Pro Pro
            340                 345                 350

Val Glu Glu Pro Val Phe Asp Glu Ser Pro Pro Pro Pro Pro Pro Pro
        355                 360                 365

Glu Asp Tyr Glu Glu Glu Glu Ala Ala Val Val Glu Tyr Ser Asp Pro
    370                 375                 380

Tyr Ala Glu Glu Asp Pro Pro Trp Ala Pro Arg Ser Tyr Leu Glu Lys
385                 390                 395                 400

Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Glu Asp Glu Leu Ser
                405                 410                 415

Phe Gln Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly
            420                 425                 430

Trp Tyr Glu Gly Val Met Asn Gly Val Thr Gly Leu Phe Pro Gly Asn
        435                 440                 445

Tyr Val Glu Ser Ile Met His Tyr Ser Glu
```

450 455

<210> 927
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410509"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 927
Xaa Gln Ser Leu Ala Ser Val Ala Tyr Leu Ile Asn Thr Leu Ala Asn
1 5 10 15

Asn Val Leu Gln Met Leu Asp Ile Gln Ala Ser Gln Leu Arg Arg Met
20 25 30

Glu Ser Ser Ile Asn His Ile Ser Gln Ala Asn
35 40

<210> 928
<211> 201
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413375"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 928
Xaa Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
1 5 10 15

Ile Leu Asp Asp Ile Gly His Gly Val Lys Val Ser Thr Gln Asn Met
20 25 30

Lys Met Gly Gly Leu Pro Arg Thr Thr Pro Pro Thr Gln Lys Pro Pro
35 40 45

Ser Pro Pro Met Ser Gly Lys Gly Thr Leu Gly Arg His Ser Pro Tyr
50 55 60

Arg Thr Leu Glu Pro Val Arg Pro Pro Val Val Pro Asn Asp Tyr Val
65 70 75 80

Pro Ser Pro Thr Arg Asn Met Ala Pro Ser Gln Gln Ser Pro Val Arg
85 90 95

Thr Ala Ser Val Asn Gln Arg Asn Arg Thr Tyr Ser Ser Gly Ser Ser
100 105 110

Gly Gly Ser His Pro Ser Ser Arg Ser Ser Ser Arg Glu Asn Ser Gly
115 120 125

Ser Gly Ser Val Gly Val Pro Ile Ala Val Pro Thr Pro Ser Pro Pro
130 135 140

Ser Val Phe Pro Gly His Pro Val Gln Phe Tyr Ser Met Asn Arg Pro
145 150 155 160

Ala Ser Arg His Thr Pro Pro Thr Ile Gly Gly Ser Leu Pro Tyr Arg

```
                165                 170                 175

Arg Pro Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln Asn Gln Met Asn
            180                 185                 190

Gly Gly Pro Phe Tyr Ser Gln Asn Pro
        195                 200


<210> 929
<211> 486
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 152; "

<220>
<221> source
<223> /note="Gene Symbol: ABI2; "

<220>
<221> source
<223> /note="Gene Name:
      abl-interactor 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414703"

<400> 929
Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro Gly Gly Arg
1               5                   10                  15

Arg Ala Leu Phe Asp Ser Tyr Thr Asn Leu Glu Arg Val Ala Asp Tyr
            20                  25                  30

Cys Glu Asn Asn Tyr Ile Gln Ser Ala Asp Lys Gln Arg Ala Leu Glu
        35                  40                  45

Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr Leu
    50                  55                  60

Ile Asn Thr Leu Ala Asn Asn Val Leu Gln Met Leu Asp Ile Gln Ala
65                  70                  75                  80

Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr
                85                  90                  95
```

```
Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu
            100                 105                 110

Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala
        115                 120                 125

Asn Leu Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr
    130                 135                 140

Ile Leu Asp Asp Ile Gly His Gly Val Lys Trp Leu Leu Arg Phe Lys
145                 150                 155                 160

Val Ser Thr Gln Asn Met Lys Met Gly Gly Leu Pro Arg Thr Thr Pro
                165                 170                 175

Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Lys Gly Thr Leu
            180                 185                 190

Gly Arg His Ser Pro Tyr Arg Thr Leu Glu Pro Val Arg Pro Pro Val
        195                 200                 205

Val Pro Asn Asp Tyr Val Pro Ser Pro Thr Arg Asn Met Ala Pro Ser
    210                 215                 220

Gln Gln Ser Pro Val Arg Thr Ala Ser Val Asn Gln Arg Asn Arg Thr
225                 230                 235                 240

Tyr Ser Ser Ser Gly Ser Ser Gly Gly Ser His Pro Ser Ser Arg Ser
                245                 250                 255

Ser Ser Arg Glu Asn Ser Gly Ser Gly Ser Val Gly Val Pro Ile Ala
            260                 265                 270

Val Pro Thr Pro Ser Pro Pro Ser Val Phe Pro Ala Pro Ala Gly Ser
        275                 280                 285

Ala Gly Thr Pro Pro Leu Pro Ala Thr Ser Ala Ser Ala Pro Ala Pro
    290                 295                 300

Leu Val Pro Ala Thr Val Pro Ser Ser Thr Ala Pro Asp Ala Ala Ala
305                 310                 315                 320
```

```
Gly Gly Ala Gln Thr Leu Ala Asp Gly Phe Thr Ser Pro Thr Pro Pro
                325                 330                 335

Val Val Ser Ser Thr Pro Pro Thr Gly His Pro Val Gln Phe Tyr Ser
            340                 345                 350

Met Asn Arg Pro Ala Ser Arg His Thr Pro Pro Thr Ile Gly Gly Ser
        355                 360                 365

Leu Pro Tyr Arg Arg Pro Pro Ser Ile Thr Ser Gln Thr Ser Leu Gln
    370                 375                 380

Asn Gln Met Asn Gly Gly Pro Phe Tyr Ser Gln Asn Pro Val Ser Asp
385                 390                 395                 400

Thr Pro Pro Pro Pro Pro Pro Val Glu Glu Pro Val Phe Asp Glu Ser
                405                 410                 415

Pro Pro Pro Pro Pro Pro Pro Glu Asp Tyr Glu Glu Glu Glu Ala Ala
            420                 425                 430

Val Val Glu Tyr Ser Asp Pro Tyr Ala Glu Glu Asp Pro Pro Trp Ala
        435                 440                 445

Pro Arg Ser Tyr Leu Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys
    450                 455                 460

Asp Lys Glu Asp Glu Leu Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val
465                 470                 475                 480

Ile Lys Lys Asn Asp Asp
                485
```

<210> 930
<211> 1892
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 153; "

<220>
<221> source
<223> /note="Gene Symbol: ASPM; "

<220>
<221> source
<223> /note="Gene Name:
abnormal spindle microtubule assembly; "

<220>
<221> source
<223> /note="Uniprot ID: Q8IZT6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000294732"

<400> 930
Met Ala Asn Arg Arg Val Gly Arg Gly Cys Trp Glu Val Ser Pro Thr
1 5 10 15

Glu Arg Arg Pro Pro Ala Gly Leu Arg Gly Pro Ala Ala Glu Glu Glu
20 25 30

Ala Ser Ser Pro Pro Val Leu Ser Leu Ser His Phe Cys Arg Ser Pro
35 40 45

Phe Leu Cys Phe Gly Asp Val Leu Leu Gly Ala Ser Arg Thr Leu Ser
50 55 60

Leu Ala Leu Asp Asn Pro Asn Glu Glu Val Ala Glu Val Lys Ile Ser
65 70 75 80

His Phe Pro Ala Ala Asp Leu Gly Phe Ser Val Ser Gln Arg Cys Phe
85 90 95

Val Leu Gln Pro Lys Glu Lys Ile Val Ile Ser Val Asn Trp Thr Pro
100 105 110

Leu Lys Glu Gly Arg Val Arg Glu Ile Met Thr Phe Leu Val Asn Asp
115 120 125

Val Leu Lys His Gln Ala Ile Leu Leu Gly Asn Ala Glu Glu Gln Lys
130 135 140

Lys Lys Lys Arg Ser Leu Trp Asp Thr Ile Lys Lys Lys Lys Ile Ser
145 150 155 160

Ala Ser Thr Ser His Asn Arg Arg Val Ser Asn Ile Gln Asn Val Asn
165 170 175

```
Lys Thr Phe Ser Val Ser Gln Lys Val Asp Arg Val Arg Ser Pro Leu
            180                 185                 190

Gln Ala Cys Glu Asn Leu Ala Met Asn Glu Gly Gly Pro Pro Thr Glu
        195                 200                 205

Asn Asn Ser Leu Ile Leu Glu Glu Asn Lys Ile Pro Ile Ser Pro Ile
    210                 215                 220

Ser Pro Ala Phe Asn Glu Cys His Gly Ala Thr Cys Leu Pro Leu Ser
225                 230                 235                 240

Val Arg Arg Ser Thr Thr Tyr Ser Ser Leu His Ala Ser Glu Asn Arg
                245                 250                 255

Glu Leu Leu Asn Val His Ser Ala Asn Val Ser Lys Val Ser Phe Asn
            260                 265                 270

Glu Lys Ala Val Thr Glu Thr Ser Phe Asn Ser Val Asn Val Asn Gly
        275                 280                 285

Gln Arg Gly Glu Asn Ser Lys Leu Ser Leu Thr Pro Asn Cys Ser Ser
    290                 295                 300

Thr Leu Asn Ile Thr Gln Ser Gln Ile His Phe Leu Ser Pro Asp Ser
305                 310                 315                 320

Phe Val Asn Asn Ser His Gly Ala Asn Asn Glu Leu Glu Leu Val Thr
                325                 330                 335

Cys Leu Ser Ser Asp Met Phe Met Lys Asp Asn Ser Gln Pro Val His
            340                 345                 350

Leu Glu Ser Thr Ile Ala His Glu Ile Tyr Gln Lys Ile Leu Ser Pro
        355                 360                 365

Asp Ser Phe Ile Lys Asp Asn Tyr Gly Leu Asn Gln Asp Leu Glu Ser
    370                 375                 380

Glu Ser Val Asn Pro Ile Leu Ser Pro Asn Gln Phe Leu Lys Asp Asn
385                 390                 395                 400
```

```
Met Ala Tyr Met Cys Thr Ser Gln Gln Thr Cys Lys Val Pro Leu Ser
                405                 410                 415

Asn Glu Asn Ser Gln Val Pro Gln Ser Pro Glu Asp Trp Arg Lys Ser
            420                 425                 430

Glu Val Ser Pro Arg Ile Pro Glu Cys Gln Gly Ser Lys Ser Pro Lys
        435                 440                 445

Ala Ile Phe Glu Glu Leu Val Glu Met Lys Ser Asn Tyr Tyr Ser Phe
    450                 455                 460

Ile Lys Gln Asn Asn Pro Lys Phe Ser Ala Val Gln Asp Ile Ser Ser
465                 470                 475                 480

His Ser His Asn Lys Gln Pro Lys Arg Arg Pro Ile Leu Ser Ala Thr
                485                 490                 495

Val Thr Lys Arg Lys Ala Thr Cys Thr Arg Glu Asn Gln Thr Glu Ile
            500                 505                 510

Asn Lys Pro Lys Ala Lys Arg Cys Leu Asn Ser Ala Val Gly Glu His
        515                 520                 525

Glu Lys Val Ile Asn Asn Gln Lys Glu Lys Glu Asp Phe His Ser Tyr
    530                 535                 540

Leu Pro Ile Ile Asp Pro Ile Leu Ser Lys Ser Lys Ser Tyr Lys Asn
545                 550                 555                 560

Glu Val Thr Pro Ser Ser Thr Thr Ala Ser Val Ala Arg Lys Arg Lys
                565                 570                 575

Ser Asp Gly Ser Met Glu Asp Ala Asn Val Arg Val Ala Ile Thr Glu
            580                 585                 590

His Thr Glu Val Arg Glu Ile Lys Arg Ile His Phe Ser Pro Ser Glu
        595                 600                 605

Pro Lys Thr Ser Ala Val Lys Lys Thr Lys Asn Val Thr Thr Pro Ile
    610                 615                 620

Ser Lys Arg Ile Ser Asn Arg Glu Lys Leu Asn Leu Lys Lys Lys Thr
```

625 630 635 640

Asp Leu Ser Ile Phe Arg Thr Pro Ile Ser Lys Thr Asn Lys Arg Thr
645 650 655

Lys Pro Ile Ile Ala Val Ala Gln Ser Ser Leu Thr Phe Ile Lys Pro
660 665 670

Leu Lys Thr Asp Ile Pro Arg His Pro Met Pro Phe Ala Ala Lys Asn
675 680 685

Met Phe Tyr Asp Glu Arg Trp Lys Glu Lys Gln Glu Gln Gly Phe Thr
690 695 700

Trp Trp Leu Asn Phe Ile Leu Thr Pro Asp Asp Phe Thr Val Lys Thr
705 710 715 720

Asn Ile Ser Glu Val Asn Ala Ala Thr Leu Leu Leu Gly Ile Glu Asn
725 730 735

Gln His Lys Ile Ser Val Pro Arg Ala Pro Thr Lys Glu Glu Met Ser
740 745 750

Leu Arg Ala Tyr Thr Ala Arg Cys Arg Leu Asn Arg Leu Arg Arg Ala
755 760 765

Ala Cys Arg Leu Phe Thr Ser Glu Lys Met Val Lys Ala Ile Lys Lys
770 775 780

Leu Glu Ile Glu Ile Glu Ala Arg Arg Leu Ile Val Arg Lys Asp Arg
785 790 795 800

His Leu Trp Lys Asp Val Gly Glu Arg Gln Lys Val Leu Asn Trp Leu
805 810 815

Leu Ser Tyr Asn Pro Leu Trp Leu Arg Ile Gly Leu Glu Thr Thr Tyr
820 825 830

Gly Glu Leu Ile Ser Leu Glu Asp Asn Ser Asp Val Thr Gly Leu Ala
835 840 845

Met Phe Ile Leu Asn Arg Leu Leu Trp Asn Pro Asp Ile Ala Ala Glu
850 855 860

```
Tyr Arg His Pro Thr Val Pro His Leu Tyr Arg Asp Gly His Glu Glu
865                 870                 875                 880

Ala Leu Ser Lys Phe Thr Leu Lys Lys Leu Leu Leu Leu Val Cys Phe
                885                 890                 895

Leu Asp Tyr Ala Lys Ile Ser Arg Leu Ile Asp His Asp Pro Cys Leu
            900                 905                 910

Phe Cys Lys Asp Ala Glu Phe Lys Ala Ser Lys Glu Ile Leu Leu Ala
        915                 920                 925

Phe Ser Arg Asp Phe Leu Ser Gly Glu Gly Asp Leu Ser Arg His Leu
    930                 935                 940

Gly Leu Leu Gly Leu Pro Val Asn His Val Gln Thr Pro Phe Asp Glu
945                 950                 955                 960

Phe Asp Phe Ala Val Thr Asn Leu Ala Val Asp Leu Gln Cys Gly Val
                965                 970                 975

Arg Leu Val Arg Thr Met Glu Leu Leu Thr Gln Asn Trp Asp Leu Ser
            980                 985                 990

Lys Lys Leu Arg Ile Pro Ala Ile  Ser Arg Leu Gln Lys  Met His
Asn
        995                 1000                1005

Val Asp  Ile Val Leu Gln Val  Leu Lys Ser Arg Gly  Ile Glu Leu
    1010                1015                1020

Ser Asp  Glu His Gly Asn Thr  Ile Leu Ser Lys Asp  Ile Val Asp
    1025                1030                1035

Arg His  Arg Glu Lys Thr Leu  Arg Leu Leu Trp Lys  Ile Ala Phe
    1040                1045                1050

Ala Phe  Gln Val Asp Ile Ser  Leu Asn Leu Asp Gln  Leu Lys Glu
    1055                1060                1065

Glu Ile  Ala Phe Leu Lys His  Thr Lys Ser Ile Lys  Lys Thr Ile
    1070                1075                1080
```

```
Ser Leu  Leu Ser Cys His Ser  Asp Asp Leu Ile Asn  Lys Lys Lys
    1085                1090                1095

Gly Lys  Arg Asp Ser Gly Ser  Phe Glu Gln Tyr Ser  Glu Asn Ile
    1100                1105                1110

Lys Leu  Leu Met Asp Trp Val  Asn Ala Val Cys Ala  Phe Tyr Asn
    1115                1120                1125

Lys Lys  Val Glu Asn Phe Thr  Val Ser Phe Ser Asp  Gly Arg Val
    1130                1135                1140

Leu Cys  Tyr Leu Ile His His  Tyr His Pro Cys Tyr  Val Pro Phe
    1145                1150                1155

Asp Ala  Ile Cys Gln Arg Thr  Thr Gln Thr Val Glu  Cys Thr Gln
    1160                1165                1170

Thr Gly  Ser Val Val Leu Asn  Ser Ser Ser Glu Ser  Asp Asp Ser
    1175                1180                1185

Ser Leu  Asp Met Ser Leu Lys  Ala Phe Asp His Glu  Asn Thr Ser
    1190                1195                1200

Glu Leu  Tyr Lys Glu Leu Leu  Glu Asn Glu Lys Lys  Asn Phe His
    1205                1210                1215

Leu Val  Arg Ser Ala Val Arg  Asp Leu Gly Gly Ile  Pro Ala Met
    1220                1225                1230

Ile Asn  His Ser Asp Met Ser  Asn Thr Ile Pro Asp  Glu Lys Val
    1235                1240                1245

Val Ile  Thr Tyr Leu Ser Phe  Leu Cys Ala Arg Leu  Leu Asp Leu
    1250                1255                1260

Arg Lys  Glu Ile Arg Ala Ala  Arg Leu Ile Gln Thr  Thr Trp Arg
    1265                1270                1275

Lys Tyr  Lys Leu Lys Thr Asp  Leu Lys Arg His Gln  Glu Arg Glu
    1280                1285                1290
```

```
Lys Ala  Ala Arg Ile Ile Gln  Leu Ala Val Ile Asn  Phe Leu Ala
    1295                 1300                 1305

Lys Gln  Arg Leu Arg Lys Arg  Val Asn Ala Ala Leu  Val Ile Gln
    1310                 1315                 1320

Lys Tyr  Trp Arg Arg Val Leu  Ala Gln Arg Lys Leu  Leu Met Leu
    1325                 1330                 1335

Lys Lys  Glu Lys Leu Glu Lys  Val Gln Asn Lys Ala  Ala Ser Leu
    1340                 1345                 1350

Ile Gln  Ala Met Trp Arg Arg  Tyr Arg Ala Lys Lys  Tyr Leu Cys
    1355                 1360                 1365

Lys Val  Lys Ala Ala Cys Lys  Ile Gln Ala Trp Tyr  Arg Cys Trp
    1370                 1375                 1380

Arg Ala  His Lys Glu Tyr Leu  Ala Ile Leu Lys Ala  Val Lys Ile
    1385                 1390                 1395

Ile Gln  Gly Cys Phe Tyr Thr  Lys Leu Glu Arg Thr  Arg Phe Leu
    1400                 1405                 1410

Asn Val  Arg Ala Ser Ala Ile  Ile Ile Gln Arg Lys  Trp Arg Ala
    1415                 1420                 1425

Ile Leu  Pro Ala Lys Ile Ala  His Glu His Phe Leu  Met Ile Lys
    1430                 1435                 1440

Arg His  Arg Ala Ala Cys Leu  Ile Gln Ala His Tyr  Arg Gly Tyr
    1445                 1450                 1455

Lys Gly  Arg Gln Val Phe Leu  Arg Gln Lys Ser Ala  Ala Leu Ile
    1460                 1465                 1470

Ile Gln  Lys Tyr Ile Arg Ala  Arg Glu Ala Gly Lys  His Glu Arg
    1475                 1480                 1485

Ile Lys  Tyr Ile Glu Phe Lys  Lys Ser Thr Val Ile  Leu Gln Ala
    1490                 1495                 1500
```

Leu Val Arg Gly Trp Leu Val Arg Lys Arg Phe Leu Glu Gln Arg
1505 1510 1515

Ala Lys Ile Arg Leu Leu His Phe Thr Ala Ala Ala Tyr Tyr His
1520 1525 1530

Leu Asn Ala Val Arg Ile Gln Arg Ala Tyr Lys Leu Tyr Leu Ala
1535 1540 1545

Val Lys Asn Ala Asn Lys Gln Val Asn Ser Val Ile Cys Ile Gln
1550 1555 1560

Arg Trp Phe Arg Ala Arg Leu Gln Glu Lys Arg Phe Ile Gln Lys
1565 1570 1575

Tyr His Ser Ile Lys Lys Ile Glu His Glu Gly Gln Glu Cys Leu
1580 1585 1590

Ser Gln Arg Asn Arg Ala Ala Ser Val Ile Gln Lys Ala Val Arg
1595 1600 1605

His Phe Leu Leu Arg Lys Lys Gln Glu Lys Phe Thr Ser Gly Ile
1610 1615 1620

Ile Lys Ile Gln Ala Leu Trp Arg Gly Tyr Ser Trp Arg Lys Lys
1625 1630 1635

Asn Asp Cys Thr Lys Ile Lys Ala Ile Arg Leu Ser Leu Gln Val
1640 1645 1650

Val Asn Arg Glu Ile Arg Glu Glu Asn Lys Leu Tyr Lys Arg Thr
1655 1660 1665

Ala Leu Ala Leu His Tyr Leu Leu Thr Tyr Lys His Leu Ser Ala
1670 1675 1680

Ile Leu Glu Ala Leu Lys His Leu Glu Val Val Thr Arg Leu Ser
1685 1690 1695

Pro Leu Cys Cys Glu Asn Met Ala Gln Ser Gly Ala Ile Ser Lys
1700 1705 1710

Ile Phe Val Leu Ile Arg Ser Cys Asn Arg Ser Ile Pro Cys Met

```
    1715                1720                1725

Glu Val  Ile Arg Tyr Ala Val  Gln Val Leu Leu Asn  Val Ser Lys
    1730                1735                1740

Tyr Glu  Lys Thr Thr Ser Ala  Val Tyr Asp Val Glu  Asn Cys Ile
    1745                1750                1755

Asp Ile  Leu Leu Glu Leu Leu  Gln Ile Tyr Arg Glu  Lys Pro Gly
    1760                1765                1770

Asn Lys  Val Ala Asp Lys Gly  Gly Ser Ile Phe Thr  Lys Thr Cys
    1775                1780                1785

Cys Leu  Leu Ala Ile Leu Leu  Lys Thr Thr Asn Arg  Ala Ser Asp
    1790                1795                1800

Val Arg  Ser Arg Ser Lys Val  Val Asp Arg Ile Tyr  Ser Leu Tyr
    1805                1810                1815

Lys Leu  Thr Ala His Lys His  Lys Met Asn Thr Glu  Arg Ile Leu
    1820                1825                1830

Tyr Lys  Gln Lys Lys Asn Ser  Ser Ile Ser Ile Pro  Phe Ile Pro
    1835                1840                1845

Glu Thr  Pro Val Arg Thr Arg  Ile Val Ser Arg Leu  Lys Pro Asp
    1850                1855                1860

Trp Val  Leu Arg Arg Asp Asn  Met Glu Glu Ile Thr  Asn Pro Leu
    1865                1870                1875

Gln Ala  Ile Gln Met Val Met  Asp Thr Leu Gly Ile  Pro Tyr
    1880                1885                1890


<210> 931
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<223> /note="Gene Name:
abnormal spindle microtubule assembly; "

<220>
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<223> /note="ENSP ID: ENSP00000356378"

<400> 931

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Met Ser Leu Arg Ala Tyr Thr Ala Arg Cys Arg Leu Asn Arg Leu Arg
1               5                  10                  15

Arg Ala Ala Cys Arg Leu Phe Thr Ser Glu Lys Met Val Lys Ala Ile
            20                  25                  30

Lys Lys Leu Glu Ile Glu Ile Glu Ala Arg Arg Leu Ile Val Arg Lys
        35                  40                  45

Asp Arg His Leu Trp Lys Asp Val Gly Glu Arg Gln Lys Val Leu Asn
    50                  55                  60

Trp Leu Leu Ser Tyr Asn Pro Leu Trp Leu Arg Ile Gly Leu Glu Thr
65                  70                  75                  80

Thr Tyr Gly Glu Leu Ile Ser Leu Glu Asp Asn Ser Asp Val Thr Gly
                85                  90                  95

Leu Ala Met Phe Ile Leu Asn Arg Leu Leu Trp Asn Pro Asp Ile Ala
            100                 105                 110

Ala Glu Tyr Arg His Pro Thr Val Pro His Leu Tyr Arg Asp Gly His
        115                 120                 125

Glu Glu Ala Leu Ser Lys Phe Thr Leu Lys Lys Leu Leu Leu Leu Val
    130                 135                 140

Cys Phe Leu Asp Tyr Ala Lys Ile Ser Arg Leu Ile Asp His Asp Pro
145                 150                 155                 160

Cys Leu Phe Cys Lys Asp Ala Glu Phe Lys Ala Ser Lys Glu Ile Leu
                165                 170                 175
```

```
Leu Ala Phe Ser Arg Asp Phe Leu Ser Gly Glu Gly Asp Leu Ser Arg
            180                 185                 190

His Leu Gly Leu Leu Gly Leu Pro Val Asn His Val Gln Thr Pro Phe
        195                 200                 205

Asp Glu Phe Asp Phe Ala Val Thr Asn Leu Ala Val Asp Leu Gln Cys
    210                 215                 220

Gly Val Arg Leu Val Arg Thr Met Glu Leu Leu Thr Gln Asn Trp Asp
225                 230                 235                 240

Leu Ser Lys Lys Leu Arg Ile Pro Ala Ile Ser Arg Leu Gln Lys Met
                245                 250                 255

His Asn Val Asp Ile Val Leu Gln Val Leu Lys Ser Arg Gly Ile Glu
            260                 265                 270

Leu Ser Asp Glu His Gly Asn Thr Ile Leu Ser Lys Asp Ile Val Asp
        275                 280                 285

Arg His Arg Glu Lys Thr Leu Arg Leu Leu Trp Lys Ile Ala Phe Ala
    290                 295                 300

Phe Gln Val Asp Ile Ser Leu Asn Leu Asp Gln Leu Lys Glu Glu Ile
305                 310                 315                 320

Ala Phe Leu Lys His Thr Lys Ser Ile Lys Lys Thr Ile Ser Leu Leu
                325                 330                 335

Ser Cys His Ser Asp Asp Leu Ile Asn Lys Lys Lys Gly Lys Arg Asp
            340                 345                 350

Ser Gly Ser Phe Glu Gln Tyr Ser Glu Asn Ile Lys Leu Leu Met Asp
        355                 360                 365

Trp Val Asn Ala Val Cys Ala Phe Tyr Asn Lys Lys Val Glu Asn Phe
    370                 375                 380

Thr Val Ser Phe Ser Asp Gly Arg Val Leu Cys Tyr Leu Ile His His
385                 390                 395                 400

Tyr His Pro Cys Tyr Val Pro Phe Asp Ala Ile Cys Gln Arg Thr Thr
```

405 410 415

Gln Thr Val Glu Cys Thr Gln Thr Gly Ser Val Val Leu Asn Ser Ser
420 425 430

Ser Glu Ser Asp Asp Ser Ser Leu Asp Met Ser Leu Lys Ala Phe Asp
435 440 445

His Glu Asn Thr Ser Glu Leu Tyr Lys Glu Leu Leu Glu Asn Glu Lys
450 455 460

Lys Asn Phe His Leu Val Arg Ser Ala Val Arg Asp Leu Gly Gly Ile
465 470 475 480

Pro Ala Met Ile Asn His Ser Asp Met Ser Asn Thr Ile Pro Asp Glu
485 490 495

Lys Val Val Ile Thr Tyr Leu Ser Phe Leu Cys Ala Arg Leu Leu Asp
500 505 510

Leu Arg Lys Glu Ile Arg Ala Ala Arg Leu Ile Gln Thr Thr Trp Arg
515 520 525

Lys Tyr Lys Leu Lys Thr Asp Leu Lys Arg His Gln Glu Arg Glu Lys
530 535 540

Ala Ala Arg Ile Ile Gln Leu Ala Val Ile Asn Phe Leu Ala Lys Gln
545 550 555 560

Arg Leu Arg Lys Arg Val Asn Ala Ala Leu Val Ile Gln Lys Tyr Trp
565 570 575

Arg Arg Val Leu Ala Gln Arg Lys Leu Leu Met Leu Lys Lys Glu Lys
580 585 590

Leu Glu Lys Val Gln Asn Lys Ala Ala Ser Leu Ile Gln Ala Met Trp
595 600 605

Arg Arg Tyr Arg Ala Lys Lys Tyr Leu Cys Lys Val Lys Ala Ala Cys
610 615 620

Lys Ile Gln Ala Trp Tyr Arg Cys Trp Arg Ala His Lys Glu Tyr Leu
625 630 635 640

Ala Ile Leu Lys Ala Val Lys Ile Ile Gln Gly Cys Phe Tyr Thr Lys
645 650 655

Leu Glu Arg Thr Arg Phe Leu Asn Val Arg Ala Ser Ala Ile Ile Ile
660 665 670

Gln Arg Lys Trp Arg Ala Ile Leu Pro Ala Lys Ile Ala His Glu His
675 680 685

Phe Leu Met Ile Lys Arg His Arg Ala Ala Cys Leu Ile Gln Ala His
690 695 700

Tyr Arg Gly Tyr Lys Gly Arg Gln Val Phe Leu Arg Gln Lys Ser Ala
705 710 715 720

Ala Leu Ile Ile Gln Lys Tyr Ile Arg Ala Arg Glu Ala Gly Lys His
725 730 735

Glu Arg Ile Lys Tyr Ile Glu Phe Lys Lys Ser Thr Val Ile Leu Gln
740 745 750

Ala Leu Val Arg Gly Trp Leu Val Arg Lys Arg Phe Leu Glu Gln Arg
755 760 765

Ala Lys Ile Arg Leu Leu His Phe Thr Ala Ala Ala Tyr Tyr His Leu
770 775 780

Asn Ala Val Arg Ile Gln Arg Ala Tyr Lys Leu Tyr Leu Ala Val Lys
785 790 795 800

Asn Ala Asn Lys Gln Val Asn Ser Val Ile Cys Ile Gln Arg Trp Phe
805 810 815

Arg Ala Arg Leu Gln Glu Lys Arg Phe Ile Gln Lys Tyr His Ser Ile
820 825 830

Lys Lys Ile Glu His Glu Gly Gln Glu Cys Leu Ser Gln Arg Asn Arg
835 840 845

Ala Ala Ser Val Ile Gln Lys Ala Val Arg His Phe Leu Leu Arg Lys
850 855 860

```
Lys Gln Glu Lys Phe Thr Ser Gly Ile Ile Lys Ile Gln Ala Leu Trp
865                 870                 875                 880

Arg Gly Tyr Ser Trp Arg Lys Lys Asn Asp Cys Thr Lys Ile Lys Ala
                885                 890                 895

Ile Arg Leu Ser Leu Gln Val Val Asn Arg Glu Ile Arg Glu Glu Asn
            900                 905                 910

Lys Leu Tyr Lys Arg Thr Ala Leu Ala Leu His Tyr Leu Leu Thr Tyr
        915                 920                 925

Lys His Leu Ser Ala Ile Leu Glu Ala Leu Lys His Leu Glu Val Val
    930                 935                 940

Thr Arg Leu Ser Pro Leu Cys Cys Glu Asn Met Ala Gln Ser Gly Ala
945                 950                 955                 960

Ile Ser Lys Ile Phe Val Leu Ile Arg Ser Cys Asn Arg Ser Ile Pro
                965                 970                 975

Cys Met Glu Val Ile Arg Tyr Ala Val Gln Val Leu Leu Asn Val Ser
            980                 985                 990

Lys Tyr Glu Lys Thr Thr Ser Ala  Val Tyr Asp Val Glu  Asn Cys
Ile
        995                 1000                1005

Asp Ile  Leu Leu Glu Leu Leu  Gln Ile Tyr Arg Glu  Lys Pro Gly
    1010                1015                1020

Asn Lys  Val Ala Asp Lys Gly  Gly Ser Ile Phe Thr  Lys Thr Cys
    1025                1030                1035

Cys Leu  Leu Ala Ile Leu Leu  Lys Thr Thr Asn Arg  Ala Ser Asp
    1040                1045                1050

Val Arg  Ser Arg Ser Lys Val  Val Asp Arg Ile Tyr  Ser Leu Tyr
    1055                1060                1065

Lys Leu  Thr Ala His Lys His  Lys Met Asn Thr Glu  Arg Ile Leu
    1070                1075                1080
```

```
Tyr Lys  Gln Lys Lys Asn Ser  Ser Ile Ser Ile Pro  Phe Ile Pro
    1085                1090                1095


Glu Thr  Pro Val Arg Thr Arg  Ile Val Ser Arg Leu  Lys Pro Asp
    1100                1105                1110


Trp Val  Leu Arg Arg Asp Asn  Met Glu Glu Ile Thr  Asn Pro Leu
    1115                1120                1125


Gln Ala  Ile Gln Met Val Met  Asp Thr Leu Gly Ile  Pro Tyr
    1130                1135                1140


<210> 932
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      abnormal spindle microtubule assembly; "

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Met Ala Asn Arg Arg Val Gly Arg Gly Cys Trp Glu Val Ser Pro Thr
1               5                  10                  15


Glu Arg Arg Pro Pro Ala Gly Leu Arg Gly Pro Ala Ala Glu Glu Glu
            20                  25                  30


Ala Ser Ser Pro Pro Val Leu Ser Leu Ser His Phe Cys Arg Ser Pro
        35                  40                  45


Phe Leu Cys Phe Gly Asp Val Leu Leu Gly Ala Ser Arg Thr Leu Ser
```

```
    50                  55                  60

Leu Ala Leu Asp Asn Pro Asn Glu Glu Val Ala Glu Val Lys Ile Ser
65                  70                  75                  80

His Phe Pro Ala Ala Asp Leu Gly Phe Ser Val Ser Gln Arg Cys Phe
                85                  90                  95

Val Leu Gln Pro Lys Glu Lys Ile Val Ile Ser Val Asn Trp Thr Pro
            100                 105                 110

Leu Lys Glu Gly Arg Val Arg Glu Ile Met Thr Phe Leu Val Asn Asp
        115                 120                 125

Val Leu Lys His Gln Ala Ile Leu Leu Gly Asn Ala Glu Glu Gln Lys
    130                 135                 140

Lys Lys Lys Arg Ser Leu Trp Asp Thr Ile Lys Lys Lys Lys Ile Ser
145                 150                 155                 160

Ala Ser Thr Ser His Asn Arg Arg Val Ser Asn Ile Gln Asn Val Asn
                165                 170                 175

Lys Thr Phe Ser Val Ser Gln Lys Val Asp Arg Val Arg Ser Pro Leu
            180                 185                 190

Gln Ala Cys Glu Asn Leu Ala Met Asn Glu Gly Gly Pro Pro Thr Glu
        195                 200                 205

Asn Asn Ser Leu Ile Leu Glu Glu Asn Lys Ile Pro Ile Ser Pro Ile
    210                 215                 220

Ser Pro Ala Phe Asn Glu Cys His Gly Ala Thr Cys Leu Pro Leu Ser
225                 230                 235                 240

Val Arg Arg Ser Thr Thr Tyr Ser Ser Leu His Ala Ser Glu Asn Arg
                245                 250                 255

Glu Leu Leu Asn Val His Ser Ala Asn Val Ser Lys Val Ser Phe Asn
            260                 265                 270

Glu Lys Ala Val Thr Glu Thr Ser Phe Asn Ser Val Asn Val Asn Gly
        275                 280                 285
```

```
Gln Arg Gly Glu Asn Ser Lys Leu Ser Leu Thr Pro Asn Cys Ser Ser
    290                 295                 300

Thr Leu Asn Ile Thr Gln Ser Gln Ile His Phe Leu Ser Pro Asp Ser
305                 310                 315                 320

Phe Val Asn Asn Ser His Gly Ala Asn Asn Glu Leu Glu Leu Val Thr
                325                 330                 335

Cys Leu Ser Ser Asp Met Phe Met Lys Asp Asn Ser Gln Pro Val His
            340                 345                 350

Leu Glu Ser Thr Ile Ala His Glu Ile Tyr Gln Lys Ile Leu Ser Pro
        355                 360                 365

Asp Ser Phe Ile Lys Asp Asn Tyr Gly Leu Asn Gln Asp Leu Glu Ser
    370                 375                 380

Glu Ser Val Asn Pro Ile Leu Ser Pro Asn Gln Phe Leu Lys Asp Asn
385                 390                 395                 400

Met Ala Tyr Met Cys Thr Ser Gln Gln Thr Cys Lys Val Pro Leu Ser
                405                 410                 415

Asn Glu Asn Ser Gln Val Pro Gln Ser Pro Glu Asp Trp Arg Lys Ser
            420                 425                 430

Glu Val Ser Pro Arg Ile Pro Glu Cys Gln Gly Ser Lys Ser Pro Lys
        435                 440                 445

Ala Ile Phe Glu Glu Leu Val Glu Met Lys Ser Asn Tyr Tyr Ser Phe
    450                 455                 460

Ile Lys Gln Asn Asn Pro Lys Phe Ser Ala Val Gln Asp Ile Ser Ser
465                 470                 475                 480

His Ser His Asn Lys Gln Pro Lys Arg Arg Pro Ile Leu Ser Ala Thr
                485                 490                 495

Val Thr Lys Arg Lys Ala Thr Cys Thr Arg Glu Asn Gln Thr Glu Ile
            500                 505                 510
```

```
Asn Lys Pro Lys Ala Lys Arg Cys Leu Asn Ser Ala Val Gly Glu His
        515                 520                 525

Glu Lys Val Ile Asn Asn Gln Lys Glu Lys Glu Asp Phe His Ser Tyr
    530                 535                 540

Leu Pro Ile Ile Asp Pro Ile Leu Ser Lys Ser Lys Ser Tyr Lys Asn
545                 550                 555                 560

Glu Val Thr Pro Ser Ser Thr Thr Ala Ser Val Ala Arg Lys Arg Lys
                565                 570                 575

Ser Asp Gly Ser Met Glu Asp Ala Asn Val Arg Val Ala Ile Thr Glu
            580                 585                 590

His Thr Glu Val Arg Glu Ile Lys Arg Ile His Phe Ser Pro Ser Glu
        595                 600                 605

Pro Lys Thr Ser Ala Val Lys Lys Thr Lys Asn Val Thr Thr Pro Ile
    610                 615                 620

Ser Lys Arg Ile Ser Asn Arg Glu Lys Leu Asn Leu Lys Lys Lys Thr
625                 630                 635                 640

Asp Leu Ser Ile Phe Arg Thr Pro Ile Ser Lys Thr Asn Lys Arg Thr
                645                 650                 655

Lys Pro Ile Ile Ala Val Ala Gln Ser Ser Leu Thr Phe Ile Lys Pro
            660                 665                 670

Leu Lys Thr Asp Ile Pro Arg His Pro Met Pro Phe Ala Ala Lys Asn
        675                 680                 685

Met Phe Tyr Asp Glu Arg Trp Lys Glu Lys Gln Glu Gln Gly Phe Thr
    690                 695                 700

Trp Trp Leu Asn Phe Ile Leu Thr Pro Asp Asp Phe Thr Val Lys Thr
705                 710                 715                 720

Asn Ile Ser Glu Val Asn Ala Ala Thr Leu Leu Leu Gly Ile Glu Asn
                725                 730                 735
```

```
Gln His Lys Ile Ser Val Pro Arg Ala Pro Thr Lys Glu Glu Met Ser
            740                 745                 750

Leu Arg Ala Tyr Thr Ala Arg Cys Arg Leu Asn Arg Leu Arg Arg Ala
        755                 760                 765

Ala Cys Arg Leu Phe Thr Ser Glu Lys Met Val Lys Ala Ile Lys Lys
    770                 775                 780

Leu Glu Ile Glu Ile Glu Ala Arg Arg Leu Ile Val Arg Lys Asp Arg
785                 790                 795                 800

His Leu Trp Lys Asp Val Gly Glu Arg Gln Lys Val Leu Asn Trp Leu
                805                 810                 815

Leu Ser Tyr Asn Pro Leu Trp Leu Arg Ile Gly Leu Glu Thr Thr Tyr
            820                 825                 830

Gly Glu Leu Ile Ser Leu Glu Asp Asn Ser Asp Val Thr Gly Leu Ala
        835                 840                 845

Met Phe Ile Leu Asn Arg Leu Leu Trp Asn Pro Asp Ile Ala Ala Glu
    850                 855                 860

Tyr Arg His Pro Thr Val Pro His Leu Tyr Arg Asp Gly His Glu Glu
865                 870                 875                 880

Ala Leu Ser Lys Phe Thr Leu Lys Lys Leu Leu Leu Leu Val Cys Phe
                885                 890                 895

Leu Asp Tyr Ala Lys Ile Ser Arg Leu Ile Asp His Asp Pro Cys Leu
            900                 905                 910

Phe Cys Lys Asp Ala Glu Phe Lys Ala Ser Lys Glu Ile Leu Leu Ala
        915                 920                 925

Phe Ser Arg Asp Phe Leu Ser Gly Glu Gly Asp Leu Ser Arg His Leu
    930                 935                 940

Gly Leu Leu Gly Leu Pro Val Asn His Val Gln Thr Pro Phe Asp Glu
945                 950                 955                 960

Phe Asp Phe Ala Val Thr Asn Leu Ala Val Asp Leu Gln Cys Gly Val
```

965 970 975

Arg Leu Val Arg Thr Met Glu Leu Leu Thr Gln Asn Trp Asp Leu Ser
980 985 990

Lys Lys Leu Arg Ile Pro Ala Ile Ser Arg Leu Gln Lys Met His Asn
995 1000 1005

Val Asp Ile Val Leu Gln Val Leu Lys Ser Arg Gly Ile Glu Leu
1010 1015 1020

Ser Asp Glu His Gly Asn Thr Ile Leu Ser Lys Asp Ile Val Asp
1025 1030 1035

Arg His Arg Glu Lys Thr Leu Arg Leu Leu Trp Lys Ile Ala Phe
1040 1045 1050

Ala Phe Gln Val Asp Ile Ser Leu Asn Leu Asp Gln Leu Lys Glu
1055 1060 1065

Glu Ile Ala Phe Leu Lys His Thr Lys Ser Ile Lys Lys Thr Ile
1070 1075 1080

Ser Leu Leu Ser Cys His Ser Asp Asp Leu Ile Asn Lys Lys Lys
1085 1090 1095

Gly Lys Arg Asp Ser Gly Ser Phe Glu Gln Tyr Ser Glu Asn Ile
1100 1105 1110

Lys Leu Leu Met Asp Trp Val Asn Ala Val Cys Ala Phe Tyr Asn
1115 1120 1125

Lys Lys Val Glu Asn Phe Thr Val Ser Phe Ser Asp Gly Arg Val
1130 1135 1140

Leu Cys Tyr Leu Ile His His Tyr His Pro Cys Tyr Val Pro Phe
1145 1150 1155

Asp Ala Ile Cys Gln Arg Thr Thr Gln Thr Val Glu Cys Thr Gln
1160 1165 1170

Thr Gly Ser Val Val Leu Asn Ser Ser Ser Glu Ser Asp Asp Ser

1175 1180 1185

Ser Leu Asp Met Ser Leu Lys Ala Phe Asp His Glu Asn Thr Ser
1190 1195 1200

Glu Leu Tyr Lys Glu Leu Leu Glu Asn Glu Lys Lys Asn Phe His
1205 1210 1215

Leu Val Arg Ser Ala Val Arg Asp Leu Gly Gly Ile Pro Ala Met
1220 1225 1230

Ile Asn His Ser Asp Met Ser Asn Thr Ile Pro Asp Glu Lys Val
1235 1240 1245

Val Ile Thr Tyr Leu Ser Phe Leu Cys Ala Arg Leu Leu Asp Leu
1250 1255 1260

Arg Lys Glu Ile Arg Ala Ala Arg Leu Ile Gln Thr Thr Trp Arg
1265 1270 1275

Lys Tyr Lys Leu Lys Thr Asp Leu Lys Arg His Gln Glu Arg Glu
1280 1285 1290

Lys Ala Ala Arg Ile Ile Gln Leu Ala Val Ile Asn Phe Leu Ala
1295 1300 1305

Lys Gln Arg Leu Arg Lys Arg Val Asn Ala Ala Leu Val Ile Gln
1310 1315 1320

Lys Tyr Trp Arg Arg Val Leu Ala Gln Arg Lys Leu Leu Met Leu
1325 1330 1335

Lys Lys Glu Lys Leu Glu Lys Val Gln Asn Lys Ala Ala Ser Leu
1340 1345 1350

Ile Gln Gly Tyr Trp Arg Arg Tyr Ser Thr Arg Gln Arg Phe Leu
1355 1360 1365

Lys Leu Lys Tyr Tyr Ser Ile Ile Leu Gln Ser Arg Ile Arg Met
1370 1375 1380

Ile Ile Ala Val Thr Ser Tyr Lys Arg Tyr Leu Trp Ala Thr Val
1385 1390 1395

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Thr Ile  Gln Arg His Trp Arg  Ala Tyr Leu Arg Arg  Lys Gln Asp
    1400                1405                1410

Gln Gln  Arg Tyr Glu Met Leu  Lys Ser Ser Thr Leu  Ile Ile Gln
    1415                1420                1425

Ser Met  Phe Arg Lys Trp Lys  Gln Arg Lys Met Gln  Ser Gln Val
    1430                1435                1440

Lys Ala  Thr Val Ile Leu Gln  Arg Ala Phe Arg Glu  Trp His Leu
    1445                1450                1455

Arg Lys  Gln Ala Lys Glu Glu  Asn Ser Ala Ile Ile  Ile Gln Ser
    1460                1465                1470

Trp Tyr  Arg Met His Lys Glu  Leu Arg Lys Tyr Ile  Tyr Ile Arg
    1475                1480                1485

Ser Cys  Val Val Ile Ile Gln  Lys Arg Phe Arg Cys  Phe Gln Ala
    1490                1495                1500

Gln Lys  Leu Tyr Lys Arg Arg  Lys Glu Ser Ile Leu  Thr Ile Gln
    1505                1510                1515

Lys Tyr  Tyr Lys Ala Tyr Leu  Lys Gly Lys Ile Glu  Arg Thr Asn
    1520                1525                1530

Tyr Leu  Gln Lys Arg Ala Ala  Ala Ile Gln Leu Gln  Ala Ala Phe
    1535                1540                1545

Arg Arg  Leu Lys Ala His Asn  Leu Cys Arg Gln Ile  Arg Ala Ala
    1550                1555                1560

Cys Val  Ile Gln Ser Tyr Trp  Arg Met Arg Gln Asp  Arg Val Arg
    1565                1570                1575

Phe Leu  Asn Leu Lys Lys Thr  Ile Ile Lys Phe Gln  Ala His Val
    1580                1585                1590

Arg Lys  His Gln Gln Arg Gln  Lys Tyr Lys Lys Met  Lys Lys Ala
    1595                1600                1605
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Ala Val  Ile Ile Gln Thr His  Phe Arg Ala Tyr Ile  Phe Ala Met
    1610                1615                1620

Lys Val  Leu Ala Ser Tyr Gln  Lys Thr Arg Ser Ala  Val Ile Val
    1625                1630                1635

Leu Gln  Ser Ala Tyr Arg Gly  Met Gln Ala Arg Lys  Met Tyr Ile
    1640                1645                1650

His Ile  Leu Thr Ser Val Ile  Lys Ile Gln Ser Tyr  Tyr Arg Ala
    1655                1660                1665

Tyr Val  Ser Lys Lys Glu Phe  Leu Ser Leu Lys Asn  Ala Thr Ile
    1670                1675                1680

Lys Leu  Gln Ser Thr Val Lys  Met Lys Gln Thr Arg  Lys Gln Tyr
    1685                1690                1695

Leu His  Leu Arg Ala Ala Ala  Leu Phe Ile Gln Gln  Cys Tyr Arg
    1700                1705                1710

Ser Lys  Lys Ile Ala Ala Gln  Lys Arg Glu Glu Tyr  Met Gln Met
    1715                1720                1725

Arg Glu  Ser Cys Ile Lys Leu  Gln Ala Phe Val Arg  Gly Tyr Leu
    1730                1735                1740

Val Arg  Lys Gln Met Arg Leu  Gln Arg Lys Ala Val  Ile Ser Leu
    1745                1750                1755

Gln Ser  Tyr Phe Arg Met Arg  Lys Ala Arg Gln Tyr  Tyr Leu Lys
    1760                1765                1770

Met Tyr  Lys Ala Ile Ile Val  Ile Gln Asn Tyr Tyr  His Ala Tyr
    1775                1780                1785

Lys Ala  Gln Val Asn Gln Arg  Lys Asn Phe Leu Gln  Val Lys Lys
    1790                1795                1800

Ala Ala  Thr Cys Leu Gln Ala  Ala Tyr Arg Gly Tyr  Lys Val Arg
    1805                1810                1815
```

Gln Leu Ile Lys Gln Gln Ser Ile Ala Ala Leu Lys Ile Gln Ser
1820 1825 1830

Ala Phe Arg Gly Tyr Asn Lys Arg Val Lys Tyr Gln Ser Val Leu
1835 1840 1845

Gln Ser Ile Ile Lys Ile Gln Arg Trp Tyr Arg Ala Tyr Lys Thr
1850 1855 1860

Leu His Asp Thr Arg Thr His Phe Leu Lys Thr Lys Ala Ala Val
1865 1870 1875

Ile Ser Leu Gln Ser Ala Tyr Arg Gly Trp Lys Val Arg Lys Gln
1880 1885 1890

Ile Arg Arg Glu His Gln Ala Ala Leu Lys Ile Gln Ser Ala Phe
1895 1900 1905

Arg Met Ala Lys Ala Gln Lys Gln Phe Arg Leu Phe Lys Thr Ala
1910 1915 1920

Ala Leu Val Ile Gln Gln Asn Phe Arg Ala Trp Thr Ala Gly Arg
1925 1930 1935

Lys Gln Cys Met Glu Tyr Ile Glu Leu Arg His Ala Val Leu Val
1940 1945 1950

Leu Gln Ser Met Trp Lys Gly Lys Thr Leu Arg Arg Gln Leu Gln
1955 1960 1965

Arg Gln His Lys Cys Ala Ile Ile Ile Gln Ser Tyr Tyr Arg Met
1970 1975 1980

His Val Gln Gln Lys Lys Trp Lys Ile Met Lys Lys Ala Ala Leu
1985 1990 1995

Leu Ile Gln Lys Tyr Tyr Arg Ala Tyr Ser Ile Gly Arg Glu Gln
2000 2005 2010

Asn His Leu Tyr Leu Lys Thr Lys Ala Ala Val Val Thr Leu Gln
2015 2020 2025

Ser Ala Tyr Arg Gly Met Lys Val Arg Lys Arg Ile Lys Asp Cys

2030 2035 2040

Asn Lys Ala Ala Val Thr Ile Gln Ser Lys Tyr Arg Ala Tyr Lys
2045 2050 2055

Thr Lys Lys Lys Tyr Ala Thr Tyr Arg Ala Ser Ala Ile Ile Ile
2060 2065 2070

Gln Arg Trp Tyr Arg Gly Ile Lys Ile Thr Asn His Gln His Lys
2075 2080 2085

Glu Tyr Leu Asn Leu Lys Lys Thr Ala Ile Lys Ile Gln Ser Val
2090 2095 2100

Tyr Arg Gly Ile Arg Val Arg Arg His Ile Gln His Met His Arg
2105 2110 2115

Ala Ala Thr Phe Ile Lys Ala Met Phe Lys Met His Gln Ser Arg
2120 2125 2130

Ile Ser Tyr His Thr Met Arg Lys Ala Ala Ile Val Ile Gln Val
2135 2140 2145

Arg Cys Arg Ala Tyr Tyr Gln Gly Lys Met Gln Arg Glu Lys Tyr
2150 2155 2160

Leu Thr Ile Leu Lys Ala Val Lys Val Leu Gln Ala Ser Phe Arg
2165 2170 2175

Gly Val Arg Val Arg Arg Thr Leu Arg Lys Met Gln Thr Ala Ala
2180 2185 2190

Thr Leu Ile Gln Ser Asn Tyr Arg Arg Tyr Arg Gln Gln Thr Tyr
2195 2200 2205

Phe Asn Lys Leu Lys Lys Ile Thr Lys Thr Val Gln Gln Arg Tyr
2210 2215 2220

Trp Ala Met Lys Glu Arg Asn Ile Gln Phe Gln Arg Tyr Asn Lys
2225 2230 2235

Leu Arg His Ser Val Ile Tyr Ile Gln Ala Ile Phe Arg Gly Lys
2240 2245 2250

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Lys Ala  Arg Arg His Leu Lys  Met Met His Ile Ala  Ala Thr Leu
    2255                 2260                 2265

Ile Gln  Arg Arg Phe Arg Thr  Leu Met Met Arg Arg  Arg Phe Leu
    2270                 2275                 2280

Ser Leu  Lys Lys Thr Ala Ile  Leu Ile Gln Arg Lys  Tyr Arg Ala
    2285                 2290                 2295

His Leu  Cys Thr Lys His His  Leu Gln Phe Leu Gln  Val Gln Asn
    2300                 2305                 2310

Ala Val  Ile Lys Ile Gln Ser  Ser Tyr Arg Arg Trp  Met Ile Arg
    2315                 2320                 2325

Lys Arg  Met Arg Glu Met His  Arg Ala Ala Thr Phe  Ile Gln Ser
    2330                 2335                 2340

Thr Phe  Arg Met His Arg Leu  His Met Arg Tyr Gln  Ala Leu Lys
    2345                 2350                 2355

Gln Ala  Ser Val Val Ile Gln  Gln Gln Tyr Gln Ala  Asn Arg Ala
    2360                 2365                 2370

Ala Lys  Leu Gln Arg Gln His  Tyr Leu Arg Gln Arg  His Ser Ala
    2375                 2380                 2385

Val Ile  Leu Gln Ala Ala Phe  Arg Gly Met Lys Thr  Arg Arg His
    2390                 2395                 2400

Leu Lys  Ser Met His Ser Ser  Ala Thr Leu Ile Gln  Ser Arg Phe
    2405                 2410                 2415

Arg Ser  Leu Leu Val Arg Arg  Arg Phe Ile Ser Leu  Lys Lys Ala
    2420                 2425                 2430

Thr Ile  Phe Val Gln Arg Lys  Tyr Arg Ala Thr Ile  Cys Ala Lys
    2435                 2440                 2445

His Lys  Leu Tyr Gln Phe Leu  His Leu Arg Lys Ala  Ala Ile Thr
    2450                 2455                 2460
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Ile Gln  Ser Ser Tyr Arg Arg  Leu Met Val Lys Lys  Lys Leu Gln
    2465                2470                2475

Glu Met  Gln Arg Ala Ala Val  Leu Ile Gln Ala Thr  Phe Arg Met
    2480                2485                2490

Tyr Arg  Thr Tyr Ile Thr Phe  Gln Thr Trp Lys His  Ala Ser Ile
    2495                2500                2505

Leu Ile  Gln Gln His Tyr Arg  Thr Tyr Arg Ala Ala  Lys Leu Gln
    2510                2515                2520

Arg Glu  Asn Tyr Ile Arg Gln  Trp His Ser Ala Val  Val Ile Gln
    2525                2530                2535

Ala Ala  Tyr Lys Gly Met Lys  Ala Arg Gln Leu Leu  Arg Glu Lys
    2540                2545                2550

His Lys  Ala Ser Ile Val Ile  Gln Ser Thr Tyr Arg  Met Tyr Arg
    2555                2560                2565

Gln Tyr  Cys Phe Tyr Gln Lys  Leu Gln Trp Ala Thr  Lys Ile Ile
    2570                2575                2580

Gln Glu  Lys Tyr Arg Ala Asn  Lys Lys Lys Gln Lys  Val Phe Gln
    2585                2590                2595

His Asn  Glu Leu Lys Lys Glu  Thr Cys Val Gln Ala  Gly Phe Gln
    2600                2605                2610

Asp Met  Asn Ile Lys Lys Gln  Ile Gln Glu Gln His  Gln Ala Ala
    2615                2620                2625

Ile Ile  Ile Gln Lys His Cys  Lys Ala Phe Lys Ile  Arg Lys His
    2630                2635                2640

Tyr Leu  His Leu Arg Ala Thr  Val Val Ser Ile Gln  Arg Arg Tyr
    2645                2650                2655

Arg Lys  Leu Thr Ala Val Arg  Thr Gln Ala Val Ile  Cys Ile Gln
    2660                2665                2670
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Ser Tyr  Tyr Arg Gly Phe Lys  Val Arg Lys Asp Ile  Gln Asn Met
    2675                2680                2685

His Arg  Ala Ala Thr Leu Ile  Gln Ser Phe Tyr Arg  Met His Arg
    2690                2695                2700

Ala Lys  Val Asp Tyr Glu Thr  Lys Lys Thr Ala Ile  Val Val Ile
    2705                2710                2715

Gln Asn  Tyr Tyr Arg Leu Tyr  Val Arg Val Lys Thr  Glu Arg Lys
    2720                2725                2730

Asn Phe  Leu Ala Val Gln Lys  Ser Val Arg Thr Ile  Gln Ala Ala
    2735                2740                2745

Phe Arg  Gly Met Lys Val Arg  Gln Lys Leu Lys Asn  Val Ser Glu
    2750                2755                2760

Glu Lys  Met Ala Ala Ile Val  Asn Gln Ser Ala Leu  Cys Cys Tyr
    2765                2770                2775

Arg Ser  Lys Thr Gln Tyr Glu  Ala Val Gln Ser Glu  Gly Val Met
    2780                2785                2790

Ile Gln  Glu Trp Tyr Lys Ala  Ser Gly Leu Ala Cys  Ser Gln Glu
    2795                2800                2805

Ala Glu  Tyr His Ser Gln Ser  Arg Ala Ala Val Thr  Ile Gln Lys
    2810                2815                2820

Ala Phe  Cys Arg Met Val Thr  Arg Lys Leu Glu Thr  Gln Lys Cys
    2825                2830                2835

Ala Ala  Leu Arg Ile Gln Phe  Phe Leu Gln Met Ala  Val Tyr Arg
    2840                2845                2850

Arg Arg  Phe Val Gln Gln Lys  Arg Ala Ala Ile Thr  Leu Gln His
    2855                2860                2865

Tyr Phe  Arg Thr Trp Gln Thr  Arg Lys Gln Phe Leu  Leu Tyr Arg
    2870                2875                2880

Lys Ala  Ala Val Val Leu Gln  Asn His Tyr Arg Ala  Phe Leu Ser
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2885 2890 2895

Ala Lys His Gln Arg Gln Val Tyr Leu Gln Ile Arg Ser Ser Val
2900 2905 2910

Ile Ile Ile Gln Ala Arg Ser Lys Gly Phe Ile Gln Lys Arg Lys
2915 2920 2925

Phe Gln Glu Ile Lys Asn Ser Thr Ile Lys Ile Gln Ala Met Trp
2930 2935 2940

Arg Arg Tyr Arg Ala Lys Lys Tyr Leu Cys Lys Val Lys Ala Ala
2945 2950 2955

Cys Lys Ile Gln Ala Trp Tyr Arg Cys Trp Arg Ala His Lys Glu
2960 2965 2970

Tyr Leu Ala Ile Leu Lys Ala Val Lys Ile Ile Gln Gly Cys Phe
2975 2980 2985

Tyr Thr Lys Leu Glu Arg Thr Arg Phe Leu Asn Val Arg Ala Ser
2990 2995 3000

Ala Ile Ile Ile Gln Arg Lys Trp Arg Ala Ile Leu Pro Ala Lys
3005 3010 3015

Ile Ala His Glu His Phe Leu Met Ile Lys Arg His Arg Ala Ala
3020 3025 3030

Cys Leu Ile Gln Ala His Tyr Arg Gly Tyr Lys Gly Arg Gln Val
3035 3040 3045

Phe Leu Arg Gln Lys Ser Ala Ala Leu Ile Ile Gln Lys Tyr Ile
3050 3055 3060

Arg Ala Arg Glu Ala Gly Lys His Glu Arg Ile Lys Tyr Ile Glu
3065 3070 3075

Phe Lys Lys Ser Thr Val Ile Leu Gln Ala Leu Val Arg Gly Trp
3080 3085 3090

Leu Val Arg Lys Arg Phe Leu Glu Gln Arg Ala Lys Ile Arg Leu
3095 3100 3105

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Leu His  Phe Thr Ala Ala Ala  Tyr Tyr His Leu Asn  Ala Val Arg
    3110                 3115                 3120

Ile Gln  Arg Ala Tyr Lys Leu  Tyr Leu Ala Val Lys  Asn Ala Asn
    3125                 3130                 3135

Lys Gln  Val Asn Ser Val Ile  Cys Ile Gln Arg Trp  Phe Arg Ala
    3140                 3145                 3150

Arg Leu  Gln Glu Lys Arg Phe  Ile Gln Lys Tyr His  Ser Ile Lys
    3155                 3160                 3165

Lys Ile  Glu His Glu Gly Gln  Glu Cys Leu Ser Gln  Arg Asn Arg
    3170                 3175                 3180

Ala Ala  Ser Val Ile Gln Lys  Ala Val Arg His Phe  Leu Leu Arg
    3185                 3190                 3195

Lys Lys  Gln Glu Lys Phe Thr  Ser Gly Ile Ile Lys  Ile Gln Ala
    3200                 3205                 3210

Leu Trp  Arg Gly Tyr Ser Trp  Arg Lys Lys Asn Asp  Cys Thr Lys
    3215                 3220                 3225

Ile Lys  Ala Ile Arg Leu Ser  Leu Gln Val Val Asn  Arg Glu Ile
    3230                 3235                 3240

Arg Glu  Glu Asn Lys Leu Tyr  Lys Arg Thr Ala Leu  Ala Leu His
    3245                 3250                 3255

Tyr Leu  Leu Thr Tyr Lys His  Leu Ser Ala Ile Leu  Glu Ala Leu
    3260                 3265                 3270

Lys His  Leu Glu Val Val Thr  Arg Leu Ser Pro Leu  Cys Cys Glu
    3275                 3280                 3285

Asn Met  Ala Gln Ser Gly Ala  Ile Ser Lys Ile Phe  Val Leu Ile
    3290                 3295                 3300

Arg Ser  Cys Asn Arg Ser Ile  Pro Cys Met Glu Val  Ile Arg Tyr
    3305                 3310                 3315
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Ala Val  Gln Val Leu Leu Asn  Val Ser Lys Tyr Glu  Lys Thr Thr
    3320                3325                3330

Ser Ala  Val Tyr Asp Val Glu  Asn Cys Ile Asp Ile  Leu Leu Glu
    3335                3340                3345

Leu Leu  Gln Ile Tyr Arg Glu  Lys Pro Gly Asn Lys  Val Ala Asp
    3350                3355                3360

Lys Gly  Gly Ser Ile Phe Thr  Lys Thr Cys Cys Leu  Leu Ala Ile
    3365                3370                3375

Leu Leu  Lys Thr Thr Asn Arg  Ala Ser Asp Val Arg  Ser Arg Ser
    3380                3385                3390

Lys Val  Val Asp Arg Ile Tyr  Ser Leu Tyr Lys Leu  Thr Ala His
    3395                3400                3405

Lys His  Lys Met Asn Thr Glu  Arg Ile Leu Tyr Lys  Gln Lys Lys
    3410                3415                3420

Asn Ser  Ser Ile Ser Ile Pro  Phe Ile Pro Glu Thr  Pro Val Arg
    3425                3430                3435

Thr Arg  Ile Val Ser Arg Leu  Lys Pro Asp Trp Val  Leu Arg Arg
    3440                3445                3450

Asp Asn  Met Glu Glu Ile Thr  Asn Pro Leu Gln Ala  Ile Gln Met
    3455                3460                3465

Val Met  Asp Thr Leu Gly Ile  Pro Tyr
    3470                3475
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Ala Ser Ser Pro Pro Val Leu Ser Leu Ser His Phe Cys Arg Ser Pro
35 40 45

Phe Leu Cys Phe Gly Asp Val Leu Leu Gly Ala Ser Arg Thr Leu Ser
50 55 60

Leu Ala Leu Asp Asn Pro Asn Glu Glu Val Ala Glu Val Lys Ile Ser
65 70 75 80

His Phe Pro Ala Ala Asp Leu Gly Phe Ser Val Ser Gln Arg Cys Phe
85 90 95

Val Leu Gln Pro Lys Glu Lys Ile Val Ile Ser Val Asn Trp Thr Pro
100 105 110

Leu Lys Glu Gly Arg Val Arg Glu Ile Met Thr Phe Leu Val Asn Asp
115 120 125

Val Leu Lys His Gln Ala Ile Leu Leu Gly Asn Ala Glu Glu Gln Lys
130 135 140

Lys Lys Lys Arg Ser Leu Trp Asp Thr Ile Lys Lys Lys Lys Ile Ser
145 150 155 160

Ala Ser Thr Ser His Asn Arg Arg Val Ser Asn Ile Gln Asn Val Asn
165 170 175

Lys Thr Phe Ser Val Ser Gln Lys Val Asp Arg Arg Tyr Arg Gln Gln
180 185 190

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Thr Tyr Phe Asn Lys Leu Lys Lys Ile Thr Lys Thr Val Gln Gln Arg
        195                 200                 205

Tyr Trp Ala Met Lys Glu Arg Asn Ile Gln Phe Gln Arg Tyr Asn Lys
    210                 215                 220

Leu Arg His Ser Val Ile Tyr Ile Gln Ala Ile Phe Arg Gly Lys Lys
225                 230                 235                 240

Ala Arg Arg His Leu Lys Met Met His Ile Ala Ala Thr Leu Ile Gln
                245                 250                 255

Arg Arg Phe Arg Thr Leu Met Met Arg Arg Arg Phe Leu Ser Leu Lys
            260                 265                 270

Lys Thr Ala Ile Leu Ile Gln Arg Lys Tyr Arg Ala His Leu Cys Thr
        275                 280                 285

Lys His His Leu Gln Phe Leu Gln Val Gln Asn Ala Val Ile Lys Ile
    290                 295                 300

Gln Ser Ser Tyr Arg Arg Trp Met Ile Arg Lys Arg Met Arg Glu Met
305                 310                 315                 320

His Arg Ala Ala Thr Phe Ile Gln Ser Thr Phe Arg Met His Arg Leu
                325                 330                 335

His Met Arg Tyr Gln Ala Leu Lys Gln Ala Ser Val Val Ile Gln Gln
            340                 345                 350

Gln Tyr Gln Ala Asn Arg Ala Ala Lys Leu Gln Arg Gln His Tyr Leu
        355                 360                 365

Arg Gln Arg His Ser Ala Val Ile Leu Gln Ala Ala Phe Arg Gly Met
    370                 375                 380

Lys Thr Arg Arg His Leu Lys Ser Met His Ser Ser Ala Thr Leu Ile
385                 390                 395                 400

Gln Ser Arg Phe Arg Ser Leu Leu Val Arg Arg Arg Phe Ile Ser Leu
                405                 410                 415
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Lys Lys Ala Thr Ile Phe Val Gln Arg Lys Tyr Arg Ala Thr Ile Cys
            420                 425                 430

Ala Lys His Lys Leu Tyr Gln Phe Leu His Leu Arg Lys Ala Ala Ile
        435                 440                 445

Thr Ile Gln Ser Ser Tyr Arg Arg Leu Met Val Lys Lys Lys Leu Gln
    450                 455                 460

Glu Met Gln Arg Ala Ala Val Leu Ile Gln Ala Thr Phe Arg Met Tyr
465                 470                 475                 480

Arg Thr Tyr Ile Thr Phe Gln Thr Trp Lys His Ala Ser Ile Leu Ile
                485                 490                 495

Gln Gln His Tyr Arg Thr Tyr Arg Ala Ala Lys Leu Gln Arg Glu Asn
            500                 505                 510

Tyr Ile Arg Gln Trp His Ser Ala Val Val Ile Gln Ala Ala Tyr Lys
        515                 520                 525

Gly Met Lys Ala Arg Gln Leu Leu Arg Glu Lys His Lys Ala Ser Ile
    530                 535                 540

Val Ile Gln Ser Thr Tyr Arg Met Tyr Arg Gln Tyr Cys Phe Tyr Gln
545                 550                 555                 560

Lys Leu Gln Trp Ala Thr Lys Ile Ile Gln Glu Lys Tyr Arg Ala Asn
                565                 570                 575

Lys Lys Lys Gln Lys Val Phe Gln His Asn Glu Leu Lys Lys Glu Thr
            580                 585                 590

Cys Val Gln Ala Gly Phe Gln Asp Met Asn Ile Lys Lys Gln Ile Gln
        595                 600                 605

Glu Gln His Gln Ala Ala Ile Ile Ile Gln Lys His Cys Lys Ala Phe
    610                 615                 620

Lys Ile Arg Lys His Tyr Leu His Leu Arg Ala Thr Val Val Ser Ile
625                 630                 635                 640
```

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Gln Arg Arg Tyr Arg Lys Leu Thr Ala Val Arg Thr Gln Ala Val Ile
                645                 650                 655

Cys Ile Gln Ser Tyr Tyr Arg Gly Phe Lys Val Arg Lys Asp Ile Gln
            660                 665                 670

Asn Met His Arg Ala Ala Thr Leu Ile Gln Ser Phe Tyr Arg Met His
        675                 680                 685

Arg Ala Lys Val Asp Tyr Glu Thr Lys Lys Thr Ala Ile Val Val Ile
    690                 695                 700

Gln Asn Tyr Tyr Arg Leu Tyr Val Arg Val Lys Thr Glu Arg Lys Asn
705                 710                 715                 720

Phe Leu Ala Val Gln Lys Ser Val Arg Thr Ile Gln Ala Ala Phe Arg
                725                 730                 735

Gly Met Lys Val Arg Gln Lys Leu Lys Asn Val Ser Glu Glu Lys Met
            740                 745                 750

Ala Ala Ile Val Asn Gln Ser Ala Leu Cys Cys Tyr Arg Ser Lys Thr
        755                 760                 765

Gln Tyr Glu Ala Val Gln Ser Glu Gly Val Met Ile Gln Glu Trp Tyr
    770                 775                 780

Lys Ala Ser Gly Leu Ala Cys Ser Gln Glu Ala Glu Tyr His Ser Gln
785                 790                 795                 800

Ser Arg Ala Ala Val Thr Ile Gln Lys Ala Phe Cys Arg Met Val Thr
                805                 810                 815

Arg Lys Leu Glu Thr Gln Lys Cys Ala Ala Leu Arg Ile Gln Phe Phe
            820                 825                 830

Leu Gln Met Ala Val Tyr Arg Arg Arg Phe Val Gln Gln Lys Arg Ala
        835                 840                 845

Ala Ile Thr Leu Gln His Tyr Phe Arg Thr Trp Gln Thr Arg Lys Gln
    850                 855                 860

Phe Leu Leu Tyr Arg Lys Ala Ala Val Val Leu Gln Asn His Tyr Arg
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865 870 875 880

Ala Phe Leu Ser Ala Lys His Gln Arg Gln Val Tyr Leu Gln Ile Arg
885 890 895

Ser Ser Val Ile Ile Ile Gln Ala Arg Ser Lys Gly Phe Ile Gln Lys
900 905 910

Arg Lys Phe Gln Glu Ile Lys Asn Ser Thr Ile Lys Ile Gln Ala Met
915 920 925

Trp Arg Arg Tyr Arg Ala Lys Lys Tyr Leu Cys Lys Val Lys Ala Ala
930 935 940

Cys Lys Ile Gln Ala Trp Tyr Arg Cys Trp Arg Ala His Lys Glu Tyr
945 950 955 960

Leu Ala Ile Leu Lys Ala Val Lys Ile Ile Gln Gly Cys Phe Tyr Thr
965 970 975

Lys Leu Glu Arg Thr Arg Phe Leu Asn Val Arg Ala Ser Ala Ile Ile
980 985 990

Ile Gln Arg Lys Trp Arg Ala Ile Leu Pro Ala Lys Ile Ala His
Glu
995 1000 1005

His Phe Leu Met Ile Lys Arg His Arg Ala Ala Cys Leu Ile Gln
1010 1015 1020

Ala His Tyr Arg Gly Tyr Lys Gly Arg Gln Val Phe Leu Arg Gln
1025 1030 1035

Lys Ser Ala Ala Leu Ile Ile Gln Lys Tyr Ile Arg Ala Arg Glu
1040 1045 1050

Ala Gly Lys His Glu Arg Ile Lys Tyr Ile Glu Phe Lys Lys Ser
1055 1060 1065

Thr Val Ile Leu Gln Ala Leu Val Arg Gly Trp Leu Val Arg Lys
1070 1075 1080

Arg Phe Leu Glu Gln Arg Ala Lys Ile Arg Leu Leu His Phe Thr

1085 1090 1095

Ala Ala Ala Tyr Tyr His Leu Asn Ala Val Arg Ile Gln Arg Ala
1100 1105 1110

Tyr Lys Leu Tyr Leu Ala Val Lys Asn Ala Asn Lys Gln Val Asn
1115 1120 1125

Ser Val Ile Cys Ile Gln Arg Trp Phe Arg Ala Arg Leu Gln Glu
1130 1135 1140

Lys Arg Phe Ile Gln Lys Tyr His Ser Ile Lys Lys Ile Glu His
1145 1150 1155

Glu Gly Gln Glu Cys Leu Ser Gln Arg Asn Arg Ala Ala Ser Val
1160 1165 1170

Ile Gln Lys Ala Val Arg His Phe Leu Leu Arg Lys Lys Gln Glu
1175 1180 1185

Lys Phe Thr Ser Gly Ile Ile Lys Ile Gln Ala Leu Trp Arg Gly
1190 1195 1200

Tyr Ser Trp Arg Lys Lys Asn Asp Cys Thr Lys Ile Lys Ala Ile
1205 1210 1215

Arg Leu Ser Leu Gln Val Val Asn Arg Glu Ile Arg Glu Glu Asn
1220 1225 1230

Lys Leu Tyr Lys Arg Thr Ala Leu Ala Leu His Tyr Leu Leu Thr
1235 1240 1245

Tyr Lys His Leu Ser Ala Ile Leu Glu Ala Leu Lys His Leu Glu
1250 1255 1260

Val Val Thr Arg Leu Ser Pro Leu Cys Cys Glu Asn Met Ala Gln
1265 1270 1275

Ser Gly Ala Ile Ser Lys Ile Phe Val Leu Ile Arg Ser Cys Asn
1280 1285 1290

Arg Ser Ile Pro Cys Met Glu Val Ile Arg Tyr Ala Val Gln Val
1295 1300 1305

```
Leu Leu  Asn Val Ser Lys Tyr  Glu Lys Thr Thr Ser  Ala Val Tyr
    1310                1315                1320

Asp Val  Glu Asn Cys Ile Asp  Ile Leu Leu Glu Leu  Leu Gln Ile
    1325                1330                1335

Tyr Arg  Glu Lys Pro Gly Asn  Lys Val Ala Asp Lys  Gly Gly Ser
    1340                1345                1350

Ile Phe  Thr Lys Thr Cys Cys  Leu Leu Ala Ile Leu  Leu Lys Thr
    1355                1360                1365

Thr Asn  Arg Ala Ser Val Ser  Ile Ser Gln Leu Pro  Phe Phe Lys
    1370                1375                1380

Ile Ile  Phe Leu Trp Ser
    1385
```

<210> 934
<211> 373
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 154; "

<220>
<221> source
<223> /note="Gene Symbol: ABO; "

<220>
<221> source
<223> /note="Gene Name:
ABO blood group (transferase A, alpha
1-3-N-acetylgalactosaminyltransferase; "

<220>
<221> source
<223> /note="transferase B,
alpha 1-3-galactosyltransferase); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483018"

<400> 934

```
Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala
1               5                  10                  15
```

```
Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe
            20                  25                  30

Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu
        35                  40                  45

Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val
    50                  55                  60

Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys
65                  70                  75                  80

Arg Lys Asp Val Leu Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu
                85                  90                  95

Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn
            100                 105                 110

Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe
        115                 120                 125

Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His
    130                 135                 140

Arg Val His Tyr Tyr Val Phe Thr Asp Gln Pro Ala Ala Val Pro Arg
145                 150                 155                 160

Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala
                165                 170                 175

Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser
            180                 185                 190

Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val Cys
        195                 200                 205

Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu
    210                 215                 220

Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg
225                 230                 235                 240
```

```
Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro
                245                 250                 255

Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser
            260                 265                 270

Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met
        275                 280                 285

Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His
    290                 295                 300

Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro
305                 310                 315                 320

Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg
                325                 330                 335

Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Arg
            340                 345                 350

Glu Arg Leu Pro Gly Ala Leu Gly Gly Leu Pro Ala Ala Pro Ser Pro
        355                 360                 365

Ser Arg Pro Trp Phe
    370


<210> 935
<211> 353
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 154; "

<220>
<221> source
<223> /note="Gene Symbol: ABO; "

<220>
<221> source
<223> /note="Gene Name:
      ABO blood group (transferase A, alpha
      1-3-N-acetylgalactosaminyltransferase; "

<220>
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<221> source
<223> /note="transferase B,
alpha 1-3-galactosyltransferase); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483265"

<400> 935

```
Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala
1               5                  10                  15

Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe
            20                  25                  30

Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu
        35                  40                  45

Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val
    50                  55                  60

Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys
65                  70                  75                  80

Arg Lys Asp Val Leu Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu
                85                  90                  95

Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn
            100                 105                 110

Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe
        115                 120                 125

Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His
    130                 135                 140

Arg Val His Tyr Tyr Val Phe Thr Asp Gln Pro Ala Ala Val Pro Arg
145                 150                 155                 160

Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala
                165                 170                 175

Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser
            180                 185                 190
```

```
Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val Cys
        195                 200                 205

Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu
    210                 215                 220

Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg
225                 230                 235                 240

Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro
                245                 250                 255

Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser
            260                 265                 270

Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met
        275                 280                 285

Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His
    290                 295                 300

Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro
305                 310                 315                 320

Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg
                325                 330                 335

Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn
            340                 345                 350

Pro
```

<210> 936
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 155; "

<220>
<221> source
<223> /note="Gene Symbol: ABRACL; "

<220>
<221> source
<223> /note="Gene Name:
ABRA C-terminal like; "

<220>
<221> source
<223> /note="Uniprot ID: Q9P1F3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356632"

<400> 936
Met Asn Val Asp His Glu Val Asn Leu Leu Val Glu Glu Ile His Arg
1   5   10   15

Leu Gly Ser Lys Asn Ala Asp Gly Lys Leu Ser Val Lys Phe Gly Val
            20   25   30

Leu Phe Arg Asp Asp Lys Cys Ala Asn Leu Phe Glu Ala Leu Val Gly
        35   40   45

Thr Leu Lys Ala Ala Lys Arg Arg Lys Ile Val Thr Tyr Pro Gly Glu
    50   55   60

Leu Leu Leu Gln Gly Val His Asp Asp Val Asp Ile Ile Leu Leu Gln
65   70   75   80

Asp

<210> 937
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 155; "

<220>
<221> source
<223> /note="Gene Symbol: ABRACL; "

<220>
<221> source
<223> /note="Gene Name:
ABRA C-terminal like; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000418406"

<400> 937
Met Asn Val Asp His Glu Val Asn Leu Leu Val Glu Glu Ile His Arg
1   5   10   15

Leu Gly Ser Lys Ser Lys Tyr Leu Thr Glu Ile Glu Tyr Phe Ser Trp
            20   25   30

Leu Tyr Leu Gly Thr Gly Glu Thr Gly Met Leu Glu Lys Pro Met Lys
        35   40   45

Gly Ser Pro Arg Ala Ser Gly His Arg Ser Gly Ser Ser Ala His Ser
    50   55   60

Pro Arg Leu
65

<210> 938
<211> 1723
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 156; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1; "

<220>
<221> source
<223> /note="Gene Name:
      absent in melanoma 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y4K1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358062"

<400> 938
Met Glu Lys Arg Ser Ser Gly Arg Arg Ser Gly Arg Arg Arg Gly Ser
1   5   10   15

Gln Lys Ser Thr Asp Ser Pro Gly Ala Asp Ala Glu Leu Pro Glu Ser
            20   25   30

```
Ala Ala Arg Asp Asp Ala Val Phe Asp Asp Glu Val Ala Pro Asn Ala
        35                  40                  45

Ala Ser Asp Asn Ala Ser Ala Glu Lys Lys Val Lys Ser Pro Arg Ala
    50                  55                  60

Ala Leu Asp Gly Gly Val Ala Ser Ala Ala Ser Pro Glu Ser Lys Pro
65                  70                  75                  80

Ser Pro Gly Thr Lys Gly Gln Leu Arg Gly Glu Ser Asp Arg Ser Lys
                85                  90                  95

Gln Pro Pro Pro Ala Ser Ser Pro Thr Lys Arg Lys Gly Arg Ser Arg
            100                 105                 110

Ala Leu Glu Ala Val Pro Ala Pro Pro Ala Ser Gly Pro Arg Ala Pro
        115                 120                 125

Ala Lys Glu Ser Pro Pro Lys Arg Val Pro Asp Pro Ser Pro Val Thr
    130                 135                 140

Lys Gly Thr Ala Ala Glu Ser Gly Glu Glu Ala Ala Arg Ala Ile Pro
145                 150                 155                 160

Arg Glu Leu Pro Val Lys Ser Ser Ser Leu Leu Pro Glu Ile Lys Pro
                165                 170                 175

Glu His Lys Arg Gly Pro Leu Pro Asn His Phe Asn Gly Arg Ala Glu
            180                 185                 190

Gly Gly Arg Ser Arg Glu Leu Gly Arg Ala Ala Gly Ala Pro Gly Ala
        195                 200                 205

Ser Asp Ala Asp Gly Leu Lys Pro Arg Asn His Phe Gly Val Gly Arg
    210                 215                 220

Ser Thr Val Thr Thr Lys Val Thr Leu Pro Ala Lys Pro Lys His Val
225                 230                 235                 240

Glu Leu Asn Leu Lys Thr Pro Lys Asn Leu Asp Ser Leu Gly Asn Glu
                245                 250                 255
```

```
His Asn Pro Phe Ser Gln Pro Val His Lys Gly Asn Thr Ala Thr Lys
            260                 265                 270

Ile Ser Leu Phe Glu Asn Lys Arg Thr Asn Ser Ser Pro Arg His Thr
        275                 280                 285

Asp Ile Arg Gly Gln Arg Asn Thr Pro Ala Ser Ser Lys Thr Phe Val
    290                 295                 300

Gly Arg Ala Lys Leu Asn Leu Ala Lys Lys Ala Lys Glu Met Glu Gln
305                 310                 315                 320

Pro Glu Lys Lys Val Met Pro Asn Ser Pro Gln Asn Gly Val Leu Val
                325                 330                 335

Lys Glu Thr Ala Ile Glu Thr Lys Val Thr Val Ser Glu Glu Glu Ile
            340                 345                 350

Leu Pro Ala Thr Arg Gly Met Asn Gly Asp Ser Ser Glu Asn Gln Ala
        355                 360                 365

Leu Gly Pro Gln Pro Asn Gln Asp Asp Lys Ala Asp Val Gln Thr Asp
    370                 375                 380

Ala Gly Cys Leu Ser Glu Pro Val Ala Ser Ala Leu Ile Pro Val Lys
385                 390                 395                 400

Asp His Lys Leu Leu Glu Lys Glu Asp Ser Glu Ala Ala Asp Ser Lys
                405                 410                 415

Ser Leu Val Leu Glu Asn Val Thr Asp Thr Ala Gln Asp Ile Pro Thr
            420                 425                 430

Thr Val Asp Thr Lys Asp Leu Pro Pro Thr Ala Met Pro Lys Pro Gln
        435                 440                 445

His Thr Phe Ser Asp Ser Gln Ser Pro Ala Glu Ser Ser Pro Gly Pro
    450                 455                 460

Ser Leu Ser Leu Ser Ala Pro Ala Pro Gly Asp Val Pro Lys Asp Thr
465                 470                 475                 480
```

```
Cys Val Gln Ser Pro Ile Ser Ser Phe Pro Cys Thr Asp Leu Lys Val
                485                 490                 495

Ser Glu Asn His Lys Gly Cys Val Leu Pro Val Ser Arg Gln Asn Asn
            500                 505                 510

Glu Lys Met Pro Leu Leu Glu Leu Gly Gly Glu Thr Thr Pro Pro Leu
        515                 520                 525

Ser Thr Glu Arg Ser Pro Glu Ala Val Gly Ser Glu Cys Pro Ser Arg
    530                 535                 540

Val Leu Val Gln Val Arg Ser Phe Val Leu Pro Val Glu Ser Thr Gln
545                 550                 555                 560

Asp Val Ser Ser Gln Val Ile Pro Glu Ser Ser Glu Val Arg Glu Val
                565                 570                 575

Gln Leu Pro Thr Cys His Ser Asn Glu Pro Glu Val Val Ser Val Ala
            580                 585                 590

Ser Cys Ala Pro Pro Gln Glu Glu Val Leu Gly Asn Glu His Ser His
        595                 600                 605

Cys Thr Ala Glu Leu Ala Ala Lys Ser Gly Pro Gln Val Ile Pro Pro
    610                 615                 620

Ala Ser Glu Lys Thr Leu Pro Ile Gln Ala Gln Ser Gln Gly Ser Arg
625                 630                 635                 640

Thr Pro Leu Met Ala Glu Ser Ser Pro Thr Asn Ser Pro Ser Ser Gly
                645                 650                 655

Asn His Leu Ala Thr Pro Gln Arg Pro Asp Gln Thr Val Thr Asn Gly
            660                 665                 670

Gln Asp Ser Pro Ala Ser Leu Leu Asn Ile Ser Ala Gly Ser Asp Asp
        675                 680                 685

Ser Val Phe Asp Ser Ser Ser Asp Met Glu Lys Phe Thr Glu Ile Ile
    690                 695                 700

Lys Gln Met Asp Ser Ala Val Cys Met Pro Met Lys Arg Lys Lys Ala
```

705 710 715 720

Arg Met Pro Asn Ser Pro Ala Pro His Phe Ala Met Pro Pro Ile His
725 730 735

Glu Asp His Leu Glu Lys Val Phe Asp Pro Lys Val Phe Thr Phe Gly
740 745 750

Leu Gly Lys Lys Lys Glu Ser Gln Pro Glu Met Ser Pro Ala Leu His
755 760 765

Leu Met Gln Asn Leu Asp Thr Lys Ser Lys Leu Arg Pro Lys Arg Ala
770 775 780

Ser Ala Glu Gln Ser Val Leu Phe Lys Ser Leu His Thr Asn Thr Asn
785 790 795 800

Gly Asn Ser Glu Pro Leu Val Met Pro Glu Ile Asn Asp Lys Glu Asn
805 810 815

Arg Asp Val Thr Asn Gly Gly Ile Lys Arg Ser Arg Leu Glu Lys Ser
820 825 830

Ala Leu Phe Ser Ser Leu Leu Ser Ser Leu Pro Gln Asp Lys Ile Phe
835 840 845

Ser Pro Ser Val Thr Ser Val Asn Thr Met Thr Thr Ala Phe Ser Thr
850 855 860

Ser Gln Asn Gly Ser Leu Ser Gln Ser Ser Val Ser Gln Pro Thr Thr
865 870 875 880

Glu Gly Ala Pro Pro Cys Gly Leu Asn Lys Glu Gln Ser Asn Leu Leu
885 890 895

Pro Asp Asn Ser Leu Lys Val Phe Asn Phe Asn Ser Ser Ser Thr Ser
900 905 910

His Ser Ser Leu Lys Ser Pro Ser His Met Glu Lys Tyr Pro Gln Lys
915 920 925

Glu Lys Thr Lys Glu Asp Leu Asp Ser Arg Ser Asn Leu His Leu Pro
930 935 940

```
Glu Thr Lys Phe Ser Glu Leu Ser Lys Leu Lys Asn Asp Asp Met Glu
945                 950                 955                 960

Lys Ala Asn His Ile Glu Ser Val Ile Lys Ser Asn Leu Pro Asn Cys
                965                 970                 975

Ala Asn Ser Asp Thr Asp Phe Met Gly Leu Phe Lys Ser Ser Arg Tyr
            980                 985                 990

Asp Pro Ser Ile Ser Phe Ser Gly  Met Ser Leu Ser Asp  Thr Met
Thr
        995                 1000                1005

Leu Arg  Gly Ser Val Gln Asn  Lys Leu Asn Pro Arg  Pro Gly Lys
    1010                1015                1020

Val Val  Ile Tyr Ser Glu Pro  Asp Val Ser Glu Lys  Cys Ile Glu
    1025                1030                1035

Val Phe  Ser Asp Ile Gln Asp  Cys Ser Ser Trp Ser  Leu Ser Pro
    1040                1045                1050

Val Ile  Leu Ile Lys Val Val  Arg Gly Cys Trp Ile  Leu Tyr Glu
    1055                1060                1065

Gln Pro  Asn Phe Glu Gly His  Ser Ile Pro Leu Glu  Glu Gly Glu
    1070                1075                1080

Leu Glu  Leu Ser Gly Leu Trp  Gly Ile Glu Asp Ile  Leu Glu Arg
    1085                1090                1095

His Glu  Glu Ala Glu Ser Asp  Lys Pro Val Val Ile  Gly Ser Ile
    1100                1105                1110

Arg His  Val Val Gln Asp Tyr  Arg Val Ser His Ile  Asp Leu Phe
    1115                1120                1125

Thr Glu  Pro Glu Gly Leu Gly  Ile Leu Ser Ser Tyr  Phe Asp Asp
    1130                1135                1140

Thr Glu  Glu Met Gln Gly Phe  Gly Val Met Gln Lys  Thr Cys Ser
    1145                1150                1155
```

```
Met Lys  Val His Trp Gly Thr  Trp Leu Ile Tyr Glu  Glu Pro Gly
    1160                1165                1170

Phe Gln  Gly Val Pro Phe Ile  Leu Glu Pro Gly Glu  Tyr Pro Asp
    1175                1180                1185

Leu Ser  Phe Trp Asp Thr Glu  Glu Ala Tyr Ile Gly  Ser Met Arg
    1190                1195                1200

Pro Leu  Lys Met Gly Gly Arg  Lys Val Glu Phe Pro  Thr Asp Pro
    1205                1210                1215

Lys Val  Val Val Tyr Glu Lys  Pro Phe Phe Glu Gly  Lys Cys Val
    1220                1225                1230

Glu Leu  Glu Thr Gly Met Cys  Ser Phe Val Met Glu  Gly Gly Glu
    1235                1240                1245

Thr Glu  Glu Ala Thr Gly Asp  Asp His Leu Pro Phe  Thr Ser Val
    1250                1255                1260

Gly Ser  Met Lys Val Leu Arg  Gly Ile Trp Val Ala  Tyr Glu Lys
    1265                1270                1275

Pro Gly  Phe Thr Gly His Gln  Tyr Leu Leu Glu Glu  Gly Glu Tyr
    1280                1285                1290

Arg Asp  Trp Lys Ala Trp Gly  Gly Tyr Asn Gly Glu  Leu Gln Ser
    1295                1300                1305

Leu Arg  Pro Ile Leu Gly Asp  Phe Ser Asn Ala His  Met Ile Met
    1310                1315                1320

Tyr Ser  Glu Lys Asn Phe Gly  Ser Lys Gly Ser Ser  Ile Asp Val
    1325                1330                1335

Leu Gly  Ile Val Ala Asn Leu  Lys Glu Thr Gly Tyr  Gly Val Lys
    1340                1345                1350

Thr Gln  Ser Ile Asn Val Leu  Ser Gly Val Trp Val  Ala Tyr Glu
    1355                1360                1365
```

```
Asn Pro  Asp Phe Thr Gly Glu  Gln Tyr Ile Leu Asp  Lys Gly Phe
    1370                1375                1380

Tyr Thr  Ser Phe Glu Asp Trp  Gly Gly Lys Asn Cys  Lys Ile Ser
    1385                1390                1395

Ser Val  Gln Pro Ile Cys Leu  Asp Ser Phe Thr Gly  Pro Arg Arg
    1400                1405                1410

Arg Asn  Gln Ile His Leu Phe  Ser Glu Pro Gln Phe  Gln Gly His
    1415                1420                1425

Ser Gln  Ser Phe Glu Glu Thr  Thr Ser Gln Ile Asp  Asp Ser Phe
    1430                1435                1440

Ser Thr  Lys Ser Cys Arg Val  Ser Gly Gly Ser Trp  Val Val Tyr
    1445                1450                1455

Asp Gly  Glu Asn Phe Thr Gly  Asn Gln Tyr Val Leu  Glu Glu Gly
    1460                1465                1470

His Tyr  Pro Cys Leu Ser Ala  Met Gly Cys Pro Pro  Gly Ala Thr
    1475                1480                1485

Phe Lys  Ser Leu Arg Phe Ile  Asp Val Glu Phe Ser  Glu Pro Thr
    1490                1495                1500

Ile Ile  Leu Phe Glu Arg Glu  Asp Phe Lys Gly Lys  Lys Ile Glu
    1505                1510                1515

Leu Asn  Ala Glu Thr Val Asn  Leu Arg Ser Leu Gly  Phe Asn Thr
    1520                1525                1530

Gln Ile  Arg Ser Val Gln Val  Ile Gly Gly Ile Trp  Val Thr Tyr
    1535                1540                1545

Glu Tyr  Gly Ser Tyr Arg Gly  Arg Gln Phe Leu Leu  Ser Pro Ala
    1550                1555                1560

Glu Val  Pro Asn Trp Tyr Glu  Phe Ser Gly Cys Arg  Gln Ile Gly
    1565                1570                1575
```

```
Ser Leu  Arg Pro Phe Val Gln  Lys Arg Ile Tyr Phe  Arg Leu Arg
    1580                1585                1590

Asn Lys  Ala Thr Gly Leu Phe  Met Ser Thr Asn Gly  Asn Leu Glu
    1595                1600                1605

Asp Leu  Lys Leu Leu Arg Ile  Gln Val Met Glu Asp  Val Gly Ala
    1610                1615                1620

Asp Asp  Gln Ile Trp Ile Tyr  Gln Glu Gly Cys Ile  Lys Cys Arg
    1625                1630                1635

Ile Ala  Glu Asp Cys Cys Leu  Thr Ile Val Gly Ser  Leu Val Thr
    1640                1645                1650

Ser Gly  Ser Lys Leu Gly Leu  Ala Leu Asp Gln Asn  Ala Asp Ser
    1655                1660                1665

Gln Phe  Trp Ser Leu Lys Ser  Asp Gly Arg Ile Tyr  Ser Lys Leu
    1670                1675                1680

Lys Pro  Asn Leu Val Leu Asp  Ile Lys Gly Gly Thr  Gln Tyr Asp
    1685                1690                1695

Gln Asn  His Ile Ile Leu Asn  Thr Val Ser Lys Glu  Lys Phe Thr
    1700                1705                1710

Gln Val  Trp Glu Ala Met Val  Leu Tyr Thr
    1715                1720


<210> 939
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 156; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1; "

<220>
<221> source
<223> /note="Gene Name:
      absent in melanoma 1; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000391419"

<400> 939
Met Gln Lys Pro Lys Thr Val Ala Trp Glu Asn Leu Gly Pro Glu Met
1   5   10   15

Ser Ala Leu Gly Thr Ala Phe Ser Arg Glu Gly Gly Arg Lys Val Glu
            20   25   30

Phe Pro Thr Asp Pro Lys Val Val Val Tyr Glu Lys Pro Phe Phe Glu
        35   40   45

Gly Lys Cys Val Glu Leu Glu Thr Gly Met Cys Ser Phe Val Met Glu
    50   55   60

Gly Gly Glu Thr Glu Glu Ala Thr Gly Asp Asp His Leu Pro Phe Thr
65   70   75   80

Ser Val Gly Ser Met Lys Val Leu Arg Gly Ile Trp Val Ala Tyr Glu
                85   90   95

Lys Pro Gly Phe Thr Gly His Gln Tyr Leu Leu Glu Glu Gly Glu Tyr
            100   105   110

Arg Asp Trp Lys Ala Trp Gly Gly Tyr Asn Gly Glu Leu Gln Ser Leu
        115   120   125

Arg Pro Ile Leu Gly Asp Phe Ser Asn Ala His Met Ile Met Tyr Ser
    130   135   140

Glu Lys Asn Phe Gly Ser Lys Gly Ser Ser Ile Asp Val Leu Gly Ile
145   150   155   160

Val Ala Asn Leu Lys Glu Thr Gly Tyr Gly Val Lys Thr Gln Ser Ile
                165   170   175

Asn Val Leu Ser Gly Val Trp Val Ala Tyr Glu Asn Pro Asp Phe Thr
            180   185   190

Gly Glu Gln Tyr Ile Leu Asp Lys Gly Phe Tyr Thr Ser Phe Glu Asp
        195   200   205

```
Trp Gly Gly Lys Asn Cys Lys Ile Ser Ser Val Gln Pro Ile Cys Leu
    210                 215                 220

Asp Ser Phe Thr Gly Pro Arg Arg Arg Asn Gln Ile His Leu Phe Ser
225                 230                 235                 240

Glu Pro Gln Phe Gln Gly His Ser Gln Ser Phe Glu Glu Thr Thr Ser
                245                 250                 255

Gln Ile Asp Asp Ser Phe Ser Thr Lys Ser Cys Arg Val Ser Gly Gly
            260                 265                 270

Ser Trp Val Val Tyr Asp Gly Glu Asn Phe Thr Gly Asn Gln Tyr Val
        275                 280                 285

Leu Glu Glu Gly His Tyr Pro Cys Leu Ser Ala Met Gly Cys Pro Pro
    290                 295                 300

Gly Ala Thr Phe Lys Ser Leu Arg Phe Ile Asp Val
305                 310                 315


<210> 940
<211> 2131
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 156; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1; "

<220>
<221> source
<223> /note="Gene Name:
      absent in melanoma 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488010"

<400> 940
Met Pro Leu Ser Pro Pro Ala Gln Gly Asp Pro Gly Glu Pro Ser Pro
1               5                   10                  15

Cys Arg Pro Pro Lys Lys His Thr Thr Phe His Leu Trp Arg Ser Lys
```

```
            20                  25                  30

Lys Lys Gln Gln Pro Ala Pro Pro Asp Cys Gly Val Phe Val Pro His
        35                  40                  45

Pro Leu Pro Ala Pro Ala Gly Glu Ala Arg Ala Leu Asp Val Val Asp
    50                  55                  60

Gly Lys Tyr Val Val Arg Asp Ser Gln Glu Phe Pro Leu His Cys Gly
65                  70                  75                  80

Glu Ser Gln Phe Phe His Thr Thr Ser Glu Ala Leu Gly Ser Leu Leu
                85                  90                  95

Leu Glu Ser Gly Ile Phe Lys Lys Ser Arg Ala Gln Pro Pro Glu Asp
            100                 105                 110

Asn Arg Arg Lys Pro Val Leu Gly Lys Leu Gly Thr Leu Phe Thr Ala
        115                 120                 125

Gly Arg Arg Arg Asn Ser Arg Asn Gly Leu Glu Ser Pro Thr Arg Ser
    130                 135                 140

Asn Ala Lys Pro Leu Ser Pro Lys Asp Val Val Ala Ser Pro Lys Leu
145                 150                 155                 160

Pro Glu Arg Glu Ser Glu Arg Ser Arg Ser Gln Ser Ser Gln Leu Lys
                165                 170                 175

Gln Thr Asp Thr Ser Glu Glu Gly Ser Pro Arg Glu Asn Pro Arg Glu
            180                 185                 190

Ala Glu Gly Glu Leu Pro Glu Ser Gly Gly Pro Ala Ala Pro Pro Asp
        195                 200                 205

Ala Glu Leu Ser Pro Arg Trp Ser Ser Ser Ala Ala Ala Val Ala Val
    210                 215                 220

Gln Gln Cys His Glu Asn Asp Ser Pro Gln Leu Glu Pro Leu Glu Ala
225                 230                 235                 240

Glu Gly Glu Pro Phe Pro Asp Ala Thr Thr Thr Ala Lys Gln Leu His
                245                 250                 255
```

```
Ser Ser Pro Gly Asn Ser Ser Arg Gln Glu Asn Ala Glu Thr Pro Ala
            260                 265                 270

Arg Ser Pro Gly Glu Asp Ala Ser Pro Gly Ala Gly His Glu Gln Glu
        275                 280                 285

Ala Phe Leu Gly Val Arg Gly Ala Pro Gly Ser Pro Thr Gln Glu Arg
    290                 295                 300

Pro Ala Gly Gly Leu Gly Glu Ala Pro Asn Gly Ala Pro Ser Val Cys
305                 310                 315                 320

Ala Glu Glu Gly Ser Leu Gly Pro Arg Asn Ala Arg Ser Gln Pro Pro
                325                 330                 335

Lys Gly Ala Ser Asp Leu Pro Gly Glu Pro Pro Ala Glu Gly Ala Ala
            340                 345                 350

His Thr Ala Ser Ser Ala Gln Ala Asp Cys Thr Ala Arg Pro Lys Gly
        355                 360                 365

His Ala His Pro Ala Lys Val Leu Thr Leu Asp Ile Tyr Leu Ser Lys
    370                 375                 380

Thr Glu Gly Ala Gln Val Asp Glu Pro Val Val Ile Thr Pro Arg Ala
385                 390                 395                 400

Glu Asp Cys Gly Asp Trp Asp Asp Met Glu Lys Arg Ser Ser Gly Arg
                405                 410                 415

Arg Ser Gly Arg Arg Arg Gly Ser Gln Lys Ser Thr Asp Ser Pro Gly
            420                 425                 430

Ala Asp Ala Glu Leu Pro Glu Ser Ala Ala Arg Asp Asp Ala Val Phe
        435                 440                 445

Asp Asp Glu Val Ala Pro Asn Ala Ala Ser Asp Asn Ala Ser Ala Glu
    450                 455                 460

Lys Lys Val Lys Ser Pro Arg Ala Ala Leu Asp Gly Gly Val Ala Ser
465                 470                 475                 480
```

Ala Ala Ser Pro Glu Ser Lys Pro Ser Pro Gly Thr Lys Gly Gln Leu
485 490 495

Arg Gly Glu Ser Asp Arg Ser Lys Gln Pro Pro Pro Ala Ser Ser Pro
500 505 510

Thr Lys Arg Lys Gly Arg Ser Arg Ala Leu Glu Ala Val Pro Ala Pro
515 520 525

Pro Ala Ser Gly Pro Arg Ala Pro Ala Lys Glu Ser Pro Pro Lys Arg
530 535 540

Val Pro Asp Pro Ser Pro Val Thr Lys Gly Thr Ala Ala Glu Ser Gly
545 550 555 560

Glu Glu Ala Ala Arg Ala Ile Pro Arg Glu Leu Pro Val Lys Ser Ser
565 570 575

Ser Leu Leu Pro Glu Ile Lys Pro Glu His Lys Arg Gly Pro Leu Pro
580 585 590

Asn His Phe Asn Gly Arg Ala Glu Gly Gly Arg Ser Arg Glu Leu Gly
595 600 605

Arg Ala Ala Gly Ala Pro Gly Ala Ser Asp Ala Asp Gly Leu Lys Pro
610 615 620

Arg Asn His Phe Gly Val Gly Arg Ser Thr Val Thr Thr Lys Val Thr
625 630 635 640

Leu Pro Ala Lys Pro Lys His Val Glu Leu Asn Leu Lys Thr Pro Lys
645 650 655

Asn Leu Asp Ser Leu Gly Asn Glu His Asn Pro Phe Ser Gln Pro Val
660 665 670

His Lys Gly Asn Thr Ala Thr Lys Ile Ser Leu Phe Glu Asn Lys Arg
675 680 685

Thr Asn Ser Ser Pro Arg His Thr Asp Ile Arg Gly Gln Arg Asn Thr
690 695 700

```
Pro Ala Ser Ser Lys Thr Phe Val Gly Arg Ala Lys Leu Asn Leu Ala
705                 710                 715                 720

Lys Lys Ala Lys Glu Met Glu Gln Pro Glu Lys Lys Val Met Pro Asn
                725                 730                 735

Ser Pro Gln Asn Gly Val Leu Val Lys Glu Thr Ala Ile Glu Thr Lys
            740                 745                 750

Val Thr Val Ser Glu Glu Glu Ile Leu Pro Ala Thr Arg Gly Met Asn
        755                 760                 765

Gly Asp Ser Ser Glu Asn Gln Ala Leu Gly Pro Gln Pro Asn Gln Asp
    770                 775                 780

Asp Lys Ala Asp Val Gln Thr Asp Ala Gly Cys Leu Ser Glu Pro Val
785                 790                 795                 800

Ala Ser Ala Leu Ile Pro Val Lys Asp His Lys Leu Leu Glu Lys Glu
                805                 810                 815

Asp Ser Glu Ala Ala Asp Ser Lys Ser Leu Val Leu Glu Asn Val Thr
            820                 825                 830

Asp Thr Ala Gln Asp Ile Pro Thr Thr Val Asp Thr Lys Asp Leu Pro
        835                 840                 845

Pro Thr Ala Met Pro Lys Pro Gln His Thr Phe Ser Asp Ser Gln Ser
    850                 855                 860

Pro Ala Glu Ser Ser Pro Gly Pro Ser Leu Ser Leu Ser Ala Pro Ala
865                 870                 875                 880

Pro Gly Asp Val Pro Lys Asp Thr Cys Val Gln Ser Pro Ile Ser Ser
                885                 890                 895

Phe Pro Cys Thr Asp Leu Lys Val Ser Glu Asn His Lys Gly Cys Val
            900                 905                 910

Leu Pro Val Ser Arg Gln Asn Asn Glu Lys Met Pro Leu Leu Glu Leu
        915                 920                 925

Gly Gly Glu Thr Thr Pro Pro Leu Ser Thr Glu Arg Ser Pro Glu Ala
```

```
    930                 935                 940

Val Gly Ser Glu Cys Pro Ser Arg Val Leu Val Gln Val Arg Ser Phe
945                 950                 955                 960

Val Leu Pro Val Glu Ser Thr Gln Asp Val Ser Ser Gln Val Ile Pro
                965                 970                 975

Glu Ser Ser Glu Val Arg Glu Val Gln Leu Pro Thr Cys His Ser Asn
            980                 985                 990

Glu Pro Glu Val Val Ser Val Ala  Ser Cys Ala Pro Pro  Gln Glu
Glu
        995                 1000                1005

Val Leu  Gly Asn Glu His Ser  His Cys Thr Ala Glu  Leu Ala Ala
    1010                1015                1020

Lys Ser  Gly Pro Gln Val Ile  Pro Pro Ala Ser Glu  Lys Thr Leu
    1025                1030                1035

Pro Ile  Gln Ala Gln Ser Gln  Gly Ser Arg Thr Pro  Leu Met Ala
    1040                1045                1050

Glu Ser  Ser Pro Thr Asn Ser  Pro Ser Ser Gly Asn  His Leu Ala
    1055                1060                1065

Thr Pro  Gln Arg Pro Asp Gln  Thr Val Thr Asn Gly  Gln Asp Ser
    1070                1075                1080

Pro Ala  Ser Leu Leu Asn Ile  Ser Ala Gly Ser Asp  Asp Ser Val
    1085                1090                1095

Phe Asp  Ser Ser Ser Asp Met  Glu Lys Phe Thr Glu  Ile Ile Lys
    1100                1105                1110

Gln Met  Asp Ser Ala Val Cys  Met Pro Met Lys Arg  Lys Lys Ala
    1115                1120                1125

Arg Met  Pro Asn Ser Pro Ala  Pro His Phe Ala Met  Pro Pro Ile
    1130                1135                1140

His Glu  Asp His Leu Glu Lys  Val Phe Asp Pro Lys  Val Phe Thr
```

1145 1150 1155

Phe Gly Leu Gly Lys Lys Lys Glu Ser Gln Pro Glu Met Ser Pro
1160 1165 1170

Ala Leu His Leu Met Gln Asn Leu Asp Thr Lys Ser Lys Leu Arg
1175 1180 1185

Pro Lys Arg Ala Ser Ala Glu Gln Ser Val Leu Phe Lys Ser Leu
1190 1195 1200

His Thr Asn Thr Asn Gly Asn Ser Glu Pro Leu Val Met Pro Glu
1205 1210 1215

Ile Asn Asp Lys Glu Asn Arg Asp Val Thr Asn Gly Gly Ile Lys
1220 1225 1230

Arg Ser Arg Leu Glu Lys Ser Ala Leu Phe Ser Ser Leu Leu Ser
1235 1240 1245

Ser Leu Pro Gln Asp Lys Ile Phe Ser Pro Ser Val Thr Ser Val
1250 1255 1260

Asn Thr Met Thr Thr Ala Phe Ser Thr Ser Gln Asn Gly Ser Leu
1265 1270 1275

Ser Gln Ser Ser Val Ser Gln Pro Thr Thr Glu Gly Ala Pro Pro
1280 1285 1290

Cys Gly Leu Asn Lys Glu Gln Ser Asn Leu Leu Pro Asp Asn Ser
1295 1300 1305

Leu Lys Val Phe Asn Phe Asn Ser Ser Ser Thr Ser His Ser Ser
1310 1315 1320

Leu Lys Ser Pro Ser His Met Glu Lys Tyr Pro Gln Lys Glu Lys
1325 1330 1335

Thr Lys Glu Asp Leu Asp Ser Arg Ser Asn Leu His Leu Pro Glu
1340 1345 1350

Thr Lys Phe Ser Glu Leu Ser Lys Leu Lys Asn Asp Asp Met Glu
1355 1360 1365

```
Lys Ala  Asn His Ile Glu Ser  Val Ile Lys Ser Asn  Leu Pro Asn
    1370                1375                1380

Cys Ala  Asn Ser Asp Thr Asp  Phe Met Gly Leu Phe  Lys Ser Ser
    1385                1390                1395

Arg Tyr  Asp Pro Ser Ile Ser  Phe Ser Gly Met Ser  Leu Ser Asp
    1400                1405                1410

Thr Met  Thr Leu Arg Gly Ser  Val Gln Asn Lys Leu  Asn Pro Arg
    1415                1420                1425

Pro Gly  Lys Val Val Ile Tyr  Ser Glu Pro Asp Val  Ser Glu Lys
    1430                1435                1440

Cys Ile  Glu Val Phe Ser Asp  Ile Gln Asp Cys Ser  Ser Trp Ser
    1445                1450                1455

Leu Ser  Pro Val Ile Leu Ile  Lys Val Val Arg Gly  Cys Trp Ile
    1460                1465                1470

Leu Tyr  Glu Gln Pro Asn Phe  Glu Gly His Ser Ile  Pro Leu Glu
    1475                1480                1485

Glu Gly  Glu Leu Glu Leu Ser  Gly Leu Trp Gly Ile  Glu Asp Ile
    1490                1495                1500

Leu Glu  Arg His Glu Glu Ala  Glu Ser Asp Lys Pro  Val Val Ile
    1505                1510                1515

Gly Ser  Ile Arg His Val Val  Gln Asp Tyr Arg Val  Ser His Ile
    1520                1525                1530

Asp Leu  Phe Thr Glu Pro Glu  Gly Leu Gly Ile Leu  Ser Ser Tyr
    1535                1540                1545

Phe Asp  Asp Thr Glu Glu Met  Gln Gly Phe Gly Val  Met Gln Lys
    1550                1555                1560

Thr Cys  Ser Met Lys Val His  Trp Gly Thr Trp Leu  Ile Tyr Glu
    1565                1570                1575
```

Glu Pro Gly Phe Gln Gly Val Pro Phe Ile Leu Glu Pro Gly Glu
1580 1585 1590

Tyr Pro Asp Leu Ser Phe Trp Asp Thr Glu Glu Ala Tyr Ile Gly
1595 1600 1605

Ser Met Arg Pro Leu Lys Met Gly Gly Arg Lys Val Glu Phe Pro
1610 1615 1620

Thr Asp Pro Lys Val Val Val Tyr Glu Lys Pro Phe Phe Glu Gly
1625 1630 1635

Lys Cys Val Glu Leu Glu Thr Gly Met Cys Ser Phe Val Met Glu
1640 1645 1650

Gly Gly Glu Thr Glu Glu Ala Thr Gly Asp Asp His Leu Pro Phe
1655 1660 1665

Thr Ser Val Gly Ser Met Lys Val Leu Arg Gly Ile Trp Val Ala
1670 1675 1680

Tyr Glu Lys Pro Gly Phe Thr Gly His Gln Tyr Leu Leu Glu Glu
1685 1690 1695

Gly Glu Tyr Arg Asp Trp Lys Ala Trp Gly Gly Tyr Asn Gly Glu
1700 1705 1710

Leu Gln Ser Leu Arg Pro Ile Leu Gly Asp Phe Ser Asn Ala His
1715 1720 1725

Met Ile Met Tyr Ser Glu Lys Asn Phe Gly Ser Lys Gly Ser Ser
1730 1735 1740

Ile Asp Val Leu Gly Ile Val Ala Asn Leu Lys Glu Thr Gly Tyr
1745 1750 1755

Gly Val Lys Thr Gln Ser Ile Asn Val Leu Ser Gly Val Trp Val
1760 1765 1770

Ala Tyr Glu Asn Pro Asp Phe Thr Gly Glu Gln Tyr Ile Leu Asp
1775 1780 1785

```
Lys Gly  Phe Tyr Thr Ser Phe  Glu Asp Trp Gly Gly  Lys Asn Cys
    1790                 1795                 1800

Lys Ile  Ser Ser Val Gln Pro  Ile Cys Leu Asp Ser  Phe Thr Gly
    1805                 1810                 1815

Pro Arg  Arg Arg Asn Gln Ile  His Leu Phe Ser Glu  Pro Gln Phe
    1820                 1825                 1830

Gln Gly  His Ser Gln Ser Phe  Glu Glu Thr Thr Ser  Gln Ile Asp
    1835                 1840                 1845

Asp Ser  Phe Ser Thr Lys Ser  Cys Arg Val Ser Gly  Gly Ser Trp
    1850                 1855                 1860

Val Val  Tyr Asp Gly Glu Asn  Phe Thr Gly Asn Gln  Tyr Val Leu
    1865                 1870                 1875

Glu Glu  Gly His Tyr Pro Cys  Leu Ser Ala Met Gly  Cys Pro Pro
    1880                 1885                 1890

Gly Ala  Thr Phe Lys Ser Leu  Arg Phe Ile Asp Val  Glu Phe Ser
    1895                 1900                 1905

Glu Pro  Thr Ile Ile Leu Phe  Glu Arg Glu Asp Phe  Lys Gly Lys
    1910                 1915                 1920

Lys Ile  Glu Leu Asn Ala Glu  Thr Val Asn Leu Arg  Ser Leu Gly
    1925                 1930                 1935

Phe Asn  Thr Gln Ile Arg Ser  Val Gln Val Ile Gly  Gly Ile Trp
    1940                 1945                 1950

Val Thr  Tyr Glu Tyr Gly Ser  Tyr Arg Gly Arg Gln  Phe Leu Leu
    1955                 1960                 1965

Ser Pro  Ala Glu Val Pro Asn  Trp Tyr Glu Phe Ser  Gly Cys Arg
    1970                 1975                 1980

Gln Ile  Gly Ser Leu Arg Pro  Phe Val Gln Lys Arg  Ile Tyr Phe
    1985                 1990                 1995

Arg Leu  Arg Asn Lys Ala Thr  Gly Leu Phe Met Ser  Thr Asn Gly
```

```
    2000                2005                2010

Asn Leu  Glu Asp Leu Lys Leu  Leu Arg Ile Gln Val  Met Glu Asp
    2015                2020                2025

Val Gly  Ala Asp Asp Gln Ile  Trp Ile Tyr Gln Glu  Gly Cys Ile
    2030                2035                2040

Lys Cys  Arg Ile Ala Glu Asp  Cys Cys Leu Thr Ile  Val Gly Ser
    2045                2050                2055

Leu Val  Thr Ser Gly Ser Lys  Leu Gly Leu Ala Leu  Asp Gln Asn
    2060                2065                2070

Ala Asp  Ser Gln Phe Trp Ser  Leu Lys Ser Asp Gly  Arg Ile Tyr
    2075                2080                2085

Ser Lys  Leu Lys Pro Asn Leu  Val Leu Asp Ile Lys  Gly Gly Thr
    2090                2095                2100

Gln Tyr  Asp Gln Asn His Ile  Ile Leu Asn Thr Val  Ser Lys Glu
    2105                2110                2115

Lys Phe  Thr Gln Val Trp Glu  Ala Met Val Leu Tyr  Thr
    2120                2125                2130


<210> 941
<211> 1661
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 157; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1L; "

<220>
<221> source
<223> /note="Gene Name:
      absent in melanoma
      1-like; "

<220>
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<223> /note="Uniprot ID:  Q8N1P7; "
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<220>
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<400> 941
Met Glu Glu Ala Gly Gly Pro Met Ala Arg Ala Lys Ala Arg Val Val
1   5   10   15

Ser Ala Thr Leu Thr Trp Arg Gln Arg Pro Pro Thr Gln Glu Glu Ile
            20   25   30

Lys His Gly Phe His Lys Val Ser Leu Val Ser Gly Ala Gln Met Glu
        35   40   45

Ala Pro Gln Lys Glu Met Phe Glu Phe Ser Arg Arg Glu Glu Val Glu
    50   55   60

Val Asn Gly Phe Ala Thr Gln Glu Glu Glu Thr Val Asn Cys Gln Gly
65   70   75   80

Pro Arg Asp Thr Ala Gly Ser Lys Asn Phe Gln Ser His Gly Pro Ile
                85   90   95

Phe Ser Lys Lys Tyr Ile Pro Pro Pro Lys Glu Lys Arg Pro Glu Gly
            100   105   110

Arg Leu Lys Glu Ala Val Asp Gln Ser Asp Gly Ser Arg Gln Ala Pro
        115   120   125

Arg Thr Glu Pro Pro Cys Val Gly Ala Met Ala Arg Thr Glu Leu Leu
    130   135   140

Val Pro Leu Pro Gly Pro Arg Glu Pro Ser Pro His Pro Gly Val Gly
145   150   155   160

Leu Thr Ser Gly Ser Ser Arg Ser Leu Glu Glu Tyr Arg Val Thr Arg
                165   170   175

Thr Val Arg Thr Thr Thr Val Val Gly Gly His Val Asp Arg Arg Met
            180   185   190

Ser Ser Ser Val Thr Val Arg Pro Val Ser Ser Gly Glu Ala Leu Pro
        195   200   205

```
Arg Gly Arg Gln Val Ser Arg Met Val Pro Pro Val Val Val Gly Ser
    210                 215                 220

Pro Pro Gly Ser Pro Ser Arg Ser Gln Ala Val Lys Val Leu Ser Asn
225                 230                 235                 240

Leu Val Pro Ala Gly His Ser Pro Pro Ala Ser His Leu Pro Arg Pro
                245                 250                 255

Thr Ala Gly Gly Pro Arg Ser Thr Gly Leu Gly Ser Thr Val Gly Ala
            260                 265                 270

Ala Leu Arg Gln Leu Pro Glu Thr Gly Thr Ala Glu Leu Lys Asp Ser
        275                 280                 285

Ser Ala Leu Ala Ser Thr Gly Ile Pro Ala Ser Ala His Leu Pro Lys
    290                 295                 300

Asn Gln Asp Ala Pro Ala Ala Cys Pro Asp Arg Asp Gln Gly Arg Ala
305                 310                 315                 320

Pro Asp Ala Arg Ala Cys Glu Leu Trp Gln Val Leu Gly Ala Pro Ser
                325                 330                 335

Ser Thr Glu Leu Pro Leu Gln Thr Ser Gln Gly Gln Ala Ser Val Pro
            340                 345                 350

Ser Ser Pro Arg Leu Glu Thr His Val Pro Ser Pro Gly Leu Thr His
        355                 360                 365

Pro Ala Lys Gln Pro Val Val Pro Thr His Pro Gly Ala Arg Leu Thr
    370                 375                 380

Pro Leu Val Leu Pro Pro Lys Lys Lys Asp Gly Pro Val Asp Pro Pro
385                 390                 395                 400

Ala Ala Thr Val Leu Pro Met Val Arg Ser Glu His Val Thr Val Pro
                405                 410                 415

Gly Gln Pro Pro Ala Pro Ser Thr Thr Arg Arg Lys Asp Val Pro Ser
            420                 425                 430
```

```
Pro Gly Gly Leu Ser Ala Pro Ser Ser Pro Arg Asn Lys Phe Val Gln
        435                 440                 445

Asn Ser Glu Asn Val Pro Val Leu Pro Phe Thr Gln Arg Glu Val Val
    450                 455                 460

Lys Gly Pro Gly Ala Pro Ala Ala Ser Ser Pro Thr Arg Lys Glu Val
465                 470                 475                 480

Val Gln Gly Ser Ser Ala Ser Ala Ala Ser Ser Pro Thr Trp Lys Glu
                485                 490                 495

Val Val Lys Gly Pro Gly Ala Pro Ala Ala Ser Ser Pro Thr Gln Lys
            500                 505                 510

Glu Val Val Gln Gly Ser Ser Ala Pro Ala Ala Leu Phe Pro Thr Trp
        515                 520                 525

Lys Glu Val Val Lys Gly Pro Gly Ala Pro Asp Ala Ser Phe Pro Thr
    530                 535                 540

Trp Lys Glu Val Val Lys Gly Pro Gly Ala Pro Ala Ala Ser Ser Pro
545                 550                 555                 560

Thr Gln Lys Glu Val Val Gln Gly Ser Gly Ala Pro Ala Ala Leu Ser
                565                 570                 575

Thr Thr Pro Lys Glu Val Val Lys Gly Pro Gly Ala Pro Ala Ala Ser
            580                 585                 590

Ser Pro Thr Gln Lys Glu Val Val Lys Gly Pro Cys Ala Pro Ala Ala
        595                 600                 605

Ser Ser Pro Thr Gln Lys Glu Val Val Gln Gly Ser Gly Ala Pro Ala
    610                 615                 620

Ala Leu Ser Pro Lys Ser Thr Glu Val Val Gln Gly Pro Lys Gly Ser
625                 630                 635                 640

Ser Ser Ile Gln Lys Glu Ala Val Gln Gly Ile Ala Gly Ser Leu Ala
                645                 650                 655

Pro Pro Leu Thr Lys Glu Glu Thr Val Gln Gly Pro Ile Ala Pro Ala
```

660 665 670

Thr Ser Leu Pro Lys Gln Asp Lys Gly Val Gln Asp Ser Glu Gly Ser
675 680 685

Pro Ile Ser Ser Leu Thr Gln Lys Glu Val Val Gln Asp Pro Asp Ala
690 695 700

Leu Pro Ala Pro Ser Ser Ser Val Asp Arg Val Ser Pro Ser Pro Gly
705 710 715 720

Gly Thr Pro Ala Pro Val Pro Thr Gly Ala Glu Ala Ser Thr Glu Ser
725 730 735

Gln Leu Val Ser Asp Pro Thr Glu Gly Lys Thr Cys Thr Glu Thr Ser
740 745 750

Arg Glu Glu Asp Glu Val Ala Leu Ala Ala Asp Leu Glu Ile Phe Leu
755 760 765

Asp Thr Leu Arg Ser Met Glu Pro Pro Glu Ile Leu Arg Thr His Arg
770 775 780

Leu Pro Arg Ala Pro Arg Ser Ser Tyr Leu Ser Met Tyr Ala Thr Leu
785 790 795 800

Pro Ala Ile Glu Glu Asp Gln Leu Gly Pro Trp Val Leu Gly Pro Gly
805 810 815

Pro Gln Glu Val Pro Ser Leu Glu Glu Lys Glu Glu Glu Glu Glu Glu
820 825 830

Glu Pro Glu Asn Pro Tyr Leu Ser Asp Asp Glu Lys Leu Gln Arg Arg
835 840 845

Gln Glu Lys Ala Gly Pro Ser Pro Ser Arg Asp Leu His Pro Ala Arg
850 855 860

Pro Thr Gln Val Ser Cys Ser Pro Leu Glu Met Met Lys Lys His Val
865 870 875 880

Ala Gly Thr Lys Gly Pro His Ser Glu Leu Gly Leu Glu Leu Gln Gly
885 890 895

```
Gly Ser Arg Pro Thr Ser Arg Leu Gly Gly Ser Leu Leu Phe Gly Ser
            900                 905                 910

Leu Val Pro Thr Ala Lys Glu Ala Ser Thr Pro Glu Pro Leu Gly Thr
        915                 920                 925

Lys Leu Ser Ala Leu Leu Pro His Gly Ala Pro Gly Leu Arg Lys Val
    930                 935                 940

Pro Gly Gln Leu Pro Leu Leu Cys Ser Glu Arg Ser Ser Pro Thr Glu
945                 950                 955                 960

Lys Leu Ala Cys Ser Leu Pro Leu Glu Gly Trp Ser Pro Ala Leu Lys
                965                 970                 975

Thr Gln Gly Lys Leu Asn Thr Arg Pro Gly Lys Val Ile Phe Phe Ser
            980                 985                 990

Glu Ser Gly Cys Gln Gly Ser Gly  Arg Glu Val Trp Gly  Asp Ile
Val
        995                 1000                1005

Asp Ala  Ser Gly Trp Ala Pro  Val Ala Ser Ile Arg  Val Val Arg
    1010                1015                1020

Gly Cys  Trp Val Leu Tyr Glu  Glu Pro Glu Phe Arg  Gly Gln Lys
    1025                1030                1035

Leu Val  Leu Pro Glu Gly Asp  Met Glu Leu Arg Thr  Pro Gly Thr
    1040                1045                1050

Lys Trp  Ser Pro Gln Gly Ile  Gly Ser Leu Arg Arg  Val Val Trp
    1055                1060                1065

Asp Tyr  Ser Thr Pro Glu Ile  Ser Leu Phe Ser Glu  Glu Gly Leu
    1070                1075                1080

Lys Gly  Glu Gln Val Lys Leu  Thr Glu Ala Leu Lys  Asn Ser Gln
    1085                1090                1095

Gly Leu  Glu Lys Pro Leu Gln  Val Ala Ser Ala Thr  Val Ser Ala
    1100                1105                1110
```

```
Gly Leu  Trp Leu Leu Tyr Pro  Lys Pro Leu Phe Glu  Asp Thr Pro
    1115                1120                1125

Tyr Ile  Leu Glu Pro Gly Glu  Tyr Pro Thr Ser Glu  Ala Trp Gly
    1130                1135                1140

Thr Ser  Asp Pro Ser Val Gly  Ser Leu Lys Pro Met  Arg Leu Gly
    1145                1150                1155

Cys Pro  Ser Val Glu Lys Pro  Gly Glu Pro Arg Ala  Val Val Tyr
    1160                1165                1170

Glu Ala  Pro Gly Phe Gln Gly  Arg Ser Trp Glu Val  Ser Arg Asp
    1175                1180                1185

Ile Tyr  Asn Leu Gln Gln Pro  Glu Asp Ser Gln Ser  Pro His Leu
    1190                1195                1200

Ala Ser  Val Gly Ser Leu Arg  Val Leu Gly Gly Cys  Trp Val Gly
    1205                1210                1215

Tyr Glu  Lys Glu Gly Phe Arg  Gly His Gln Tyr Leu  Leu Glu Glu
    1220                1225                1230

Gly Glu  Tyr Pro Asp Trp Ser  His Trp Gly Gly Tyr  Asp Glu Leu
    1235                1240                1245

Leu Thr  Ser Leu Arg Val Ile  Arg Thr Asp Phe Gly  Asp Pro Ala
    1250                1255                1260

Val Val  Leu Phe Glu Ala Met  Asp Phe Glu Gly His  Gly Val Glu
    1265                1270                1275

Val Ser  Lys Ala Leu Pro Asp  Val Glu Leu Val Gln  His Gly Pro
    1280                1285                1290

Ser Thr  Gln Ala Ile His Val  Leu Ser Gly Val Trp  Val Ala Tyr
    1295                1300                1305

Gln Glu  Val Gly Phe Ser Gly  Glu Gln Tyr Val Leu  Glu Lys Gly
    1310                1315                1320
```

```
Val Tyr  Arg Asn Cys Glu Asp  Trp Gly Ala Gly Asn  Ser Thr Leu
    1325                1330                1335

Ala Ser  Leu Gln Pro Val Leu  Gln Val Gly Glu His  Asp Leu His
    1340                1345                1350

Phe Val  Ser Lys Ile Gln Leu  Phe Ser Arg Pro Asp  Phe Leu Gly
    1355                1360                1365

Asp His  Phe Ser Phe Glu Asp  Asp Gln Ala Ala Leu  Pro Ala Ser
    1370                1375                1380

Phe Arg  Pro Gln Ser Cys Arg  Val His Gly Gly Ser  Trp Ile Leu
    1385                1390                1395

Phe Asp  Glu Thr Asn Phe Glu  Gly Asp Gln His Ile  Leu Ser Glu
    1400                1405                1410

Gly Glu  Phe Pro Thr Leu Thr  Ala Met Gly Cys Leu  Ala Ser Thr
    1415                1420                1425

Val Leu  Gly Ser Leu Gln Lys  Val Ser Leu His Phe  Ser Glu Pro
    1430                1435                1440

Ser Ile  Phe Leu Tyr Gly Leu  Glu Cys Phe Glu Gly  Lys Glu Ile
    1445                1450                1455

Glu Leu  Ser Arg Glu Val Arg  Ser Leu Gln Ala Glu  Gly Phe Asn
    1460                1465                1470

Asn His  Val Leu Ser Val Arg  Ile Lys Gly Gly Ile  Trp Val Leu
    1475                1480                1485

Cys Glu  His Ser Asp Phe Arg  Gly Arg Gln Trp Leu  Val Gly Ser
    1490                1495                1500

Cys Glu  Ile Thr Asn Trp Leu  Thr Tyr Ser Gly Thr  Gln Arg Val
    1505                1510                1515

Gly Ser  Leu Tyr Pro Ile Lys  Gln Arg Arg Val Tyr  Phe Arg Leu
    1520                1525                1530
```

```
Trp Asn  Ala Ala Leu Gly Gly  Phe Leu Ala Val Pro  Asp His Val
    1535                1540                1545

Glu Asp  Met Lys Ala Gly Arg  Val Val Val Ala Asp  Pro Gln Ala
    1550                1555                1560

Gly Gly  Ser Cys Ile Trp Tyr  Tyr Glu Asp Gly Leu  Leu Lys Asn
    1565                1570                1575

Gln Met  Ala Pro Thr Met Ser  Leu Gln Val Ile Gly  Pro Pro Ser
    1580                1585                1590

Pro Gly  Ser Lys Val Val Leu  Trp Ala Glu Ser Arg  Leu Pro Arg
    1595                1600                1605

Gln Thr  Trp Ser Ile Ser Glu  Ser Gly His Ile Cys  Ser Gln Met
    1610                1615                1620

Phe Glu  Gly Gln Ile Leu Asp  Val Lys Gly Gly Arg  Gly Tyr Asp
    1625                1630                1635

Arg Asp  His Val Val Leu Trp  Glu Pro Asp Glu Asp  Arg Ala Ser
    1640                1645                1650

Gln Ile  Trp Thr Ile His Val  Leu
    1655                1660


<210> 942
<211> 352
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 157; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1L; "

<220>
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<223> /note="Gene Name:
      absent in melanoma
      1-like; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000363323"

<400> 942

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Met Glu Glu Ala Gly Gly Pro Met Ala Arg Ala Lys Ala Arg Val Asp
1               5                  10                  15

Gly Pro Val Asp Pro Pro Ala Ala Thr Val Leu Pro Met Val Arg Ser
            20                  25                  30

Glu His Val Thr Val Pro Gly Gln Pro Pro Ala Pro Ser Thr Thr Arg
        35                  40                  45

Arg Lys Asp Val Pro Ser Pro Gly Val Asp Arg Val Ser Pro Ser Pro
    50                  55                  60

Gly Gly Thr Pro Ala Pro Val Pro Thr Gly Ala Glu Ala Ser Thr Glu
65                  70                  75                  80

Ser Gln Leu Val Ser Asp Pro Thr Glu Gly Lys Thr Cys Thr Glu Thr
                85                  90                  95

Ser Arg Glu Glu Asp Glu Val Ala Leu Ala Ala Asp Leu Glu Ile Phe
            100                 105                 110

Leu Asp Thr Leu Arg Ser Met Glu Pro Pro Glu Ile Leu Arg Thr His
        115                 120                 125

Arg Leu Pro Arg Ala Pro Arg Ser Ser Tyr Leu Ser Met Tyr Ala Thr
    130                 135                 140

Leu Pro Ala Ile Glu Glu Asp Gln Leu Gly Pro Trp Val Leu Gly Pro
145                 150                 155                 160

Gly Pro Gln Glu Val Pro Ser Leu Glu Glu Lys Glu Glu Glu Glu Glu
                165                 170                 175

Glu Glu Pro Glu Asn Pro Tyr Leu Ser Asp Asp Glu Lys Leu Gln Arg
            180                 185                 190

Arg Gln Glu Lys Ala Gly Pro Ser Pro Ser Arg Asp Leu His Pro Ala
        195                 200                 205

Arg Pro Thr Gln Val Ser Cys Ser Pro Leu Glu Met Met Lys Lys His
    210                 215                 220
```

```
Val Ala Gly Thr Lys Gly Pro His Ser Glu Leu Gly Leu Glu Leu Gln
225                 230                 235                 240

Gly Gly Ser Arg Pro Thr Ser Arg Leu Gly Gly Ser Leu Leu Phe Gly
                245                 250                 255

Ser Leu Val Pro Thr Ala Lys Glu Ala Ser Thr Pro Glu Pro Leu Gly
            260                 265                 270

Thr Lys Leu Ser Ala Leu Leu Pro His Gly Ala Pro Gly Leu Arg Lys
        275                 280                 285

Val Pro Gly Gln Leu Pro Leu Leu Cys Ser Glu Arg Ser Ser Pro Thr
    290                 295                 300

Glu Lys Leu Ala Cys Ser Leu Pro Leu Glu Gly Trp Pro Ser Leu Lys
305                 310                 315                 320

Asp Pro Gly Gln Ala Glu His Gln Ala Trp Lys Gly Asp Leu Leu Leu
                325                 330                 335

Arg Val Trp Leu Pro Arg Gln Trp Gln Gly Gly Leu Gly Arg His Arg
            340                 345                 350


<210> 943
<211> 296
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 157; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1L; "

<220>
<221> source
<223> /note="Gene Name:
      absent in melanoma
      1-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000409834"
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 943
Xaa Ser Gln Gly Leu Glu Lys Pro Leu Gln Val Ala Ser Ala Thr Val
1 5 10 15

Ser Ala Gly Leu Trp Leu Leu Tyr Pro Lys Pro Leu Phe Glu Asp Thr
20 25 30

Pro Tyr Ile Leu Glu Pro Gly Glu Tyr Pro Thr Ser Glu Ala Trp Gly
35 40 45

Thr Ser Asp Pro Ser Val Gly Ser Leu Lys Pro Met Arg Leu Ala Val
50 55 60

Val Tyr Glu Ala Pro Gly Phe Gln Gly Arg Ser Trp Glu Val Ser Arg
65 70 75 80

Asp Ile Tyr Asn Leu Gln Gln Pro Glu Asp Ser Gln Ser Pro His Leu
85 90 95

Ala Ser Val Gly Ser Leu Arg Val Leu Gly Gly Cys Trp Val Gly Tyr
100 105 110

Glu Lys Glu Gly Phe Arg Gly His Gln Tyr Leu Leu Glu Glu Gly Glu
115 120 125

Tyr Pro Asp Trp Ser His Trp Gly Gly Tyr Asp Glu Leu Leu Thr Ser
130 135 140

Leu Arg Val Ile Arg Thr Asp Phe Gly Asp Pro Ala Val Val Leu Phe
145 150 155 160

Glu Ala Met Asp Phe Glu Gly His Gly Val Glu Val Ser Lys Ala Leu
165 170 175

Pro Asp Val Glu Leu Val Gln His Gly Pro Ser Thr Gln Ala Ile His
180 185 190

Val Leu Ser Gly Val Trp Val Ala Tyr Gln Glu Val Gly Phe Ser Gly
195 200 205

```
Glu Gln Tyr Val Leu Glu Lys Gly Val Tyr Arg Asn Cys Glu Asp Trp
    210                 215                 220

Gly Ala Gly Asn Ser Thr Leu Ala Ser Leu Gln Pro Val Leu Gln Val
225                 230                 235                 240

Gly Glu His Asp Leu His Phe Val Ser Lys Ile Gln Leu Phe Ser Arg
                245                 250                 255

Pro Asp Phe Leu Gly Asp His Phe Ser Phe Glu Asp Asp Gln Ala Ala
            260                 265                 270

Leu Pro Ala Ser Phe Arg Pro Gln Ser Cys Arg Val His Gly Gly Ser
        275                 280                 285

Trp Ile Leu Phe Asp Glu Thr Asn
    290                 295


<210> 944
<211> 466
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 157; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1L; "

<220>
<221> source
<223> /note="Gene Name:
      absent in melanoma
      1-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428746"

<400> 944
Met Glu Glu Ala Gly Gly Pro Met Ala Arg Ala Lys Ala Arg Val Val
1               5                   10                  15

Ser Ala Thr Leu Thr Trp Arg Gln Arg Pro Pro Thr Gln Glu Glu Ile
            20                  25                  30
```

```
Lys His Gly Phe His Lys Val Ser Leu Val Ser Gly Ala Gln Met Glu
        35                  40                  45

Ala Pro Gln Lys Glu Met Phe Glu Phe Ser Arg Arg Glu Glu Val Glu
    50                  55                  60

Val Asn Gly Phe Ala Thr Gln Glu Glu Glu Thr Val Asn Cys Gln Gly
65                  70                  75                  80

Pro Arg Asp Thr Ala Gly Ser Lys Asn Phe Gln Ser His Gly Pro Ile
                85                  90                  95

Phe Ser Lys Lys Tyr Ile Pro Pro Pro Lys Glu Lys Arg Pro Glu Gly
            100                 105                 110

Arg Leu Lys Glu Ala Val Asp Gln Ser Asp Gly Ser Arg Gln Ala Pro
        115                 120                 125

Arg Thr Glu Pro Pro Cys Val Gly Ala Met Ala Arg Thr Glu Leu Leu
    130                 135                 140

Val Pro Leu Pro Gly Pro Arg Glu Pro Ser Pro His Pro Gly Val Gly
145                 150                 155                 160

Leu Thr Ser Gly Ser Ser Arg Ser Leu Glu Glu Tyr Arg Val Thr Arg
                165                 170                 175

Thr Val Arg Thr Thr Thr Val Val Gly Gly His Val Asp Arg Arg Met
            180                 185                 190

Ser Ser Ser Val Thr Val Arg Pro Val Ser Ser Gly Glu Ala Leu Pro
        195                 200                 205

Arg Gly Arg Gln Val Ser Arg Met Val Pro Pro Val Val Val Gly Ser
    210                 215                 220

Pro Pro Gly Ser Pro Ser Arg Ser Gln Ala Val Lys Val Leu Ser Asn
225                 230                 235                 240

Leu Val Pro Ala Gly His Ser Pro Pro Ala Ser His Leu Pro Arg Pro
                245                 250                 255
```

```
Thr Ala Gly Gly Pro Arg Ser Thr Gly Leu Gly Ser Thr Val Gly Ala
            260                 265                 270

Ala Leu Arg Gln Leu Pro Glu Thr Gly Thr Ala Glu Leu Lys Asp Ser
        275                 280                 285

Ser Ala Leu Ala Ser Thr Gly Ile Pro Ala Ser Ala His Leu Pro Lys
    290                 295                 300

Asn Gln Asp Ala Pro Ala Ala Cys Pro Asp Arg Asp Gln Gly Arg Ala
305                 310                 315                 320

Pro Asp Ala Arg Ala Cys Glu Leu Trp Gln Val Leu Gly Ala Pro Ser
                325                 330                 335

Ser Thr Glu Leu Pro Leu Gln Thr Ser Gln Gly Gln Ala Ser Val Pro
            340                 345                 350

Ser Ser Pro Arg Leu Glu Thr His Val Pro Ser Pro Gly Leu Thr His
        355                 360                 365

Pro Ala Lys Gln Pro Val Val Pro Thr His Pro Gly Ala Arg Leu Thr
    370                 375                 380

Pro Leu Val Leu Pro Pro Lys Lys Lys Asp Gly Pro Val Asp Pro Pro
385                 390                 395                 400

Ala Ala Thr Val Leu Pro Met Val Arg Ser Glu His Val Thr Val Pro
                405                 410                 415

Gly Gln Pro Pro Ala Pro Ser Thr Thr Arg Arg Lys Asp Val Pro Ser
            420                 425                 430

Pro Gly Gly Leu Ser Ala Pro Ser Ser Pro Arg Asn Lys Phe Val Gln
        435                 440                 445

Asn Ser Glu Asn Val Pro Val Leu Pro Phe Thr Gln Arg Glu Val Val
    450                 455                 460

Lys Gly
465
```

<210> 945

<211> 787
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 157; "

<220>
<221> source
<223> /note="Gene Symbol: AIM1L; "

<220>
<221> source
<223> /note="Gene Name:
absent in melanoma
1-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433931"

<400> 945

```
Met Met Lys Lys His Val Ala Gly Thr Lys Gly Pro His Ser Glu Leu
1               5                   10                  15

Gly Leu Glu Leu Gln Gly Gly Ser Arg Pro Thr Ser Arg Leu Gly Gly
            20                  25                  30

Ser Leu Leu Phe Gly Ser Leu Val Pro Thr Ala Lys Glu Ala Ser Thr
        35                  40                  45

Pro Glu Pro Leu Gly Thr Lys Leu Ser Ala Leu Leu Pro His Gly Ala
    50                  55                  60

Pro Gly Leu Arg Lys Val Pro Gly Gln Leu Pro Leu Leu Cys Ser Glu
65                  70                  75                  80

Arg Ser Ser Pro Thr Glu Lys Leu Ala Cys Ser Leu Pro Leu Glu Gly
                85                  90                  95

Trp Ser Pro Ala Leu Lys Thr Gln Gly Lys Leu Asn Thr Arg Pro Gly
            100                 105                 110

Lys Val Ile Phe Phe Ser Glu Ser Gly Cys Gln Gly Ser Gly Arg Glu
        115                 120                 125

Val Trp Gly Asp Ile Val Asp Ala Ser Gly Trp Ala Pro Val Ala Ser
    130                 135                 140
```

```
Ile Arg Val Val Arg Gly Cys Trp Val Leu Tyr Glu Glu Pro Glu Phe
145                 150                 155                 160

Arg Gly Gln Lys Leu Val Leu Pro Glu Gly Asp Met Glu Leu Arg Thr
                165                 170                 175

Pro Gly Thr Lys Trp Ser Pro Gln Gly Ile Gly Ser Leu Arg Arg Val
            180                 185                 190

Val Trp Asp Tyr Ser Thr Pro Glu Ile Ser Leu Phe Ser Glu Glu Gly
        195                 200                 205

Leu Lys Gly Glu Gln Val Lys Leu Thr Glu Ala Leu Lys Asn Ser Gln
    210                 215                 220

Gly Leu Glu Lys Pro Leu Gln Val Ala Ser Ala Thr Val Ser Ala Gly
225                 230                 235                 240

Leu Trp Leu Leu Tyr Pro Lys Pro Leu Phe Glu Asp Thr Pro Tyr Ile
                245                 250                 255

Leu Glu Pro Gly Glu Tyr Pro Thr Ser Glu Ala Trp Gly Thr Ser Asp
            260                 265                 270

Pro Ser Val Gly Ser Leu Lys Pro Met Arg Leu Gly Cys Pro Ser Val
        275                 280                 285

Glu Lys Pro Gly Glu Pro Arg Ala Val Val Tyr Glu Ala Pro Gly Phe
    290                 295                 300

Gln Gly Arg Ser Trp Glu Val Ser Arg Asp Ile Tyr Asn Leu Gln Gln
305                 310                 315                 320

Pro Glu Asp Ser Gln Ser Pro His Leu Ala Ser Val Gly Ser Leu Arg
                325                 330                 335

Val Leu Gly Gly Cys Trp Val Gly Tyr Glu Lys Glu Gly Phe Arg Gly
            340                 345                 350

His Gln Tyr Leu Leu Glu Glu Gly Glu Tyr Pro Asp Trp Ser His Trp
        355                 360                 365
```

```
Gly Gly Tyr Asp Glu Leu Leu Thr Ser Leu Arg Val Ile Arg Thr Asp
    370                 375                 380

Phe Gly Asp Pro Ala Val Val Leu Phe Glu Ala Met Asp Phe Glu Gly
385                 390                 395                 400

His Gly Val Glu Val Ser Lys Ala Leu Pro Asp Val Glu Leu Val Gln
                405                 410                 415

His Gly Pro Ser Thr Gln Ala Ile His Val Leu Ser Gly Val Trp Val
            420                 425                 430

Ala Tyr Gln Glu Val Gly Phe Ser Gly Glu Gln Tyr Val Leu Glu Lys
        435                 440                 445

Gly Val Tyr Arg Asn Cys Glu Asp Trp Gly Ala Gly Asn Ser Thr Leu
    450                 455                 460

Ala Ser Leu Gln Pro Val Leu Gln Val Gly Glu His Asp Leu His Phe
465                 470                 475                 480

Val Ser Lys Ile Gln Leu Phe Ser Arg Pro Asp Phe Leu Gly Asp His
                485                 490                 495

Phe Ser Phe Glu Asp Asp Gln Ala Ala Leu Pro Ala Ser Phe Arg Pro
            500                 505                 510

Gln Ser Cys Arg Val His Gly Gly Ser Trp Ile Leu Phe Asp Glu Thr
        515                 520                 525

Asn Phe Glu Gly Asp Gln His Ile Leu Ser Glu Gly Glu Phe Pro Thr
    530                 535                 540

Leu Thr Ala Met Gly Cys Leu Ala Ser Thr Val Leu Gly Ser Leu Gln
545                 550                 555                 560

Lys Val Ser Leu His Phe Ser Glu Pro Ser Ile Phe Leu Tyr Gly Leu
                565                 570                 575

Glu Cys Phe Glu Gly Lys Glu Ile Glu Leu Ser Arg Glu Val Arg Ser
            580                 585                 590
```

```
Leu Gln Ala Glu Gly Phe Asn Asn His Val Leu Ser Val Arg Ile Lys
        595                 600                 605

Gly Gly Ile Trp Val Leu Cys Glu His Ser Asp Phe Arg Gly Arg Gln
    610                 615                 620

Trp Leu Val Gly Ser Cys Glu Ile Thr Asn Trp Leu Thr Tyr Ser Gly
625                 630                 635                 640

Thr Gln Arg Val Gly Ser Leu Tyr Pro Ile Lys Gln Arg Arg Val Tyr
                645                 650                 655

Phe Arg Leu Trp Asn Ala Ala Leu Gly Gly Phe Leu Ala Val Pro Asp
            660                 665                 670

His Val Glu Asp Met Lys Ala Gly Arg Val Val Val Ala Asp Pro Gln
        675                 680                 685

Ala Gly Gly Ser Cys Ile Trp Tyr Tyr Glu Asp Gly Leu Leu Lys Asn
    690                 695                 700

Gln Met Ala Pro Thr Met Ser Leu Gln Val Ile Gly Pro Pro Ser Pro
705                 710                 715                 720

Gly Ser Lys Val Val Leu Trp Ala Glu Ser Arg Leu Pro Arg Gln Thr
                725                 730                 735

Trp Ser Ile Ser Glu Ser Gly His Ile Cys Ser Gln Met Phe Glu Gly
            740                 745                 750

Gln Ile Leu Asp Val Lys Gly Gly Arg Gly Tyr Asp Arg Asp His Val
        755                 760                 765

Val Leu Trp Glu Pro Asp Glu Asp Arg Ala Ser Gln Ile Trp Thr Ile
    770                 775                 780

His Val Leu
785
```

<210> 946
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 158; "

<220>
<221> source
<223> /note="Gene Symbol: AIM2; "

<220>
<221> source
<223> /note="Gene Name:
absent in melanoma 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000357111"

<400> 946
Met Val Ala Gln Gln Glu Ser Ile Arg Glu Gly Phe Gln Lys Arg Cys
1 5 10 15

Leu Pro Val Met Val Leu Lys Ala Lys Lys Pro Phe Thr Phe Glu Thr
20 25 30

Gln Glu Gly Lys Gln Glu Met Phe His Ala Thr Val Ala Thr Glu Lys
35 40 45

Glu Phe Phe Phe Val Lys Val Phe Asn Thr Leu Leu Lys Asp Lys Phe
50 55 60

Ile Pro Lys Arg Ile Ile Ile Ile Ala Arg Tyr Tyr Arg His Ser Gly
65 70 75 80

Phe Leu Glu Val Asn Ser Ala Ser Arg Val Leu Asp Ala Glu Ser Asp
85 90 95

Gln Lys Val Asn Val Pro Leu Asn Ile Ile Arg Lys Ala Gly Glu Thr
100 105 110

Pro Lys Ile Asn Thr Leu Gln Thr Gln Pro Leu Gly Thr Ile Val Asn
115 120 125

Gly Leu Phe Val Val Gln Lys Val Thr Glu Lys Lys Lys Asn Ile Leu
130 135 140

Phe Asp Leu Ser Asp Asn Thr Gly Lys Met Glu Val Leu Gly Val Arg
145 150 155 160

Asn Glu Asp Thr Met Lys Cys
165

<210> 947
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 158; "

<220>
<221> source
<223> /note="Gene Symbol: AIM2; "

<220>
<221> source
<223> /note="Gene Name:
absent in melanoma 2; "

<220>
<221> source
<223> /note="Uniprot ID: O14862; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000357112"

<400> 947
Met Glu Ser Lys Tyr Lys Glu Ile Leu Leu Leu Thr Gly Leu Asp Asn
1 5 10 15

Ile Thr Asp Glu Glu Leu Asp Arg Phe Lys Phe Phe Leu Ser Asp Glu
20 25 30

Phe Asn Ile Ala Thr Gly Lys Leu His Thr Ala Asn Arg Ile Gln Val
35 40 45

Ala Thr Leu Met Ile Gln Asn Ala Gly Ala Val Ser Ala Val Met Lys
50 55 60

Thr Ile Arg Ile Phe Gln Lys Leu Asn Tyr Met Leu Leu Ala Lys Arg
65 70 75 80

Leu Gln Glu Glu Lys Glu Lys Val Asp Lys Gln Tyr Lys Ser Val Thr
85 90 95

Lys Pro Lys Pro Leu Ser Gln Ala Glu Met Ser Pro Ala Ala Ser Ala

```
            100                 105                 110

Ala Ile Arg Asn Asp Val Ala Lys Gln Arg Ala Ala Pro Lys Val Ser
        115                 120                 125

Pro His Val Lys Pro Glu Gln Lys Gln Met Val Ala Gln Gln Glu Ser
    130                 135                 140

Ile Arg Glu Gly Phe Gln Lys Arg Cys Leu Pro Val Met Val Leu Lys
145                 150                 155                 160

Ala Lys Lys Pro Phe Thr Phe Glu Thr Gln Glu Gly Lys Gln Glu Met
                165                 170                 175

Phe His Ala Thr Val Ala Thr Glu Lys Glu Phe Phe Phe Val Lys Val
            180                 185                 190

Phe Asn Thr Leu Leu Lys Asp Lys Phe Ile Pro Lys Arg Ile Ile Ile
        195                 200                 205

Ile Ala Arg Tyr Tyr Arg His Ser Gly Phe Leu Glu Val Asn Ser Ala
    210                 215                 220

Ser Arg Val Leu Asp Ala Glu Ser Asp Gln Lys Val Asn Val Pro Leu
225                 230                 235                 240

Asn Ile Ile Arg Lys Ala Gly Glu Thr Pro Lys Ile Asn Thr Leu Gln
                245                 250                 255

Thr Gln Pro Leu Gly Thr Ile Val Asn Gly Leu Phe Val Val Gln Lys
            260                 265                 270

Val Thr Glu Lys Lys Lys Asn Ile Leu Phe Asp Leu Ser Asp Asn Thr
        275                 280                 285

Gly Lys Met Glu Val Leu Gly Val Arg Asn Glu Asp Thr Met Lys Cys
    290                 295                 300

Lys Glu Gly Asp Lys Val Arg Leu Thr Phe Phe Thr Leu Ser Lys Asn
305                 310                 315                 320

Gly Glu Lys Leu Gln Leu Thr Ser Gly Val His Ser Thr Ile Lys Val
                325                 330                 335
```

Ile Lys Ala Lys Lys Lys Thr
340

<210> 948
<211> 355
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 158; "

<220>
<221> source
<223> /note="Gene Symbol: AIM2; "

<220>
<221> source
<223> /note="Gene Name:
absent in melanoma 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483485"

<400> 948
Met Glu Ser Lys Tyr Lys Glu Ile Leu Leu Leu Thr Gly Leu Asp Asn
1 5 10 15

Ile Thr Asp Glu Glu Leu Asp Arg Phe Lys Phe Phe Leu Ser Asp Glu
20 25 30

Phe Asn Ile Ala Thr Gly Lys Leu His Thr Ala Asn Arg Ile Gln Val
35 40 45

Ala Thr Leu Met Ile Gln Asn Ala Gly Ala Val Ser Ala Val Met Lys
50 55 60

Thr Ile Arg Ile Phe Gln Lys Leu Asn Tyr Met Leu Leu Ala Lys Arg
65 70 75 80

Leu Gln Glu Glu Lys Glu Lys Val Asp Lys Gln Tyr Lys Ser Val Thr
85 90 95

Lys Pro Lys Pro Leu Ser Gln Ala Glu Met Ser Pro Ala Ala Ser Ala
100 105 110

```
Ala Ile Arg Asn Asp Val Ala Lys Gln Arg Ala Ala Pro Lys Val Ser
        115                 120                 125

Pro His Val Lys Pro Glu Gln Lys Gln Met Val Ala Gln Gln Glu Ser
    130                 135                 140

Ile Arg Glu Gly Phe Gln Lys Arg Cys Leu Pro Val Met Val Leu Lys
145                 150                 155                 160

Ala Lys Lys Pro Phe Thr Phe Glu Thr Gln Glu Gly Lys Gln Glu Met
                165                 170                 175

Phe His Ala Thr Val Ala Thr Glu Lys Glu Phe Phe Phe Val Lys Val
            180                 185                 190

Phe Asn Thr Leu Leu Lys Asp Lys Phe Ile Pro Lys Arg Ile Ile Ile
        195                 200                 205

Ile Ala Arg Tyr Tyr Arg His Ser Gly Phe Leu Glu Val Asn Ser Ala
    210                 215                 220

Ser Arg Val Leu Asp Ala Glu Ser Asp Gln Lys Val Asn Val Pro Leu
225                 230                 235                 240

Asn Ile Ile Arg Lys Ala Gly Glu Thr Pro Lys Ile Asn Thr Leu Gln
                245                 250                 255

Thr Gln Pro Leu Gly Thr Ile Val Asn Gly Leu Phe Val Val Gln Lys
            260                 265                 270

Val Thr Glu Lys Lys Lys Asn Ile Leu Phe Asp Leu Ser Asp Asn Thr
        275                 280                 285

Gly Lys Met Glu Val Leu Gly Val Arg Asn Glu Asp Thr Met Lys Cys
    290                 295                 300

Lys Glu Gly Asp Lys Val Arg Leu Thr Phe Phe Thr Leu Ser Lys Asn
305                 310                 315                 320

Gly Glu Lys Leu Gln Leu Thr Ser Gly Val His Ser Thr Ile Lys Val
                325                 330                 335

Ile Lys Ala Lys Lys Lys His Arg Glu Val Lys Arg Thr Asn Ser Ser
```

340 345 350

Gln Leu Val
355

<210> 949
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 159; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC002310.11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454241"

<400> 949
Met Thr Asp Pro Ser Leu Gly Leu Thr Val Pro Met Ala Pro Pro Leu
1 5 10 15

Ala Pro Leu Pro Pro Arg Asp Pro Asn Gly Ala Gly Ser Glu Trp Arg
20 25 30

Lys Pro Gly Ala Val Ser Phe Ala Asp Val Ala Val Tyr Phe Ser Arg
35 40 45

Glu Glu Trp Gly Cys Leu Arg Pro Ala Gln Arg Ala Leu Tyr Arg Asp
50 55 60

Val Met Arg Glu Thr Tyr Gly His Leu Gly Ala Leu Gly Val Gly Gly
65 70 75 80

Ser Lys Pro Ala Leu Ile Ser Trp Val Glu Glu Lys Ala Glu Leu Trp
85 90 95

Asp Pro Ala Ala Gln Asp Pro Glu Val Ala Lys Cys Pro Thr Glu Ala
100 105 110

```
Asp Pro Asp Ser Arg Asn Lys Glu Glu Glu Arg Gln Arg Glu Gly Thr
        115                 120                 125

Gly Ala Leu Glu Lys Pro Asp Pro Val Ala Ala Gly Ser Pro Gly Leu
    130                 135                 140

Lys Ala Pro Gln Ala Pro Phe Ala Gly Leu Glu Gln Leu Ser Lys Ala
145                 150                 155                 160

Arg Arg Arg Ser Arg Pro Arg Phe Phe Ala His Pro Pro Val Pro Arg
                165                 170                 175

Ala Asp Gln Arg His Gly Cys Tyr Val Cys Gly Lys Ser Phe Ala Trp
            180                 185                 190

Arg Ser Thr Leu Val Glu His Ile Tyr Ser His Arg Gly Glu Lys Pro
        195                 200                 205

Phe His Cys Ala Asp Cys Gly Lys Gly Phe Gly His Ala Ser Ser Leu
    210                 215                 220

Ser Lys His Arg Ala Ile His Arg Gly Glu Arg Pro His Arg Cys Pro
225                 230                 235                 240

Glu Cys Gly Arg Ala Phe Met Arg Arg Thr Ala Leu Thr Ser His Leu
                245                 250                 255

Arg Val His Thr Gly Glu Lys Pro Tyr Arg Cys Pro Gln Cys Gly Arg
            260                 265                 270

Cys Phe Gly Leu Lys Thr Gly Met Ala Lys His Gln Trp Val His Arg
        275                 280                 285

Pro Gly Gly Glu Gly Arg Arg Gly Arg Arg Pro Gly Gly Leu Ser Val
    290                 295                 300

Thr Leu Thr Pro Val Arg Gly Asp Leu Asp Pro Pro Val Gly Phe Gln
305                 310                 315                 320

Leu Tyr Pro Glu Ile Phe Gln Glu Cys Gly
                325                 330
```

<210> 950
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 160; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC002310.13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455659"

<400> 950
Met Ala Pro Pro Leu Ala Pro Leu Pro Pro Arg Asp Pro Asn Gly Ala
1 5 10 15

Gly Pro Glu Trp Arg Glu Pro Gly Ala Val Ser Phe Ala Asp Val Ala
20 25 30

Val Tyr Phe Cys Arg Glu Glu Trp Gly Cys Leu Arg Pro Ala Gln Arg
35 40 45

Ala Leu Tyr Arg Asp Val Met Arg Glu Thr Tyr Gly His Leu Ser Ala
50 55 60

Leu Gly Val Gly Gly Ser Lys Pro Ala Leu Ile Ser Trp Val Glu Glu
65 70 75 80

Lys Ala Glu Leu Trp Asp Pro Ala Ala Gln Asp Pro Glu
85 90

<210> 951
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 161; "

<220>

<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC002398.9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468389"

<400> 951
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
1 5 10 15

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
20 25 30

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
35 40 45

Glu Gln Ser Gln Ile Lys Gly
50 55

<210> 952
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 162; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC002985.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469669"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 952
Xaa Gln Glu Val Lys Glu Ala Ala Arg Leu Ala Arg Glu Lys Ser Gln
1   5   10   15

Asp Gly Gly Glu Leu Thr Ser Pro Ala Leu Gly Leu Ala Ser His Gln
            20   25   30

Val Pro Pro Ser Pro Leu Val Ser Ala Asn Gly Pro Gly Glu Glu Lys
        35   40   45

Leu Phe Arg Ser Gln Ser Ala Asp Ala Pro Gly Pro Thr Glu Arg Glu
    50   55   60

Arg Leu Lys Lys Met Leu Ser Glu Gly Trp Leu Ser Trp Arg Leu Arg
65   70   75   80

Gln Leu Gln Arg

<210> 953
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 162; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC002985.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471765"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 953
Xaa Gln Glu Val Lys Glu Ala Ala Arg Leu Ala Arg Glu Lys Ser Gln
1   5   10   15

```
Asp Gly Gly Glu Leu Thr Ser Pro Ala Leu Gly Leu Ala Ser His Gln
            20                  25                  30

Val Pro Pro Ser Pro Leu Val Ser Ala Asn Gly Pro Gly Glu Glu Lys
        35                  40                  45

Leu Phe Arg Ser Gln Ser Ala Asp Ala Pro Gly Pro Thr Glu Arg Glu
    50                  55                  60

Arg Leu Lys Lys Met Leu Ser Glu Gly Trp Leu Ser Trp Arg Leu Arg
65                  70                  75                  80

Gln Leu Gln Arg
```

<210> 954
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 163; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC003002.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472894"

<400> 954

```
Met Ala Glu Met Asn Pro Ala Gln Gly His Val Val Phe Glu Asp Val
1               5                   10                  15

Ala Ile Tyr Phe Ser Gln Glu Glu Trp Gly His Leu Asp Glu Ala Gln
            20                  25                  30

Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Leu Ala Leu Leu Ser
        35                  40                  45

Ser Leu Gly Ser Trp His Gly Ala Glu Asp Glu Glu Ala Pro Ser Gln
```

```
    50                  55                  60

Gln Gly Phe Ser Val Gly Val Ser Glu Val Thr Ala Ser Lys Pro Cys
65                  70                  75                  80

Leu Ser Ser Gln Lys Val His Pro Ser Glu Thr Cys Gly Pro Pro Leu
                85                  90                  95

Lys Asp Ile Leu Cys Leu
            100


<210> 955
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 164; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC003002.6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471870"

<400> 955
Met Asn Leu Thr Glu Gly Pro Leu Ala Met Ala Glu Met Asp Pro Thr
1               5                   10                  15

Gln Gly Arg Val Val Phe Glu Asp Val Ala Ile Tyr Phe Ser Gln Glu
            20                  25                  30

Glu Trp Gly His Leu Asp Glu Ala Gln Arg Leu Leu Tyr Arg Asp Val
        35                  40                  45

Met Leu Glu Asn Leu Ala Leu Leu Ser Ser Leu Gly Phe Ile Ala Val
    50                  55                  60

Ala Ala Met Leu Met Asp Ala Gly Gln Asp Tyr Met Val Phe Glu Asp
65                  70                  75                  80
```

```
Val Ala Ile His Phe Ser Gln Glu Glu Trp Gly Ile Leu Asn Asp Val
                85                  90                  95


Gln Arg His Leu His Ser Asp Val Met Leu
            100                 105


<210> 956
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 164; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC003002.6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472277"

<400> 956
Met Asn Leu Thr Glu Gly Pro Leu Ala Met Ala Glu Met Asp Pro Thr
1               5                   10                  15


Gln Asp Tyr Met Val Phe Glu Asp Val Ala Ile His Phe Ser Gln Glu
            20                  25                  30


Glu Trp Gly Ile Leu Asn Asp Val Gln Arg His Leu His Ser Asp Val
        35                  40                  45


Met Leu Glu Asn Phe Ala Leu Leu Ser Ser Val Gly Cys Trp His Gly
    50                  55                  60


Ala Lys Asp Glu Glu Ala Pro Ser Lys Gln Cys Val Ser Val Gly Val
65                  70                  75                  80


Ser Gln Val Thr Thr Leu Lys Pro Ala Leu Ser Thr Gln Lys Ala Gln
                85                  90                  95


Pro Cys Glu Thr Cys Ser Ser Leu Leu Lys Asp Ile Leu His Leu Ala
```

```
            100                 105                 110

Glu His Asp Gly Thr His Pro Lys Arg Thr Ala Lys Leu Tyr Leu His
        115                 120                 125

Gln Lys Glu His Leu Arg Glu Lys Leu Thr Arg Ser Asp Glu Gly Arg
    130                 135                 140

Pro Ser Phe Val Asn Asp Ser Val His Leu Ala Lys Arg Asn Leu Thr
145                 150                 155                 160

Cys Met Gln Gly Gly Lys Asp Phe Thr Gly Asp Ser Asp Leu Gln Gln
                165                 170                 175

Gln Ala Leu
```

<210> 957
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 165; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC003005.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471625"

<400> 957

```
Met Ala Ala Ala Ala Leu Arg Asp Pro Ala Gln Gly Tyr Val Thr Phe
1               5                   10                  15

Glu Asp Val Ala Val Tyr Phe Ser Gln Glu Glu Trp Arg Leu Leu Asp
            20                  25                  30

Asp Ala Gln Arg Leu Leu Tyr Arg Asn Val Met Leu Glu Asn Phe Thr
        35                  40                  45
```

```
Leu Leu Ala Ser Leu Ala Gly Leu Cys Asp Leu
    50                  55


<210> 958
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 165; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC003005.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472846"

<400> 958
Met Ala Ala Ala Ala Leu Arg Asp Pro Ala Gln Gly Tyr Val Thr Phe
1               5                   10                  15


Glu Asp Val Ala Val Tyr Phe Ser Gln Glu Glu Trp Arg Leu Leu Asp
            20                  25                  30


Asp Ala Gln Arg Leu Leu Tyr Arg Asn Val Met Leu Glu Asn Phe Thr
        35                  40                  45


Leu Leu Ala Ser Leu Gly Leu Cys Asp Leu
    50                  55


<210> 959
<211> 148
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 166; "

<220>
<221> source
<223> /note="Gene Symbol:; "
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<220>
<221> source
<223> /note="Gene Name:
AC003006.7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472160"

<400> 959
Met Ala Ala Val Ala Leu Arg Asp Ser Ala Gln Gly Thr Val Thr Phe
1 5 10 15

Glu Asp Val Ala Val Asn Phe Ser Gln Glu Glu Trp Ser Leu Leu Ser
20 25 30

Glu Ala Gln Arg Cys Leu Tyr His Asp Val Met Leu Glu Asn Leu Thr
35 40 45

Leu Ile Ser Ser Leu Gly Cys Trp Tyr Gly Ala Lys Asp Glu Thr Pro
50 55 60

Ser Lys Gln Thr Leu Ser Ile Gln Gln Glu Ser Pro Leu Arg Thr His
65 70 75 80

Trp Thr Gly Val Cys Thr Lys Lys Val His Leu Trp Gly Met Cys Gly
85 90 95

Pro Leu Leu Gly Asp Ile Leu His Gln Gly Thr Gln His Asn Gln Lys
100 105 110

Leu Asn Gly Phe Gly Ala Tyr Glu Lys Lys Leu Asp Asp Asp Ala Asn
115 120 125

His His Gln Asp Gln Lys Gln His Ile Gly Glu Lys Ser Tyr Arg Ser
130 135 140

Asn Ala Lys Gly
145

<210> 960
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 167; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004076.7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472152"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 960
Xaa Gln Gly Pro Leu Ala Met Ala Glu Met Asp Pro Thr Gln Arg Gln
1 5 10 15

Asp Leu Thr Leu Ser Pro Lys Leu Glu Tyr Ser Gly Met Ile Ile Ala
20 25 30

His Cys His Leu Glu Pro Leu Gly Ser Ser Asp Pro Pro Ala Ser Ala
35 40 45

Ser Gln Val Ala Gly Thr Thr Gly Arg Lys Asn Glu Gly Arg Asp Gln
50 55 60

Leu Ser Met Pro Leu Glu Ala Ile
65 70

<210> 961
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 168; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC004076.9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470969"

<400> 961
Met Ala Ala Ala Glu Pro Met Gly Pro Ala Gln Val Pro Met Asn Ser
1 5 10 15

Glu Val Ile Val Asp Pro Ile Gln Gly Gln Val Asn Phe Glu Asp Val
20 25 30

Phe Val Tyr Phe Ser Gln Glu Glu Trp Val Leu Leu Asp Glu Ala Gln
35 40 45

Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Ala Leu Met Ala
50 55 60

Ser Leu Gly Ile Pro Gln Thr Met Ala Ala Phe Gly Leu Lys Tyr Leu
65 70 75 80

Leu Asn Asp Thr Gly Tyr Thr Ser Ser Lys Ser Asn Thr Ile Thr Ala
85 90 95

Thr Asp Ser Pro Ala Asp Leu Pro Arg Lys Pro Glu Pro His Thr Pro
100 105 110

Ser Trp Ser Trp Lys Lys Gln Ala Met Ser Ile Arg Thr Val Leu Trp
115 120 125

His Pro Thr Gly
130

<210> 962
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 169; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004158.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485454"

<400> 962
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 963
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 170; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC004231.7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459812"

<400> 963

```
Met Ser Tyr Ser Cys Cys Leu Pro Ser Leu Gly Cys Arg Thr Ser Cys
1               5                   10                  15

Ser Ser Arg Pro Cys Val Pro Pro Ser Cys His Gly Tyr Thr Leu Pro
            20                  25                  30

Gly Ala Cys Asn Ile Pro Ala Asn Val Ser Asn Cys Asn Trp Phe Cys
        35                  40                  45

Glu Gly Ser Phe Asn Gly Ser Glu Lys Glu Thr Met Gln Phe Leu Asn
    50                  55                  60

Asp Arg Leu Ala Ser Tyr Leu Glu Lys Val Arg Gln Leu Glu Arg Asp
65                  70                  75                  80

Asn Ala Glu Leu Glu Lys Leu Ile Gln Glu Arg Ser Gln Gln Gln Glu
                85                  90                  95

Pro Leu Leu Cys Pro Ser Tyr Gln Ser Tyr Phe Lys Thr Ile Glu Glu
            100                 105                 110

Leu Gln Gln Lys Ile Leu Cys Ala Lys Ala Glu Asn Ala Arg Leu Val
        115                 120                 125

Val Asn Ile Asp Asn Ala Lys Leu Ala Ser Asp Asp Phe Arg Ser Lys
    130                 135                 140

Tyr Gln Thr Glu Gln Ser Leu Arg Leu Leu Val Glu Ser Asp Ile Asn
145                 150                 155                 160

Ser Ile Arg Arg Ile Leu Asp Glu Leu Thr Leu Cys Lys Ser Asp Leu
                165                 170                 175

Glu Ser Gln Val Glu Ser Leu Arg Glu Glu Leu Ile Cys Leu Lys Lys
            180                 185                 190

Asn His Glu Glu Glu Val Asn Thr Leu Arg Ser Gln Leu Gly Asp Arg
```

195 200 205

Leu Asn Val Glu Val Asp Thr Ala Pro Thr Val Asp Leu Asn Gln Val
210 215 220

Leu Asn Glu Thr Arg Ser Gln Tyr Glu Ala Leu Val Glu Thr Asn Arg
225 230 235 240

Arg Glu Val Glu Gln Trp Phe Ala Thr Gln Thr Glu Glu Leu Asn Lys
245 250 255

Gln Val Val Ser Ser Ser Glu Gln Leu Gln Ser Cys Gln Ala Glu Ile
260 265 270

Ile Glu Leu Arg Arg Thr Val Asn Ala Leu Glu Ile Glu Leu Gln Ala
275 280 285

Gln His Asn Leu Arg Asp Ser Leu Glu Asn Thr Leu Thr Glu Ser Glu
290 295 300

Ala His Tyr Ser Ser Gln Leu Ser Gln Val Gln Ser Leu Ile Thr Asn
305 310 315 320

Val Glu Ser Gln Leu Ala Glu Ile Arg Cys Asp Leu Glu Arg Gln Asn
325 330 335

Gln Glu Tyr Gln Val Leu Leu Asp Val Arg Ala Arg Leu Glu Cys Glu
340 345 350

Ile Asn Thr Tyr Arg Ser Leu Leu Glu Ser Glu Asp Cys Lys Leu Pro
355 360 365

Cys Asn Pro Cys Ala Thr Thr Asn Ala Ser Gly Asn Ser Cys Gly Pro
370 375 380

Cys Gly Thr Ser Gln Lys Gly Cys Cys Asn
385 390

<210> 964
<211> 153
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 171; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004556.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478035"

<400> 964

```
Met Ala Arg Asn Val Val Tyr Pro Leu Tyr Arg Leu Gly Gly Pro Gln
1               5                  10                  15

Leu Arg Val Phe Arg Thr Asn Phe Phe Ile Gln Leu Val Arg Pro Gly
            20                  25                  30

Val Ala Gln Pro Glu Asp Thr Val Gln Phe Arg Ile Pro Met Glu Met
        35                  40                  45

Thr Arg Val Asp Leu Arg Asn Tyr Leu Glu Gly Ile Tyr Asn Val Pro
    50                  55                  60

Val Ala Ala Val Arg Thr Arg Val Gln His Gly Ser Asn Lys Arg Arg
65                  70                  75                  80

Asp His Arg Asn Val Arg Ile Lys Lys Pro Asp Tyr Lys Val Ala Tyr
                85                  90                  95

Val Gln Leu Ala His Gly Gln Thr Phe Thr Phe Pro Asp Leu Phe Pro
            100                 105                 110

Glu Lys Asp Glu Ser Pro Glu Gly Ser Thr Ala Asp Asp Leu Tyr Ser
        115                 120                 125

Met Leu Glu Glu Glu Arg Gln Gln Arg Gln Ser Ser Asp Pro Arg Arg
    130                 135                 140

Gly Gly Val Pro Ser Trp Phe Gly Leu
145                 150
```

<210> 965
<211> 531
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 172; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004754.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471331"

<400> 965
Met Leu Asp His Lys Asp Leu Glu Ala Glu Ile His Pro Leu Lys Asn
1 5 10 15

Glu Glu Arg Lys Ser Gln Glu Asn Leu Gly Asn Pro Ser Lys Asn Glu
20 25 30

Asp Asn Val Lys Ser Ala Pro Pro Gln Ser Arg Leu Ser Arg Cys Arg
35 40 45

Ala Ala Ala Phe Phe Leu Ser Leu Phe Leu Cys Leu Phe Val Val Phe
50 55 60

Val Val Ser Phe Val Ile Pro Cys Pro Asp Arg Pro Ala Ser Gln Arg
65 70 75 80

Met Trp Arg Ile Asp Tyr Ser Ala Ala Val Ile Tyr Asp Phe Leu Ala
85 90 95

Val Asp Asp Ile Asn Gly Asp Arg Ile Gln Asp Val Leu Phe Leu Tyr
100 105 110

Lys Asn Thr Asn Ser Ser Asn Asn Phe Ser Arg Ser Cys Val Asp Glu
115 120 125

Gly Phe Ser Ser Pro Cys Thr Phe Ala Ala Ala Val Ser Gly Ala Asn
130 135 140

```
Gly Ser Thr Leu Trp Glu Arg Pro Val Ala Gln Asp Val Ala Leu Val
145                 150                 155                 160

Glu Cys Ala Val Pro Gln Pro Arg Gly Ser Glu Ala Pro Ser Ala Cys
                165                 170                 175

Ile Leu Val Gly Arg Pro Ser Ser Phe Ile Ala Val Asn Leu Phe Thr
            180                 185                 190

Gly Glu Thr Leu Trp Asn His Ser Ser Ser Phe Ser Gly Asn Ala Ser
        195                 200                 205

Ile Leu Ser Pro Leu Leu Gln Val Pro Asp Val Asp Gly Asp Gly Ala
    210                 215                 220

Pro Asp Leu Leu Val Leu Thr Gln Glu Arg Glu Glu Val Ser Gly His
225                 230                 235                 240

Leu Tyr Ser Gly Ser Thr Gly His Gln Ile Gly Leu Arg Gly Ser Leu
                245                 250                 255

Gly Val Asp Gly Glu Ser Gly Phe Leu Leu His Val Thr Arg Thr Gly
            260                 265                 270

Ala His Tyr Ile Leu Phe Pro Cys Ala Ser Ser Leu Cys Gly Cys Ser
        275                 280                 285

Val Lys Gly Leu Tyr Glu Lys Val Thr Gly Ser Gly Gly Pro Phe Lys
    290                 295                 300

Ser Asp Pro His Trp Glu Ser Met Leu Asn Ala Thr Thr Arg Arg Met
305                 310                 315                 320

Leu Ser His Ser Ser Gly Ala Val Arg Tyr Leu Met His Val Pro Gly
                325                 330                 335

Asn Ala Gly Ala Asp Val Leu Leu Val Gly Ser Glu Ala Phe Val Leu
            340                 345                 350

Leu Asp Gly Gln Glu Leu Thr Pro Arg Trp Thr Pro Lys Ala Ala His
        355                 360                 365
```

```
Val Leu Arg Lys Pro Ile Phe Gly Arg Tyr Lys Pro Asp Thr Leu Ala
    370                 375                 380

Val Ala Val Glu Asn Gly Thr Gly Thr Asp Arg Gln Ile Leu Phe Leu
385                 390                 395                 400

Asp Leu Gly Thr Gly Ala Val Leu Cys Ser Leu Ala Leu Pro Ser Leu
                405                 410                 415

Pro Gly Gly Pro Leu Ser Ala Ser Leu Pro Thr Ala Asp His Arg Ser
            420                 425                 430

Ala Phe Phe Phe Trp Gly Leu His Glu Leu Gly Ser Thr Ser Glu Thr
        435                 440                 445

Glu Thr Gly Glu Ala Arg His Ser Leu Tyr Met Phe His Pro Thr Leu
    450                 455                 460

Pro Arg Val Leu Leu Glu Leu Ala Asn Val Ser Thr His Ile Val Ala
465                 470                 475                 480

Phe Asp Gly Ser His Trp Ala Thr Ala Glu Arg Leu Leu Asp Gly Ala
                485                 490                 495

Glu Leu Ala Pro Arg Pro Ala Cys Pro Arg Leu Val Thr Gly Val Trp
            500                 505                 510

Glu Ala Ala Arg Leu Cys Ile Leu Leu Pro Gly Ile Arg Trp Leu Ile
        515                 520                 525

Tyr Trp Phe
    530


<210> 966
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 173; "

<220>
<221> source
<223> /note="Gene Symbol:; "
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<220>
<221> source
<223> /note="Gene Name:
AC004813.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485143"

<400> 966
Met Thr Leu Lys Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Val Leu Asn Glu Leu Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 967
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 174; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>

<221> source
<223> /note="Gene Name:
AC004824.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485570"

<400> 967
Thr Gly Ala Arg His Tyr Ala Gln Leu Ile Phe Val Phe Leu Ile Glu
1 5 10 15

Met Gly Phe His Arg Val Gly Gln Ala Gly Leu Lys Leu Leu Thr Ser
20 25 30

Gly Asp Pro Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val
35 40 45

Ser His Cys Ala Arg Pro Gly Gln Phe Ile Ile Leu Arg Tyr Leu
50 55 60

<210> 968
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 175; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004824.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485939"

<400> 968
Thr Gly Ala Arg His Tyr Ala Gln Leu Ile Phe Val Phe Leu Ile Glu
1 5 10 15

Met Gly Phe His Arg Val Gly Gln Ala Gly Leu Lys Leu Leu Thr Ser
20 25 30

Gly Asp Pro Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val

35 40 45

Ser His Cys Ala Arg Pro Gly Gln Phe Ile Ile Leu Arg Tyr Leu
50 55 60

<210> 969
<211> 317
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 176; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004853.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485535"

<400> 969
Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
1 5 10 15

Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
20 25 30

Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
35 40 45

Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
50 55 60

Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
65 70 75 80

Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
85 90 95

Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
100 105 110

```
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
        115                 120                 125

Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
    130                 135                 140

Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
145                 150                 155                 160

Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
                165                 170                 175

Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
            180                 185                 190

Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
        195                 200                 205

Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
    210                 215                 220

Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
225                 230                 235                 240

Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
                245                 250                 255

Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
            260                 265                 270

Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
        275                 280                 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
    290                 295                 300

Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
305                 310                 315
```

<210> 970
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 177; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC004953.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485307"

<400> 970
Met Leu Leu Arg Leu Thr Ser Asn Ser Trp Ala Gln Thr Ile Leu Pro
1 5 10 15

Pro Gln Pro Pro Lys Val Leu Gly Leu Gln Val Pro Gly Asn Ser Trp
20 25 30

Asp Arg Gly Glu Gly Ser Val Gly Ala Gln Val Arg Arg Met Val Asp
35 40 45

Ser Arg Asp Gln Gln Ser Phe Ser Asp Leu Asn Ala Leu Ser Pro Arg
50 55 60

Leu Glu Cys Ser Gly Met Ile Ser Ala His Cys Asn Leu Cys Leu Gln
65 70 75 80

Gly Ser Ser Asp Ser Leu Val Ser Ala Ser Gln
85 90

<210> 971
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 178; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>

<221> source
<223> /note="Gene Name:
AC005042.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486420"

<400> 971
Leu Pro Pro Pro Ser Gln Ser Leu Leu Val Glu Glu Gly
1 5 10

<210> 972
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 179; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC005477.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485077"

<400> 972
Met Leu Ile Ser Lys Ile Asp Val Gln Val Glu Cys Tyr Ile Ile Ser
1 5 10 15

Glu Glu Glu Ala Ser Ser Pro Ser Leu Arg Gly Glu Asn Gly Leu Val
20 25 30

Glu Glu Trp Ser Leu Asn Ser Val Leu Lys Tyr Val Gln Asp Cys Phe
35 40 45

Met Trp Lys Ala Glu Arg Lys Asn Ile Pro Gly Asp Glu Met Phe Gln
50 55 60

Gln Gly His Arg Ala Glu Glu Ser Asn Ser Asn Arg Asn Trp Leu Ala
65 70 75 80

Trp Thr

<210> 973
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 180; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC005480.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485283"

<400> 973
Met Arg Ala Lys Trp Arg Lys Lys Arg Met Cys Ser Leu Lys His Lys
1 5 10 15

Arg Arg Lys Met Arg Gln Arg Ser Lys
20 25

<210> 974
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 181; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC005779.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466282"

<400> 974

```
Ile Val Ala Gly Cys Arg Leu Leu Pro Asp Ile Arg Gly Val Pro Gly
1               5                   10                  15


Thr Glu Pro Glu Lys Asp Pro Gly Pro Arg Ala
            20                  25


<210> 975
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 182; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC005943.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468614"

<400> 975
Met Val Thr Arg Phe Leu Gly Pro Arg Tyr Arg Glu Leu Val Lys Asn
1               5                   10                  15


Trp Val Pro Thr Ala Tyr Thr Trp Gly Ala Val Gly Ala Val Gly Leu
            20                  25                  30


Val Trp Ala Thr Asp Trp Arg Leu Ile Leu Asp Trp Val Pro Tyr Ile
        35                  40                  45


Asn Gly Lys Phe Lys Lys Asp Asn
    50                  55


<210> 976
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 183; "

<220>
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<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006026.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485594"

<400> 976
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Pro Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Ser Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 977
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 184; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006328.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485474"

<400> 977
Met Gly Pro Thr Val Leu Gly Gln Gly Glu Glu Gly Gln Pro Glu Ala
1 5 10 15

Gly Ala Cys Ser Gly Leu Leu Gln Pro Pro Lys Arg Pro Ile Val Phe
20 25 30

Lys Glu Lys Leu Thr Met Lys Thr Asp Ser Leu Met Glu Glu Lys Leu
35 40 45

Glu Cys Ser Leu Trp Cys Cys Leu Ser Asp Pro Ser Ile Pro Gly Arg
50 55 60

Cys Cys Val Leu Glu Arg Arg Ile Val Pro Trp Met Gln Gln Glu Ser
65 70 75 80

Tyr Ser Ser Ser Ser Pro Ile Arg Ser Val Asp Ser Asp Glu Pro Asn
85 90 95

Leu Thr Ser Val Leu Glu Arg Leu Glu Asp Thr Lys Asp Asn Ser Ser
100 105 110

Ser Val Arg Lys Glu Thr Lys Leu Phe Ser Leu Phe Leu Ile Asn Ile
115 120 125

Ile Phe Arg Asn
130

<210> 978
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 185; "

<220>

<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006386.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485436"

<400> 978
Met Arg Ala Lys Trp Arg Lys Lys Arg Thr Leu Arg Leu Lys Arg Gln
1 5 10 15

Arg Arg Lys Met Arg Gln Lys Ser Lys
20 25

<210> 979
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 186; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006445.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485950"

<400> 979
Pro Ala Pro Ala Pro Ala Pro Pro Ala Pro Pro Ala Pro Gly Pro Ala
1 5 10 15

Pro Gly Pro Gly Gly Gly Gly Gly Gly Gly Ala Gly Gly Gly Gly Cys
20 25 30

Gly Cys Gly Leu Val Ala Met Val
35 40

<210> 980

<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 187; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006449.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479002"

<400> 980

Met	Arg	Asp	Val	Gly	Gly	Lys	Arg	Arg	Gly	Leu	His	Pro	Phe	Ile
1				5				10				15		

Pro	Ser	Leu	Gly	Pro	Val	Phe	Lys	Ser	Asn	Leu	Thr	Ala	Thr	Val	Val
			20					25				30			

Gln	Ser	Gly	Glu	Cys	Lys	Arg	Leu	Gly	Lys	Val	Gly	Glu	Gln	Pro	Leu
		35					40					45			

Gly	Asp	Glu	Asn	Pro	Ser	Leu	Trp	Phe	Gly	Leu	Arg	Glu	Gly	Arg	Ser
	50					55				60					

Val	Leu	Gly	Gly	Val	Ser	Trp	Phe	Gln	Cys	Thr	Glu	Ser	Leu	Gly	Pro
65				70					75						80

Leu	Thr	Leu	Gln	His	Gly	Asn	Leu	Gly	Val	Asp	Leu	Leu	Leu	Phe	Pro
				85					90					95	

Ser	Arg	Gln	Lys	Leu	Ser	Phe	Ala	Leu	Ser	Gly	Pro	Ala	Leu	Gly	Lys
			100					105				110			

Gly	Val	Gly	Val	Asn	Glu	Gln	Leu	Phe
		115				120		

<210> 981
<211> 121
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 188; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006449.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485082"

<400> 981
Met Arg Asp Val Gly Gly Lys Arg Arg Arg Gly Leu His Pro Phe Ile
1 5 10 15

Pro Ser Leu Gly Pro Val Phe Lys Ser Asn Leu Thr Ala Thr Val Val
20 25 30

Gln Ser Gly Glu Cys Lys Arg Leu Gly Lys Val Gly Glu Gln Pro Leu
35 40 45

Gly Asp Glu Asn Pro Ser Leu Trp Phe Gly Leu Arg Glu Gly Arg Ser
50 55 60

Val Leu Gly Gly Val Ser Trp Phe Gln Cys Thr Glu Ser Leu Gly Pro
65 70 75 80

Leu Thr Leu Gln His Gly Asn Leu Gly Val Asp Leu Leu Leu Phe Pro
85 90 95

Ser Arg Gln Lys Leu Ser Phe Ala Leu Ser Gly Pro Ala Leu Gly Lys
100 105 110

Gly Val Gly Val Asn Glu Gln Leu Phe
115 120

<210> 982
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 189; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006486.9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470087"

<400> 982

```
Met Lys Thr Pro Ala Asp Thr Gly Asp Ser Gly Lys Val Thr Thr Val
1               5                   10                  15

Val Ala Thr Leu Gly Gln Gly Pro Glu Arg Ser Gln Glu Val Ala Tyr
            20                  25                  30

Thr Asp Ile Lys Val Ile Gly Asn Gly Ser Phe Gly Val Val Tyr Gln
        35                  40                  45

Ala Arg Leu Ala Glu Thr Arg Glu Leu Val Ala Ile Lys Lys Val Leu
    50                  55                  60

Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met Arg Lys Leu
65                  70                  75                  80

Asp His Cys Asn Ile Val Arg Leu Arg Tyr Phe Phe Tyr Ser Ser Gly
                85                  90                  95

Glu Lys Lys Asp Glu Leu Tyr Leu Asn Leu Val Leu Glu Tyr Val Pro
            100                 105                 110

Glu Thr Val Tyr Arg Val Ala Arg His Phe Thr Lys Ala Lys Leu Thr
        115                 120                 125

Ile Pro Ile Leu Tyr Val Lys Val Tyr Met Tyr Gln Leu Phe Arg Ser
    130                 135                 140

Leu Ala Tyr Ile His Ser Gln Gly Val Cys His Arg Asp Ile Lys Pro
145                 150                 155                 160
```

Gln Asn Leu Leu Val Asp Pro
165

<210> 983
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 190; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006538.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467958"

<400> 983
Met Val Lys Leu Leu Val Ala Lys Ile Leu Cys Met Val Gly Val Phe
1 5 10 15

Phe Phe Met Leu Leu Gly Ser Leu Leu Pro Val Lys Ile Ile Glu Thr
20 25 30

Asp Phe Glu Lys Ala His Arg Ser Lys Lys Ile Leu Ser Leu Cys Asn
35 40 45

Thr Phe Gly Gly Gly Val Phe Leu Ala Thr Cys Phe Asn Ala Leu Leu
50 55 60

Pro Ala Val Arg Glu Lys Ala Arg Ser Gly Val Leu Ala Ala Gly Thr
65 70 75 80

Ser Pro Pro Gly Pro Gly Arg Pro Pro Ala Ala Gly Lys Met Pro Glu
85 90 95

Gln Ser Asn Asp Tyr Arg Val Val Val
100 105

<210> 984

<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 191; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC006994.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485225"

<400> 984
Met Pro Val Ile Leu Leu Leu Thr Tyr Phe Arg His His Phe Cys Pro
1 5 10 15

Phe Pro Leu Pro Glu Arg Asn Ser Val Leu Val Phe Leu Leu Pro Leu
20 25 30

Leu Thr Phe Tyr Asn Ser Ile Tyr Gly Val Leu Asn Cys Gly Pro Pro
35 40 45

Lys Ile Cys Pro Ser Leu Asn Pro Gly Ala Tyr Lys Cys Asp Leu Ile
50 55 60

Trp Glu Lys Ser Leu Thr Asp Glu Ile Lys Leu Lys Ile Leu Pro Trp
65 70 75 80

Ile Asn Gln Val Asp Ala Lys Ser Asn Lys Lys Val Ser Val Gln Glu
85 90 95

Glu Lys Arg Arg Ile Thr Glu Lys Lys Ala Met
100 105

<210> 985
<211> 197
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 192; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC007040.11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475641"

<400> 985

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Met Trp Phe Met Tyr Leu Leu Ser Trp Leu Ser Leu Phe Ile Gln Val
1               5                  10                  15

Ala Phe Ile Thr Leu Ala Val Ala Ala Gly Leu Tyr Tyr Leu Ala Glu
            20                  25                  30

Leu Ile Glu Glu Tyr Thr Val Ala Thr Ser Arg Ile Ile Lys Tyr Met
        35                  40                  45

Ile Trp Phe Ser Thr Ala Val Leu Ile Gly Leu Tyr Val Phe Glu Arg
    50                  55                  60

Phe Pro Thr Ser Met Ile Gly Val Gly Leu Phe Thr Asn Leu Val Tyr
65                  70                  75                  80

Phe Gly Leu Leu Gln Thr Phe Pro Phe Ile Met Leu Thr Ser Pro Asn
                85                  90                  95

Phe Ile Leu Ser Cys Gly Leu Val Val Val Asn His Tyr Leu Ala Phe
            100                 105                 110

Gln Phe Phe Ala Glu Glu Tyr Tyr Pro Phe Ser Glu Val Leu Ala Tyr
        115                 120                 125

Phe Thr Phe Cys Leu Trp Ile Ile Pro Phe Ala Phe Phe Val Ser Leu
    130                 135                 140

Ser Ala Gly Glu Asn Val Leu Pro Ser Thr Met Gln Pro Gly Gly Leu
145                 150                 155                 160

Gly Leu Gly Arg Ser Thr Gly His Gly Asp Ser Cys Thr Asp Phe Tyr
```

```
                165                 170                 175

Lys Asp Pro Pro Ser Val Thr Thr Ile Trp Lys Thr Pro Gly Leu Glu
            180                 185                 190

Asp Ser Gln Arg Arg
        195


<210> 986
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 192; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC007040.11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475757"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 986
Xaa Met Tyr Leu Leu Ser Trp Leu Ser Leu Phe Ile Gln Val Ala Phe
1               5                   10                  15

Ile Thr Leu Ala Val Ala Ala Gly Leu Tyr Tyr Leu Ala Glu Leu Ile
            20                  25                  30

Glu Glu Tyr Thr Val Ala Thr Ser Arg Ile Ile Lys Tyr Met Ile Trp
        35                  40                  45

Ser


<210> 987
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<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 193; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC007163.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485176"

<400> 987
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Cys Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 988
<211> 429
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 194; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC007325.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481613"

<400> 988
Met Asp Ser Leu Trp Gly Pro Gly Ala Gly Ser His Pro Phe Gly Val
1 5 10 15

His Asn Thr Arg Leu Ser Pro Asp Leu Cys Pro Gly Lys Ile Val Leu
20 25 30

Arg Ala Leu Lys Glu Ser Gly Ala Gly Met Pro Glu Gln Asp Lys Asp
35 40 45

Pro Arg Val Gln Glu Asn Pro Gly Asp Gln Arg Arg Val Pro Glu Val
50 55 60

Thr Gly Asp Ala Pro Ser Ala Phe Arg Pro Leu Arg Asp Asn Gly Gly
65 70 75 80

Leu Ser Pro Phe Val Pro Gly Pro Gly Pro Leu Gln Thr Asp Leu His
85 90 95

Ala Gln Arg Ser Glu Ile Arg Tyr Asn Gln Thr Ser Gln Thr Ser Trp
100 105 110

Thr Ser Ser Cys Thr Asn Arg Asn Ala Ile Ser Ser Ser Tyr Ser Ser
115 120 125

Thr Gly Gly Leu Pro Gly Leu Lys Arg Arg Arg Gly Pro Ala Ser Ser
130 135 140

His Cys Gln Leu Thr Leu Ser Ser Ser Lys Thr Val Ser Glu Asp Arg

```
145                 150                 155                 160

Pro Gln Ala Val Ser Ser Gly His Thr Gln Cys Glu Lys Ala Ala Asp
                165                 170                 175

Ile Ala Pro Gly Gln Thr Leu Thr Leu Arg Asn Asp Ser Ser Thr Ser
            180                 185                 190

Glu Ala Ser Arg Pro Ser Thr His Lys Phe Pro Leu Leu Pro Arg Arg
        195                 200                 205

Arg Gly Glu Pro Leu Met Leu Pro Pro Pro Val Glu Leu Gly Tyr Arg
    210                 215                 220

Val Thr Val Glu Asp Leu Asp Arg Glu Lys Glu Ala Ala Phe Gln Arg
225                 230                 235                 240

Ile Asn Ser Ala Leu Gln Val Glu Asp Lys Ala Ile Ser Asp Cys Arg
                245                 250                 255

Pro Ser Arg Pro Ser His Thr Leu Ser Ser Leu Ala Thr Gly Thr Ser
            260                 265                 270

Gly Leu Pro Ala Val Ser Lys Ala Pro Ser Met Asp Ala Gln Gln Glu
        275                 280                 285

Thr His Lys Ser Gln Asp Cys Leu Gly Leu Leu Ala Pro Leu Ala Ser
    290                 295                 300

Ala Ala Glu Val Pro Ser Thr Ala Pro Val Ser Gly Lys Lys His Arg
305                 310                 315                 320

Pro Pro Gly Pro Leu Phe Ser Ser Ser Asp Pro Leu Pro Ala Thr Ser
                325                 330                 335

Ser His Ser Arg Asp Ser Ala Gln Val Thr Ser Leu Ile Pro Ala Pro
            340                 345                 350

Phe Pro Ala Ala Ser Met Asp Ala Gly Met Gly Arg Thr Arg Pro Gly
        355                 360                 365

Thr Ser Ala Pro Ala Ala Ala Ala Ala Ala Pro Pro Pro Ser Thr Leu
    370                 375                 380
```

```
Asn Pro Thr Leu Gly Ser Leu Leu Glu Trp Met Glu Ala Leu His Ile
385                 390                 395                 400


Ser Gly Pro Gln Pro Gln Leu Gln Gln Val Pro Arg Gly Gln Asn Gln
                405                 410                 415


Arg Ser Gln Thr Ser Arg Thr Ser Ser Cys Pro Lys Arg
            420                 425


<210> 989
<211> 600
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 195; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC007325.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481127"

<400> 989
Met Ala Leu Arg Arg Ala Leu Pro Ala Leu Arg Pro Cys Ile Pro Arg
1               5                   10                  15


Phe Val Pro Leu Ser Thr Ala Pro Ala Ser Arg Glu Gln Pro Ala Ala
            20                  25                  30


Gly Pro Ala Ala Val Pro Gly Gly Gly Ser Ala Thr Ala Val Arg Pro
        35                  40                  45


Pro Val Pro Ala Val Asp Phe Gly Asn Ala Gln Glu Ala Tyr Arg Ser
    50                  55                  60


Arg Arg Thr Trp Glu Leu Ala Arg Ser Leu Leu Val Leu Arg Leu Cys
65                  70                  75                  80
```

```
Ala Trp Pro Ala Leu Leu Ala Arg His Glu Gln Leu Leu Tyr Val Ser
                85                  90                  95

Arg Lys Leu Leu Gly Gln Arg Leu Phe Asn Lys Leu Met Lys Met Thr
            100                 105                 110

Phe Tyr Gly His Phe Val Ala Gly Glu Asp Gln Glu Ser Ile Gln Pro
        115                 120                 125

Leu Leu Arg His Tyr Arg Ala Phe Gly Val Ser Ala Ile Leu Asp Tyr
    130                 135                 140

Gly Val Glu Glu Asp Leu Ser Pro Glu Glu Ala Glu His Lys Glu Met
145                 150                 155                 160

Glu Ser Cys Thr Ser Ala Ala Glu Arg Asp Gly Ser Gly Thr Asn Lys
                165                 170                 175

Arg Asp Lys Gln Tyr Gln Ala His Trp Ala Phe Gly Asp Arg Arg Asn
            180                 185                 190

Gly Val Ile Ser Ala Arg Thr Tyr Phe Tyr Ala Asn Glu Ala Lys Cys
        195                 200                 205

Asp Ser His Met Glu Thr Phe Leu Arg Cys Ile Glu Ala Ser Gly Arg
    210                 215                 220

Val Ser Asp Asp Gly Phe Ile Ala Ile Lys Leu Thr Ala Leu Gly Arg
225                 230                 235                 240

Pro Gln Phe Leu Leu Gln Phe Ser Glu Val Leu Ala Lys Trp Arg Cys
                245                 250                 255

Phe Phe His Gln Met Ala Val Glu Gln Gly Gln Ala Gly Leu Ala Ala
            260                 265                 270

Met Asp Thr Lys Leu Glu Val Ala Val Leu Gln Glu Ser Val Ala Lys
        275                 280                 285

Leu Gly Ile Ala Ser Arg Ala Glu Ile Glu Asp Trp Phe Thr Ala Glu
    290                 295                 300

Thr Leu Gly Val Ser Gly Thr Met Asp Leu Leu Asp Trp Ser Ser Leu
```

```
305                 310                 315                 320

Ile Asp Ser Arg Thr Lys Leu Ser Lys His Leu Val Val Pro Asn Ala
                325                 330                 335

Gln Thr Gly Gln Leu Glu Pro Leu Leu Ser Arg Phe Thr Glu Glu Glu
            340                 345                 350

Glu Leu Gln Met Thr Arg Met Leu Gln Arg Met Asp Val Leu Ala Lys
        355                 360                 365

Lys Ala Thr Glu Met Gly Val Arg Leu Met Val Asp Ala Glu Gln Thr
    370                 375                 380

Tyr Phe Gln Pro Ala Ile Ser Arg Leu Thr Leu Glu Met Gln Arg Lys
385                 390                 395                 400

Phe Asn Val Glu Lys Pro Leu Ile Phe Asn Thr Tyr Gln Cys Tyr Leu
                405                 410                 415

Lys Asp Ala Tyr Asp Asn Val Thr Leu Asp Val Glu Leu Ala Arg Arg
            420                 425                 430

Glu Gly Trp Cys Phe Gly Ala Lys Leu Val Arg Gly Ala Tyr Leu Ala
        435                 440                 445

Gln Glu Arg Ala Arg Ala Ala Glu Ile Gly Tyr Glu Asp Pro Ile Asn
    450                 455                 460

Pro Thr Tyr Glu Ala Thr Asn Ala Met Tyr His Arg Cys Leu Asp Tyr
465                 470                 475                 480

Val Leu Glu Glu Leu Lys His Asn Ala Lys Ala Lys Val Met Val Ala
                485                 490                 495

Ser His Asn Glu Asp Thr Val Arg Phe Ala Leu Arg Arg Met Glu Glu
            500                 505                 510

Leu Gly Leu His Pro Ala Asp His Gln Val Tyr Phe Gly Gln Leu Leu
        515                 520                 525

Gly Met Cys Asp Gln Ile Ser Phe Pro Leu Gly Gln Ala Gly Tyr Pro
    530                 535                 540
```

```
Val Tyr Lys Tyr Val Pro Tyr Gly Pro Val Met Glu Val Leu Pro Tyr
545                 550                 555                 560

Leu Ser Arg Arg Ala Leu Glu Asn Ser Ser Leu Met Lys Gly Thr His
                565                 570                 575

Arg Glu Arg Gln Leu Leu Trp Leu Glu Leu Leu Arg Arg Leu Arg Thr
            580                 585                 590

Gly Asn Leu Phe His Arg Pro Ala
        595                 600


<210> 990
<211> 492
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 195; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC007325.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482462"

<400> 990
Met Lys Met Thr Phe Tyr Gly His Phe Val Ala Gly Glu Asp Gln Glu
1               5                   10                  15

Ser Ile Gln Pro Leu Leu Arg His Tyr Arg Ala Phe Gly Val Ser Ala
            20                  25                  30

Ile Leu Asp Tyr Gly Val Glu Glu Asp Leu Ser Pro Glu Glu Ala Glu
        35                  40                  45

His Lys Glu Met Glu Ser Cys Thr Ser Ala Ala Glu Arg Asp Gly Ser
    50                  55                  60
```

```
Gly Thr Asn Lys Arg Asp Lys Gln Tyr Gln Ala His Trp Ala Phe Gly
65                  70                  75                  80

Asp Arg Arg Asn Gly Val Ile Ser Ala Arg Thr Tyr Phe Tyr Ala Asn
                85                  90                  95

Glu Ala Lys Cys Asp Ser His Met Glu Thr Phe Leu Arg Cys Ile Glu
            100                 105                 110

Ala Ser Gly Arg Val Ser Asp Asp Gly Phe Ile Ala Ile Lys Leu Thr
        115                 120                 125

Ala Leu Gly Arg Pro Gln Phe Leu Leu Gln Phe Ser Glu Val Leu Ala
    130                 135                 140

Lys Trp Arg Cys Phe Phe His Gln Met Ala Val Glu Gln Gly Gln Ala
145                 150                 155                 160

Gly Leu Ala Ala Met Asp Thr Lys Leu Glu Val Ala Val Leu Gln Glu
                165                 170                 175

Ser Val Ala Lys Leu Gly Ile Ala Ser Arg Ala Glu Ile Glu Asp Trp
            180                 185                 190

Phe Thr Ala Glu Thr Leu Gly Val Ser Gly Thr Met Asp Leu Leu Asp
        195                 200                 205

Trp Ser Ser Leu Ile Asp Ser Arg Thr Lys Leu Ser Lys His Leu Val
    210                 215                 220

Val Pro Asn Ala Gln Thr Gly Gln Leu Glu Pro Leu Leu Ser Arg Phe
225                 230                 235                 240

Thr Glu Glu Glu Glu Leu Gln Met Thr Arg Met Leu Gln Arg Met Asp
                245                 250                 255

Val Leu Ala Lys Lys Ala Thr Glu Met Gly Val Arg Leu Met Val Asp
            260                 265                 270

Ala Glu Gln Thr Tyr Phe Gln Pro Ala Ile Ser Arg Leu Thr Leu Glu
        275                 280                 285

Met Gln Arg Lys Phe Asn Val Glu Lys Pro Leu Ile Phe Asn Thr Tyr
```

290 295 300

Gln Cys Tyr Leu Lys Asp Ala Tyr Asp Asn Val Thr Leu Asp Val Glu
305 310 315 320

Leu Ala Arg Arg Glu Gly Trp Cys Phe Gly Ala Lys Leu Val Arg Gly
325 330 335

Ala Tyr Leu Ala Gln Glu Arg Ala Arg Ala Ala Glu Ile Gly Tyr Glu
340 345 350

Asp Pro Ile Asn Pro Thr Tyr Glu Ala Thr Asn Ala Met Tyr His Arg
355 360 365

Cys Leu Asp Tyr Val Leu Glu Glu Leu Lys His Asn Ala Lys Ala Lys
370 375 380

Val Met Val Ala Ser His Asn Glu Asp Thr Val Arg Phe Ala Leu Arg
385 390 395 400

Arg Met Glu Glu Leu Gly Leu His Pro Ala Asp His Gln Val Tyr Phe
405 410 415

Gly Gln Leu Leu Gly Met Cys Asp Gln Ile Ser Phe Pro Leu Gly Gln
420 425 430

Ala Gly Tyr Pro Val Tyr Lys Tyr Val Pro Tyr Gly Pro Val Met Glu
435 440 445

Val Leu Pro Tyr Leu Ser Arg Arg Ala Leu Glu Asn Ser Ser Leu Met
450 455 460

Lys Gly Thr His Arg Glu Arg Gln Leu Leu Trp Leu Glu Leu Leu Arg
465 470 475 480

Arg Leu Arg Thr Gly Asn Leu Phe His Arg Pro Ala
485 490

<210> 991
<211> 220
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 196; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC007325.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482514"

<400> 991

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Met Glu Arg Tyr Ala Gly Ala Leu Glu Glu Val Ala Asp Gly Ala Arg
1               5                  10                  15

Gln Gln Glu Arg His Tyr Gln Leu Leu Ser Ala Leu Gln Ser Leu Val
            20                  25                  30

Lys Glu Leu Pro Ser Ser Phe Gln Gln Arg Leu Ser Tyr Thr Thr Leu
        35                  40                  45

Ser Asp Leu Ala Leu Ala Leu Leu Asp Gly Thr Val Phe Glu Ile Val
    50                  55                  60

Gln Gly Leu Leu Glu Ile Gln His Leu Thr Glu Lys Ser Leu Tyr Asn
65                  70                  75                  80

Gln Arg Leu Arg Leu Gln Asn Glu His Arg Val Leu Arg Gln Ala Leu
                85                  90                  95

Arg Gln Lys His Gln Glu Ala Gln Gln Ala Cys Arg Pro His Asn Leu
            100                 105                 110

Pro Val Leu Gln Ala Ala Gln Gln Arg Glu Leu Glu Ala Val Glu His
        115                 120                 125

Arg Ile Arg Glu Glu Gln Arg Ala Met Asp Gln Lys Ile Val Leu Glu
    130                 135                 140

Leu Asp Arg Lys Val Ala Asp Gln Gln Ser Thr Leu Glu Lys Ala Gly
145                 150                 155                 160
```

```
Val Ala Gly Phe Tyr Val Thr Thr Asn Pro Gln Glu Leu Met Leu Gln
                165                 170                 175

Met Asn Leu Leu Glu Leu Ile Arg Lys Leu Gln Gln Arg Gly Cys Trp
            180                 185                 190

Ala Gly Lys Ala Ala Leu Gly Leu Gly Gly Pro Trp Gln Leu Pro Ala
        195                 200                 205

Ala Gln Cys Asp Gln Lys Gly Ser Pro Val Pro Pro
    210                 215                 220


<210> 992
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 197; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC007326.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485226"

<400> 992
Met Asn Pro Ser Glu Met Gln Arg Lys Gly Pro Pro Arg Arg Trp Tyr
1               5                   10                  15

Leu Gln Val Tyr Pro Thr Ala Pro Lys Arg Gln Arg Pro Ser Arg Thr
            20                  25                  30

Gly His Asp Asp Asp Gly Gly Phe Val Glu Lys Lys Arg Gly Lys Cys
        35                  40                  45

Gly Glu Lys Gln Glu Arg Ser Asp Cys Tyr Cys Val Cys Val Glu Arg
    50                  55                  60

Ser Arg His Arg Arg Leu His Phe Val Met Cys
65                  70                  75
```

<210> 993
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 198; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC007557.5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485284"

<400> 993
Ser Ala Lys Glu Lys Leu Arg Ser Gln Gly Ile Arg Arg Asp Lys Ser
1 5 10 15

Arg Ala Ala Ser Gln Gly Val Arg Lys Gly
20 25

<210> 994
<211> 190
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 199; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC007906.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485088"

<400> 994
Met Ser Leu Pro Ile Phe Val Phe Ser Phe Asn Leu Glu His Val Phe

```
1               5                   10                  15

Val Phe Leu Leu Ser Leu Ser Phe Gly Leu Asp Phe Ile Leu Leu Pro
            20                  25                  30

Phe Phe Ser Ser Phe Pro Ser Thr Glu Ala Val Gly Lys Phe Ser Gly
        35                  40                  45

Leu Ile Thr Arg Gly Ile Leu Arg Ser Pro Arg Ser Phe Ala Phe Ala
    50                  55                  60

Met Ala Ser Asp Ile Ile Arg Leu Ala Phe Ser Cys Leu Leu Ser Asp
65                  70                  75                  80

Ser Thr Phe Phe Leu Cys Phe Phe Ser Asp Met Thr Leu Thr Trp Val
                85                  90                  95

Phe Cys Asn Leu Val Tyr Val Pro Glu Pro Ser Leu Phe Leu Glu Asp
            100                 105                 110

Gly Gly Leu Pro Leu Gly Leu Phe Thr Glu Asp Ile Phe Gly Val Arg
        115                 120                 125

Gln Arg Leu Ala Leu Cys Phe Phe Thr Thr Pro Gly Ser Ala Gln Glu
    130                 135                 140

Lys Ser Ile Glu Arg Arg Phe Leu Asn Gly Leu Phe Ser Lys Leu Gln
145                 150                 155                 160

Pro Arg Asp Ala Gln Pro Ser Thr Asn Thr His Phe Asp Leu Ser Thr
                165                 170                 175

His Phe Cys Leu Gly Lys Phe Ile Ser Thr Val His Pro Ile
            180                 185                 190


<210> 995
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 200; "

<220>
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<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008074.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485379"

<400> 995

Met	Glu	Ala	Ile	Phe	Ser	Ala	Ala	Glu	Ser	Gly	Phe	Ser	Gly	Ser	Leu
1				5				10					15		

Val	Gly	Ser	Asn	Ile	Pro	Asn	Pro	Ala	Ala	Tyr	Met	Gly	Thr	Ile	Thr
		20					25					30			

Gly	Cys	Phe	Leu	Leu	Pro	Val	Lys	Arg	Met	Phe	Arg	Val	Ser	Ile	Pro
		35					40					45			

Lys	Glu	Asp	Lys	Ser	Phe	Leu	Leu	Leu	Trp	Glu	Pro	Pro	His	Trp	Tyr
	50					55					60				

Leu	Lys	Pro	Cys	Ala	Ser	Trp	Ile	Ser	Cys	Ser	Ser	Val	His	Thr	Ser
65					70					75					80

Ser	Asn	Ser	Pro	Leu	Ser	Gly	Lys	Ala	Ser	Leu	Val	Phe	Ile	Gly	Lys
				85					90					95	

Val	Leu	Val	Ser	Ser	Lys	Cys	Phe	Arg	Glu	Val	Thr	Ser	Ser	Ser	Ala
		100					105					110			

Ser	Gly	Thr	Ser	Met	Glu	Gly	Lys	His	Ala	Ser	Lys	Ile	Arg	Ser	Arg
		115					120					125			

Arg	Phe	Lys	Lys	Leu	Val	Asn	Thr
	130				135		

<210> 996
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 201; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008522.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485146"

<400> 996

```
Met Ala Leu Ser Val Gly Ser Leu Gln Cys Val Ala Arg Pro Gly Leu
1               5                   10                  15

His Gln Gly Gly Ala Arg Gln Ala Val Ser Gln Asp Gly Arg His Leu
            20                  25                  30

Ala Leu Pro Val Ile Asp Ala Phe Thr Gln Gly Ala Ala Val His Ala
        35                  40                  45

Gln Leu Gln Val Leu Ala Leu Leu Val Gly His Gly Gln Val Phe Arg
    50                  55                  60

His Thr Asp Gly Lys Gly Gln Val Ala Thr His Leu Pro His Lys His
65                  70                  75                  80

Cys Gly Pro Tyr Ile Ala Gly Val His Leu His Ile Val Ala Thr Leu
                85                  90                  95

Pro Phe His Asp Thr Gln Ala Leu Gly Ile Ala Val Pro Thr Thr Gly
            100                 105                 110

Gly Ala Ile His Lys Gly Gly Arg Gln Val Ile Cys His Ser Leu Val
        115                 120                 125

Asp Phe Leu Ile Cys Thr Leu Met Val Gly Phe Glu Asp Asn Ser Asp
    130                 135                 140

Leu Trp Glu Gly Ala Cys Thr Arg Phe Asn Arg Met Gly Arg Lys Gln
145                 150                 155                 160

Asn Gly Val Thr Leu Cys Ser Lys Ser Ser Pro Pro Phe
                165                 170
```

<210> 997
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 202; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008622.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485124"

<400> 997
Glu Ser Arg Gly Gly Pro Val Arg Ile Ala Gly Ile Thr Gly Val Cys
1 5 10 15

<210> 998
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 203; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008641.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485568"

<400> 998
Met Ser Arg Leu Val Arg Gly Ser Ser Leu Leu Thr Tyr Leu Val Val
1 5 10 15

Ala Leu Val Leu Gln Ser Arg

20

<210> 999
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 204; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008686.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485049"

<400> 999
Trp Leu Thr Pro Val Ile Pro Ala Leu Gly Glu Ala Glu Val Gly Gly
1 5 10 15

Leu Leu Glu Ser Arg Ser Ser Arg Arg Ser Cys Ala Met Ile Ala Pro
20 25 30

Leu His Ser Ser Leu Gly Asp Arg Ala Arg Pro Arg Leu Lys Lys Lys
35 40 45

Lys Lys Lys Lys Lys Arg Lys Lys Arg Ser Leu Ile Leu Arg Pro Cys
50 55 60

Leu Thr Leu Ser Pro Arg Leu Thr Cys Asn Gly Thr Ile Leu Ala His
65 70 75 80

Cys Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser
85 90 95

Gln Val Ala Gly Ile Thr Gly Thr His His His Thr Arg Leu Ile Phe
100 105 110

Val Phe Leu Val Glu Ser Pro Cys Trp Ser Ala Ile Val Ser Ser Ala
115 120 125

<210> 1000
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 205; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008759.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485338"

<400> 1000
Lys Lys Ile Leu Gly Arg Ala Gln Trp Leu Met Pro Val Ile Pro Ala
1 5 10 15

Leu Trp Glu Ala Glu Gly Leu Ala Leu Ser Pro Arg Leu Glu Cys
20 25 30

<210> 1001
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 206; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC008810.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485645"

<400> 1001
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

```
His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
            20                  25                  30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
        35                  40                  45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
    50                  55                  60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65                  70                  75                  80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
                85                  90                  95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
            100                 105                 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
        115                 120


<210> 1002
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 207; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC008914.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485310"

<400> 1002
Arg Cys Ala Trp Ala Thr Arg Ala Lys Leu His Leu Lys Lys Lys Lys
1               5                   10                  15
```

Lys Lys Thr Gln Lys Thr Asn Lys
20

<210> 1003
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 208; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009022.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485261"

<400> 1003
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 1004
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 209; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009060.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485576"

<400> 1004

Leu	Val	Met	Thr	Leu	Asn	Glu	His	Ala	Ala	Phe	Lys	His	Leu	Phe	Asn
1				5				10					15		

Lys	Ala	His	Leu	Ala	Pro	Pro	Leu	Ile	His	Leu	Thr	Leu	Ser	Gly	His
		20					25					30			

Ser	Thr	Cys	Phe	Arg	Glu	His	Arg	Val	Gly	Gly	Lys	Val	Thr	Asp	Gln
		35					40					45			

Gln	Asp	Pro	Lys	Ala	Glu	Glu	Phe	Phe	Leu	Val	Gln	Asn	Lys	Met	Lys
	50					55					60				

Ser	Leu	Pro	Cys	Leu	Leu	Leu	Ser	Thr	Gln	Thr	Arg	Gln	Pro	Ser	Asp
65				70					75					80	

Phe	Ser	Ile	Phe	Ser	Pro	Pro	Phe	Pro	Pro	Phe	Tyr	Ser	Thr	Lys	Pro
				85					90					95	

Pro	Leu	Ser	Ser	Trp	Pro	Val	Leu	Asn	Glu	Leu	Leu	Gly	Thr	Pro	Pro
			100					105					110		

Arg	Arg	Gly	Gly	Gly	Gln	Ala	Gly	Gly	Leu	Leu	Thr	Ser	Gln		
		115					120					125			

<210> 1005
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 210; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009060.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485574"

<400> 1005
Met Val Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn
1 5 10 15

Lys Ala His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His
20 25 30

Ser Thr Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Ile Asp Gln
35 40 45

Gln Asp Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys
50 55 60

Ser Leu Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp
65 70 75 80

Phe Ser Ile Phe Ser Pro Pro Phe Pro Leu Phe Tyr Ser Thr Lys Pro
85 90 95

Pro Leu Ser Ser Trp Pro Val Leu Asn Glu Leu Leu Gly Thr Pro Pro
100 105 110

Arg Arg Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120 125

<210> 1006
<211> 178

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 211; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009065.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485405"

<400> 1006

Glu	Leu	Ser	Ser	Gln	Lys	Thr	Gly	Gly	Asn	Leu	Asp	Arg	His	Thr	Ala
1				5				10						15	
Ser	Lys	Pro	Thr	Ala	Leu	Leu	Gln	Pro	Gly	Pro	Gly	Trp	Gln	Arg	Gly
			20					25					30		
Ala	Ala	Cys	Cys	Leu	Gln	Ile	Leu	Pro	Glu	Ser	Arg	Val	Cys	Phe	Pro
		35					40					45			
Thr	Gly	Leu	Pro	Leu	Ala	Arg	Lys	Val	Thr	Lys	Leu	Ser	Trp	Val	Gly
	50					55					60				
Tyr	Lys	Leu	Gln	Gly	Arg	Glu	Leu	Gln	Trp	Pro	Val	Tyr	Arg	Glu	Glu
65					70					75					80
Leu	Glu	Leu	Glu	Arg	Leu	Leu	Trp	Arg	Arg	Arg	Pro	Gly	Asp	Arg	Asp
				85					90					95	
Leu	Arg	Arg	Thr	Gly	Asp	Leu	Arg	Leu	Gly	Glu	Arg	Asp	Leu	Leu	Leu
			100					105					110		
Ile	Arg	Gly	Gly	Asp	Leu	Arg	His	Ile	Gly	Gly	Gly	Gly	Asn	Ile	Leu
		115					120					125			
Leu	Gly	Gly	Leu	Asn	Leu	Leu	Gly	Gly	Gly	Leu	Gly	Gln	Gly	Ala	Ser
	130					135					140				

```
Thr Ala Val Ala Val Ile Ser Trp Pro Ser Ile Cys Pro Pro Pro Ser
145                 150                 155                 160


Met Cys Phe Ser Ala Phe Ser Ala Ser Ser Gly Phe Ser Asn Ser Thr
                165                 170                 175


Tyr Ala



<210> 1007
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 212; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC009121.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485751"

<400> 1007
Ser Cys Ser Ala Ser Thr Leu Ser Gly Gly Asp Leu Gly Ser Arg Thr
1               5                   10                  15


Pro Ala Gly Pro Pro Glu Asn Glu Ser Ala
            20                  25


<210> 1008
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 213; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
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<221> source
<223> /note="Gene Name:
AC009133.22; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404873"

<400> 1008
Met Asp Ala Glu Gly Leu Ala Leu Leu Leu Pro Pro Val Thr Leu Ala
1 5 10 15

Ala Leu Val Asp Ser Trp Leu Arg Glu Asp Cys Pro Gly Leu Asn Tyr
20 25 30

Ala Ala Leu Val Ser Gly Ala Gly Pro Ser Gln Ala Ala Leu Trp Ala
35 40 45

Lys Ser Pro Gly Val Leu Ala Gly Gln Pro Phe Phe Asp Ala Ile Phe
50 55 60

Thr Gln Leu Asn Cys Gln Val Ser Trp Phe Leu Pro Glu Gly Ser Lys
65 70 75 80

Leu Val Pro Val Ala Arg Val Ala Glu Val Arg Gly Pro Ala His Cys
85 90 95

Leu Leu Leu Gly Glu Arg Val Ala Leu Asn Thr Leu Ala Arg Cys Ser
100 105 110

Gly Ile Ala Ser Ala Ala Ala Ala Ala Val Glu Ala Ala Arg Gly Ala
115 120 125

Gly Trp Thr Gly His Val Ala Gly Thr Arg Lys Thr Thr Pro Gly Phe
130 135 140

Arg Leu Val Glu Lys Tyr Gly Leu Leu Val Gly Gly Ala Ala Ser His
145 150 155 160

Arg Tyr Asp Leu

<210> 1009
<211> 359
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 214; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009133.23; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000476774"

<400> 1009
Met Ala Ala Ser Ser Ser Glu Ile Ser Glu Met Lys Gly Val Glu Glu
1 5 10 15

Ser Pro Lys Val Pro Gly Glu Gly Pro Gly His Ser Glu Ala Glu Thr
20 25 30

Gly Pro Pro Gln Val Leu Ala Gly Val Pro Asp Gln Pro Glu Ala Pro
35 40 45

Gln Pro Gly Pro Asn Thr Thr Ala Ala Pro Val Asp Ser Gly Pro Lys
50 55 60

Ala Gly Leu Ala Pro Glu Thr Thr Glu Thr Pro Ala Gly Ala Ser Glu
65 70 75 80

Thr Ala Gln Ala Thr Asp Leu Ser Leu Ser Pro Gly Gly Glu Ser Lys
85 90 95

Ala Asn Cys Ser Pro Glu Asp Pro Cys Gln Glu Thr Val Ser Lys Pro
100 105 110

Glu Val Ser Lys Glu Ala Thr Ala Asp Gln Gly Ser Arg Leu Glu Ser
115 120 125

Ala Ala Pro Pro Glu Pro Ala Pro Glu Pro Ala Pro Gln Pro Asp Pro
130 135 140

Arg Pro Asp Ser Gln Pro Thr Pro Lys Pro Ala Leu Gln Pro Glu Leu
145 150 155 160

```
Pro Thr Gln Glu Asp Pro Thr Pro Glu Ile Leu Ser Glu Ser Val Gly
                165                 170                 175

Glu Lys Gln Glu Asn Gly Ala Val Val Pro Leu Gln Ala Gly Asp Gly
            180                 185                 190

Glu Glu Gly Pro Ala Pro Glu Pro His Ser Pro Pro Ser Lys Lys Ser
        195                 200                 205

Pro Pro Ala Asn Gly Ala Pro Pro Arg Val Leu Gln Gln Leu Val Glu
    210                 215                 220

Glu Asp Arg Met Arg Arg Ala His Ser Gly His Pro Gly Ser Pro Arg
225                 230                 235                 240

Gly Ser Leu Ser Arg His Pro Ser Ser Gln Leu Ala Gly Pro Gly Val
                245                 250                 255

Glu Gly Gly Glu Gly Thr Gln Lys Pro Arg Asp Tyr Ile Ile Leu Ala
            260                 265                 270

Ile Leu Ser Cys Phe Cys Pro Met Trp Pro Val Asn Ile Val Ala Phe
        275                 280                 285

Ala Tyr Ala Val Met Pro Ala Ala Gly Gly Arg Gly Arg Gly Pro Ala
    290                 295                 300

Ser Gly Pro Gly Ser Gln Ala Leu Lys His Arg Gly Ala Gly Gly Gly
305                 310                 315                 320

Ser Pro His His His Arg Leu Leu Arg His Gln Leu Arg Arg Val Pro
                325                 330                 335

Ala Leu Val Ala Tyr Val Pro Cys Ser Gly Pro Trp Arg His Cys Gly
            340                 345                 350

Gln Tyr Gly Gly Ala Ser Val
        355
```

<210> 1010
<211> 123
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 215; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009286.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487241"

<400> 1010
Met Ala Trp Thr Pro Leu Leu Leu Leu Leu Leu Ser His Cys Thr Gly
1 5 10 15

Ser Leu Ser Gln Pro Val Leu Thr Gln Pro Thr Ser Leu Ser Ala Ser
20 25 30

Pro Gly Ala Ser Ala Arg Phe Thr Cys Thr Leu Arg Ser Gly Ile Asn
35 40 45

Val Gly Thr Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Leu
50 55 60

Pro Arg Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly
65 70 75 80

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Thr Asn
85 90 95

Ala Gly Leu Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp
100 105 110

Tyr Tyr Cys Ala Ile Trp Tyr Ser Ser Thr Ser
115 120

<210> 1011
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 216; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009336.19; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424734"

<400> 1011

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Met Val Met Ser Ser Tyr Met Val Asn Ser Lys Tyr Val Asp Pro Lys
1               5                  10                  15

Phe Pro Pro Cys Glu Glu Tyr Leu Gln Gly Gly Tyr Leu Gly Glu Gln
            20                  25                  30

Gly Ala Asp Tyr Tyr Gly Gly Gly Ala Gln Gly Ala Asp Phe Gln Pro
        35                  40                  45

Pro Gly Leu Tyr Pro Arg Pro Asp Phe Gly Glu Gln Pro Phe Gly Gly
    50                  55                  60

Ser Gly Pro Gly Pro Gly Ser Ala Leu Pro Ala Arg Gly His Gly Gln
65                  70                  75                  80

Glu Pro Gly Gly Pro Gly Gly His Tyr Ala Ala Pro Gly Glu Pro Cys
                85                  90                  95

Pro Ala Pro Pro Ala Pro Pro Pro Ala Pro Leu Pro Gly Ala Arg Ala
            100                 105                 110

Tyr Ser Gln Ser Asp Pro Lys Gln Pro Pro Ser Gly Thr Ala Leu Lys
        115                 120                 125

Gln Pro Ala Val Val Tyr Pro Trp Met Lys Lys Val His Val Asn Ser
    130                 135                 140

Gly Ile
145
```

<210> 1012
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 217; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009491.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485137"

<400> 1012
Met His Leu His Arg His Leu Leu Cys Gln Ala Thr Gly Thr Cys Gly
1 5 10 15

Asn Gly Asp Ile His Ala Val Ser Val Val Cys Ser His Arg Arg Arg
20 25 30

Cys Leu Asp Ser Glu Glu Val Thr Glu Ile Cys Ser Ser Asp Phe Ile
35 40 45

Pro Gly Arg Asp Cys Val Gly Glu Ser Gly Pro Met Ile Gly Met Leu
50 55 60

Ser Arg Ser Gln Gly Leu Leu Gly Lys Gly Arg Gln His Asp Lys Gly
65 70 75 80

Lys Ser Lys Val Glu Gln Ser Ser Tyr Thr Leu Asn Trp Pro Pro Met
85 90 95

Gly Ala Gly Glu Gly Ala Gly Pro His Pro Pro Leu Thr Ser Leu Tyr
100 105 110

Pro His Leu Tyr Leu Met Ile Trp Leu Leu Lys Leu Ser Val Leu Lys
115 120 125

<210> 1013

<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 218; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
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<223> /note="Gene Name:
AC009491.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485446"

<400> 1013

Met	His	Leu	Leu	Gly	Gly	Leu	Leu	Leu	Gln	Gln	Ser
1				5				10			

Ala	Glu	Thr	Trp	Pro	Leu	Leu	Ala	Val	Ser	Val	Val
		15				20				25	

Gly	Ser	His	Trp	Arg	Arg	Arg	Cys	Phe	Asp	Cys	Glu
		30				35				40	

Val	Ile	Thr	Arg	Asn	Cys	Ser	Ser	Asp	Ser	Ile	Pro
		45				50				55	

Glu	Arg	Gly	Ser	Val	Gln	Glu	Ile	Gly	Pro	Met	Gly
		60				65				70	

Ile	Gly	Ile	Leu	Ser	Val	Ser	Gln	Gly	Leu	Ser	Gln
		75				80				85	

Ile	Gly	Arg	Lys	His	Asp	Lys	Gly	Lys	Ser	Lys	Leu
		90				95				100	

Glu	Lys	Tyr	Ser	His	Thr	Ser	Asn	Trp	Pro	Leu	Thr
		105				110				115	

His	Ala	Gly	Glu	Gly	Val	Gly	Pro	His	Pro	Pro	Leu
		120				125				130	

Thr	Arg	Leu	His	Leu	Gln	Pro	Tyr	Leu	Thr	Phe	Leu
		135				140				145	

Leu	Leu	Ile	Leu	Ser	Val	Pro	Glu				
		150				155					

<210> 1014
<211> 314
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 219; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC009758.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485078"

<400> 1014

```
Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
1               5                  10                  15

Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
            20                  25                  30

Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
        35                  40                  45

Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
    50                  55                  60

Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
65                  70                  75                  80

Pro Gln Ala Leu Ala Ile Phe Trp Phe Arg Ala Gly Asp Ile Ser Leu
                85                  90                  95

Asp Arg Cys Ile Thr Gln Leu Phe Phe Ile His Ser Thr Phe Ile Ser
            100                 105                 110

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
        115                 120                 125

Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
    130                 135                 140

Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
```

```
145                 150                 155                 160

Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
                165                 170                 175

Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
            180                 185                 190

Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
        195                 200                 205

Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
    210                 215                 220

His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
225                 230                 235                 240

Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
                245                 250                 255

Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
            260                 265                 270

Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
        275                 280                 285

Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
    290                 295                 300

Val Val Gln Phe Leu Phe Ile Lys Gln Lys
305                 310


<210> 1015
<211> 555
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 220; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
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<221> source
<223> /note="Gene Name:
AC009950.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439558"

<400> 1015

```
Met Gly Arg Gly Phe Arg Met Phe Thr Met Thr Arg Ala Met Glu Glu
1               5                  10                  15

Ala Leu Phe Gln His Phe Met His Gln Lys Leu Gly Ile Ala Tyr Ala
            20                  25                  30

Ile His Lys Pro Phe Pro Phe Phe Glu Gly Leu Leu Asp Asn Ser Ile
        35                  40                  45

Ile Thr Lys Arg Met Tyr Met Glu Ser Leu Glu Ala Cys Arg Asn Leu
    50                  55                  60

Ile Pro Val Ser Arg Val Val His Asn Ile Leu Thr Gln Leu Glu Arg
65                  70                  75                  80

Thr Phe Asn Leu Ser Leu Leu Val Thr Leu Phe Ser Gln Ile Asn Leu
                85                  90                  95

Arg Glu Tyr Pro Asn Leu Val Thr Ile Tyr Arg Ser Phe Lys Arg Val
            100                 105                 110

Gly Ala Ser Tyr Glu Trp Gln Ser Arg Asp Thr Pro Ile Leu Leu Glu
        115                 120                 125

Ala Pro Thr Gly Leu Ala Glu Gly Ser Ser Leu His Thr Pro Leu Ala
    130                 135                 140

Leu Pro Pro Pro Gln Pro Pro Gln Pro Ser Cys Ser Pro Cys Ala Pro
145                 150                 155                 160

Arg Val Ser Glu Pro Gly Thr Ser Ser Gln Gln Ser Asp Glu Ile Leu
                165                 170                 175

Ser Glu Ser Pro Ser Pro Ser Asp Pro Val Leu Pro Leu Pro Ala Leu
            180                 185                 190
```

```
Ile Gln Glu Gly Arg Ser Thr Ser Val Thr Asn Asp Lys Leu Thr Ser
        195                 200                 205

Lys Met Asn Ala Glu Glu Asp Ser Glu Glu Met Pro Ser Leu Leu Thr
    210                 215                 220

Ser Thr Val Gln Val Ala Ser Asp Asn Leu Ile Pro Gln Ile Arg Asp
225                 230                 235                 240

Lys Glu Asp Pro Gln Glu Met Pro His Ser Pro Leu Gly Ser Met Pro
                245                 250                 255

Glu Ile Arg Asp Asn Ser Pro Glu Pro Asn Asp Pro Glu Glu Pro Gln
            260                 265                 270

Glu Val Ser Ser Thr Pro Ser Asp Lys Lys Gly Lys Lys Arg Lys Arg
        275                 280                 285

Cys Ile Trp Ser Thr Pro Lys Arg Arg His Lys Lys Lys Ser Leu Pro
    290                 295                 300

Gly Gly Thr Ala Ser Ser Arg His Gly Ile Gln Lys Lys Leu Lys Arg
305                 310                 315                 320

Val Asp Gln Val Pro Gln Lys Lys Asp Asp Ser Thr Cys Asn Ser Thr
                325                 330                 335

Val Glu Thr Arg Ala Gln Lys Ala Arg Thr Glu Cys Ala Arg Lys Ser
            340                 345                 350

Arg Ser Glu Glu Ile Ile Asp Gly Thr Ser Glu Met Asn Glu Gly Lys
        355                 360                 365

Arg Ser Gln Lys Thr Pro Ser Thr Pro Arg Arg Val Thr Gln Gly Ala
    370                 375                 380

Ala Ser Pro Gly His Gly Ile Gln Glu Lys Leu Gln Val Val Asp Lys
385                 390                 395                 400

Val Thr Gln Arg Lys Asp Asp Ser Thr Trp Asn Ser Glu Val Met Met
                405                 410                 415

Arg Val Gln Lys Ala Arg Thr Lys Cys Ala Arg Lys Ser Arg Leu Lys
```

```
            420                 425                 430

Glu Lys Lys Lys Glu Lys Asp Ile Cys Ser Ser Ser Lys Arg Arg Phe
        435                 440                 445

Gln Lys Asn Ile His Arg Arg Gly Lys Pro Lys Ser Asp Thr Val Asp
    450                 455                 460

Phe His Cys Ser Lys Leu Pro Val Thr Cys Gly Glu Ala Lys Gly Ile
465                 470                 475                 480

Leu Tyr Lys Lys Lys Met Lys His Gly Ser Ser Val Lys Cys Ile Arg
                485                 490                 495

Asn Glu Asp Gly Thr Trp Leu Thr Pro Asn Glu Phe Glu Val Glu Gly
            500                 505                 510

Lys Gly Arg Asn Ala Lys Asn Trp Lys Arg Asn Ile Arg Cys Glu Gly
        515                 520                 525

Met Thr Leu Gly Glu Leu Leu Lys Ser Gly Leu Leu Leu Cys Pro Pro
    530                 535                 540

Arg Ile Asn Leu Lys Arg Glu Leu Asn Ser Lys
545                 550                 555


<210> 1016
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 221; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC009977.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485119"
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<400> 1016
Lys His Lys Lys Lys Val Ile Glu Arg Trp Ser Leu Ala Leu Leu Pro
1   5   10   15

Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Lys Leu Arg Leu
            20   25   30

Pro

<210> 1017
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 222; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC010184.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485684"

<400> 1017
Arg Ala Ala Ala Pro Ala His Ala Ala Pro Ser Arg Ser Cys Pro Ala
1   5   10   15

Gly Ser Ala Thr Leu Glu Pro
            20

<210> 1018
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 223; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC010287.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485180"

<400> 1018
Met Pro Ile Ile Pro Ser Leu Trp Glu Ala Gly Arg Ser Leu Glu Ala
1 5 10 15

Arg Ser Ser Lys Ile Phe Cys Ile Leu Ile Val Val Val Thr Gln
20 25 30

Leu Tyr Lys Phe Val Lys Ile Gln Arg Thr Ile His Leu Lys Gly Arg
35 40 45

Leu Leu Leu Tyr Glu Val Tyr Leu Ile Asn Asn Gln Pro Lys Asn Leu
50 55 60

Cys Ser His Phe Ser Phe Pro Thr Thr Tyr Ile Lys Lys Glu Arg Leu
65 70 75 80

Trp Leu Gly Pro Val Ala His Thr Tyr Asn Pro Ser Thr Leu Gly Gly
85 90 95

Arg Gly Gly Trp Ile Thr Arg Gly Gln Glu Phe Lys Thr Ser Leu Ala
100 105 110

Asn Met Val Glu Pro Cys Leu Tyr
115 120

<210> 1019
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 224; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC010412.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485147"

<400> 1019
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Ser Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Pro Leu Pro Thr Gln Thr Gln Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Ile Phe Tyr Ser Thr Lys Leu Pro Leu
85 90 95

Ser Ser Trp Pro Val Leu Asn Glu Leu Leu Ser Thr Pro Pro Arg Arg
100 105 110

Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 1020
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 225; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC010547.9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463741"

<400> 1020
Met Ala Ala Met Pro Leu Lys Ala Gln Tyr Gln Glu Met Val Thr Phe
1   5   10   15

Glu Asp Val Ala Val His Phe Thr Lys Thr Glu Trp Thr Gly Leu Ser
            20   25   30

Pro Ala Gln Arg Ala Leu Tyr Arg Ser Val Met Leu Glu Asn Phe Gly
        35   40   45

Asn Leu Thr Ala Leu Gly Tyr Pro Val Pro Lys Pro Ala Leu Ile Ser
    50   55   60

Leu Leu Glu Arg Gly Asp Met Ala Trp Gly Leu Glu Ala Gln Asp Asp
65   70   75   80

Pro Pro Ala Glu Arg Thr Lys Asn Val Cys Lys Val Ile Leu
                85   90

<210> 1021
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 226; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC010642.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467774"

<400> 1021
Met Asp Pro Glu Asp Glu Gly Val Ala Gly Val Met Ser Val Gly Pro
1   5   10   15

```
Pro Ala Ala Arg Leu Gln Val Thr Ile Thr Thr Ile Thr Thr Ala Ala
            20                  25                  30

Gly Ser Gly Gln Ala Ser Pro Ala Gln Thr Asp Pro Phe Thr Ser Arg
        35                  40                  45

Arg Asp Glu Ser Gly Thr Ala Val Asn Ala Leu Asp Thr Trp Gly Asn
    50                  55                  60

Ser Asp Ala Gly Arg Gly Val Val Thr Val Leu Ala Gly Gln Arg Gly
65                  70                  75                  80

Gly Arg Asp Ser Asn Gln Ala Pro Gly Pro Arg Met Arg Met Leu His
                85                  90                  95

Ala Ala Leu Ser Ser Pro Gly Leu Gly Ser Val Ile Pro Glu Arg Ile
            100                 105                 110

Glu Gln Ala His Leu Leu Arg Ser Ala Pro Pro Arg Arg His Pro Cys
        115                 120                 125

Pro Phe Gln Glu Gly Leu Ser Ser Cys
    130                 135


<210> 1022
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 227; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC010646.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000473056"

<400> 1022
Met Arg Lys Glu Ala Val Gln Arg Gly Arg Ile Pro His Ser Leu Pro
1               5                   10                  15
```

Gly Ala Val Ala Ala Ser Ser Gly Ser Pro Pro Gly Ser Ala Leu Ala
            20   25   30

Ala Val Ala Ser Gly Gly Asp Leu Phe Pro Gly Gln Pro Val
        35   40   45

<210> 1023
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 228; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC010655.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485293"

<400> 1023
Ser His Leu Phe Asn Asn Tyr Leu Leu Asn Val Lys Met Thr Leu Gly
1   5   10   15

Ser Val Phe Ala Ser Val
            20

<210> 1024
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 229; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:

AC011043.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482855"

<400> 1024
Met Tyr Ser Phe Pro Thr Thr Val Val Glu Glu Arg Leu Ser Leu Ser
1 5 10 15

Ile His Leu Val Thr Phe Pro Thr Val Ser Arg Glu Ile Leu Leu Glu
20 25 30

Ile Thr Ser Gln Thr Asn Lys Lys Gln Ser Trp Glu Met Tyr Asp Thr
35 40 45

His Ser Ala Lys Glu Ile Gly Ile Ile Ala Gly Glu Gln Ile Gln Lys
50 55 60

Thr Gln Ala Val Pro Tyr Ile Cys Phe Leu Leu Arg His Gln Leu Ile
65 70 75 80

Ser Gln Ser Ser Gln Val Arg Val Glu Ala Met Tyr Ser Leu Leu Phe
85 90 95

Leu Gly Thr Leu Leu Gln Gly Gly Lys Gly Gln Glu Val Leu Leu Glu
100 105 110

Asp Ala Leu Arg Ala Arg Ala Pro
115 120

<210> 1025
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 230; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC011155.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485198"

<400> 1025
Gly Lys Asp Ala Lys Glu Lys Lys Gln Leu Thr Tyr Asn Ser Ser Ser
1   5   10   15

Tyr Ile Ser Trp Thr Val Gly Met Tyr His Val Phe His Leu His Cys
            20   25   30

Thr Cys Leu Arg His Arg Ile Ser Leu Arg
        35   40

<210> 1026
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 231; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC011295.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478066"

<400> 1026
Met Gly Pro Ala Val Leu Gly Gln Gly Glu Glu Gly Gln Pro Glu Ala
1   5   10   15

Arg Ala Cys Ser Gly Leu Leu Gln Pro Pro Lys Arg Pro Ile Val Phe
            20   25   30

Lys Glu Lys Leu Thr Met Lys Thr Asp Ser Leu Met Glu Glu Lys Leu
        35   40   45

Glu Cys Ser Leu Trp Cys Cys Leu Ser Asp Pro Ser Thr Pro Gly Arg
    50   55   60

Cys Cys Val Leu Glu Arg Arg Ile Val Pro Trp Met Gln Gln Glu Ser

65 70 75 80

Tyr Ser Ser Ser Ser Pro Ile Trp Ser Val Asp Ser Asp Glu Pro Asn
85 90 95

Leu Thr Ser Val Leu Glu Arg Leu Glu Asp Thr Lys Asp Asn Ser Ser
100 105 110

Val Arg Lys Glu Thr Lys Leu Phe Ser Leu Phe Leu Met Asn Ile Ile
115 120 125

Phe Arg Asn
130

<210> 1027
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 232; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC011380.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487555"

<400> 1027
Asn Ser Gln Ser Gly Thr Arg Glu Ala Glu Thr Gly Arg Arg Lys Lys
1 5 10 15

<210> 1028
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 233; "

<220>
<221> source

<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC011513.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469421"

<400> 1028
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
130 135 140

Pro Lys Pro Ser Ile Ser Ser Asn
145 150

<210> 1029
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 233; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC011513.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469926"

<400> 1029
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly
50 55 60

Tyr Ser Trp
65

<210> 1030
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 234; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC011530.4; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000468837"

<400> 1030
Pro Leu Val Cys Lys Lys Ile Ala Gln Glu Arg Leu Thr Val Leu Leu
1   5   10   15

Phe Leu Glu Asp Cys Ile Ile Thr Ala Cys Gln Glu Gly Leu Ile Cys
            20   25   30

Thr Trp Ala Arg Pro Gly Lys Ala Phe Thr Asp Glu Glu Thr Glu Ala
        35   40   45

Gln Thr Gly Glu Gly Ser Trp Pro Arg Ser Pro Ser Lys Ser Val Val
    50   55   60

Glu Glu Leu Gly Ala Ser Glu Leu Ala Gln Asp Lys Tyr Val Ala Asp
65   70   75   80

Phe Leu Gln Trp Ala Glu Pro Ile Val Val Arg Leu Lys Glu Val Arg
                85   90   95

Leu Gln Arg Asp Asp Phe Glu Ile Leu Lys Val Ile Gly Arg Gly Ala
            100   105   110

Phe Ser Glu Val Ala Val Val Lys Met Lys Gln Thr Gly Gln Val Tyr
        115   120   125

Ala Met Lys Ile
    130

<210> 1031
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 234; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC011530.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469741"

<400> 1031
Pro Leu Val Cys Lys Lys Ile Ala Gln Glu Arg Leu Thr Val Leu Leu
1   5   10   15

Phe Leu Glu Asp Cys Ile Ile Thr Ala Cys Gln Glu Gly Leu Ile Cys
            20   25   30

Thr Trp Ala Arg Pro Gly Lys Ala Glu Leu Gly Ala Ser Glu Leu Ala
        35   40   45

Gln Asp Lys Tyr Val Ala Asp Phe Leu Gln Trp Ala Glu Pro Ile Val
    50   55   60

Val Arg Leu Lys Glu Val Arg Leu Gln Arg Asp Asp Phe Glu Ile Leu
65   70   75   80

Lys Val Ile Gly Arg Gly Ala Phe Ser Glu Val Ala Val Val Lys Met
                85   90   95

Lys Gln Thr Gly Gln Val Tyr Ala Met Lys Ile
            100   105

<210> 1032
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 234; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC011530.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471312"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1032
Xaa Gly Val Ala Ala Glu Pro Gly Thr Pro Phe Ser Ile Gly Arg Phe
1 5 10 15

Ala Thr Leu Thr Leu Gln Glu Arg Arg Asp Arg Gly Ala Glu Lys Glu
20 25 30

His Lys Arg Tyr His Ser Leu Gly Asn Ile Ser Arg Gly Gly Ser Gly
35 40 45

Gly Ser Gly Ser Gly Gly Glu Lys Pro Ser Gly Pro Val Pro Arg Ser
50 55 60

Arg Leu Asp Pro Ala Lys Val Leu Gly Thr Ala Leu Cys Pro Arg Ile
65 70 75 80

His Glu Val Pro Leu Leu Glu Pro Leu Val Cys Lys Lys Ile Ala Gln
85 90 95

Glu Arg Leu Thr Val Leu Leu Phe Leu Glu Asp Cys Ile Ile Thr Ala
100 105 110

Cys Gln Glu Gly Leu Ile Cys Thr Trp Ala Arg Pro Gly Lys Ala Arg
115 120 125

Ser Pro Ser Trp
130

<210> 1033
<211> 56
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 234; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC011530.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472333"

<400> 1033
Pro Leu Val Cys Lys Lys Ile Ala Gln Glu Arg Leu Thr Val Leu Leu
1 5 10 15

Phe Leu Glu Asp Cys Ile Ile Thr Ala Cys Gln Glu Gly Leu Ile Cys
20 25 30

Thr Trp Ala Arg Pro Gly Lys Ala Pro Gln Ile Gln Gly Phe Pro Lys
35 40 45

Cys Gly Ser Arg Thr Thr Cys Ile
50 55

<210> 1034
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 235; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC011841.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481644"

<400> 1034
Met Tyr Ser Phe Pro Thr Thr Val Val Glu Glu Arg Leu Ser Leu Ser
1 5 10 15

Ile His Leu Val Thr Phe Pro Thr Val Ser Arg Glu Ile Leu Leu Glu
20 25 30

Ile Thr Ser Gln Thr Asn Lys Lys Gln Ser Trp Glu Met Tyr Asp Thr
35 40 45

```
His Ser Ala Lys Glu Ile Gly Ile Ile Ala Gly Glu Gln Ile Gln Lys
    50                  55                  60

Thr Gln Ala Val Pro Tyr Ile Cys Phe Leu Leu Arg His Gln Leu Ile
65                  70                  75                  80

Ser Gln Ser Ser Gln Val Arg Val Glu Ala Met Tyr Ser Leu Leu Phe
                85                  90                  95

Leu Gly Thr Leu Leu Gln Gly Gly Lys Gly Gln Glu Val Leu Leu Glu
            100                 105                 110

Asp Ala Leu Arg Ala Arg Ala Pro
        115                 120


<210> 1035
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 236; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC012005.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485052"

<400> 1035
Met Arg Ala Lys Trp Arg Lys Lys Arg Thr Leu Arg Leu Lys Arg Gln
1               5                   10                  15

Arg Arg Lys Met Arg Gln Lys Ser Lys
            20                  25


<210> 1036
<211> 132
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 237; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
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<223> /note="Gene Name:
AC012005.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485564"

<400> 1036
Met Gly Pro Thr Val Leu Gly Gln Gly Glu Glu Gly Gln Pro Glu Ala
1 5 10 15

Gly Ala Cys Ser Gly Leu Leu Gln Pro Pro Lys Arg Pro Ile Val Phe
20 25 30

Lys Glu Lys Leu Thr Met Lys Thr Asp Ser Leu Met Glu Glu Lys Leu
35 40 45

Glu Cys Ser Leu Trp Cys Cys Leu Ser Asp Pro Ser Ile Pro Gly Arg
50 55 60

Cys Cys Val Leu Glu Arg Arg Ile Val Pro Trp Met Gln Gln Glu Ser
65 70 75 80

Tyr Ser Ser Ser Ser Pro Ile Arg Ser Val Asp Ser Asp Glu Pro Asn
85 90 95

Leu Thr Ser Val Leu Glu Arg Leu Glu Asp Thr Lys Asp Asn Ser Ser
100 105 110

Ser Val Arg Lys Glu Thr Lys Leu Phe Ser Leu Phe Leu Ile Asn Ile
115 120 125

Ile Phe Arg Asn
130

<210> 1037
<211> 194

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 238; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482274"

<400> 1037
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1 5 10 15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
20 25 30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
35 40 45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
50 55 60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65 70 75 80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
85 90 95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
100 105 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
115 120 125

Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile
130 135 140

```
Pro Ser Phe Ile Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser
145                 150                 155                 160


Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys
                165                 170                 175


Asn Ala Lys Lys Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu
            180                 185                 190


Glu Asp
```

<210> 1038
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 238; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486181"

<400> 1038

```
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1               5                   10                  15


Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20                  25                  30


Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35                  40                  45


Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
    50                  55                  60


Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65                  70                  75                  80
```

```
Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85                  90                  95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100                 105                 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115                 120                 125

Leu Ile Arg Gln Arg His Ile Ser Pro Arg Arg
    130                 135


<210> 1039
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 239; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC012314.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481655"

<400> 1039
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1               5                   10                  15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20                  25                  30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35                  40                  45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
    50                  55                  60
```

```
Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65                  70                  75                  80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85                  90                  95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100                 105                 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115                 120                 125

Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile
    130                 135                 140

Pro Ser Phe Ile Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser
145                 150                 155                 160

Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys
                165                 170                 175

Asn Ala Lys Lys Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu
            180                 185                 190

Glu Asp
```

<210> 1040
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 239; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486047"

<400> 1040
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1   5   10   15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20   25   30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35   40   45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
    50   55   60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65   70   75   80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85   90   95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100   105   110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115   120   125

Leu Ile Arg Gln Arg His Ile Ser Pro Arg Arg
    130   135

<210> 1041
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 240; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC012314.5; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000480135"

<400> 1041
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1 5 10 15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
20 25 30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
35 40 45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
50 55 60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65 70 75 80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
85 90 95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
100 105 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
115 120 125

Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile
130 135 140

Pro Ser Phe Ile Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser
145 150 155 160

Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys
165 170 175

Asn Ala Lys Lys Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu
180 185 190

Glu Asp

<210> 1042

<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 240; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485843"

<400> 1042

Met	Pro	Val	Ala	Arg	Ser	Trp	Val	Cys	Arg	Lys	Thr	Tyr	Val	Thr	Pro
1				5				10						15	
Arg	Arg	Pro	Phe	Glu	Lys	Ser	Arg	Leu	Asp	Gln	Glu	Leu	Lys	Leu	Ile
		20					25					30			
Gly	Glu	Tyr	Gly	Leu	Arg	Asn	Lys	Arg	Glu	Val	Trp	Arg	Val	Lys	Phe
	35					40					45				
Thr	Leu	Ala	Lys	Ile	Arg	Lys	Ala	Ala	Arg	Glu	Leu	Leu	Thr	Leu	Asp
50					55					60					
Glu	Lys	Asp	Pro	Arg	Arg	Leu	Phe	Glu	Gly	Asn	Ala	Leu	Leu	Arg	Arg
65				70					75						80
Leu	Val	Arg	Ile	Gly	Val	Leu	Asp	Glu	Gly	Lys	Met	Lys	Leu	Asp	Tyr
			85					90					95		
Ile	Leu	Gly	Leu	Lys	Ile	Glu	Asp	Phe	Leu	Glu	Arg	Arg	Leu	Gln	Thr
		100					105					110			
Gln	Val	Phe	Lys	Leu	Gly	Leu	Ala	Lys	Ser	Ile	His	His	Ala	Arg	Val
	115					120					125				
Leu	Ile	Arg	Gln	Arg	His	Ile	Ser	Pro	Arg	Arg					
130					135										

<210> 1043
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 241; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478449"

<400> 1043
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1 5 10 15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
20 25 30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
35 40 45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
50 55 60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65 70 75 80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
85 90 95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
100 105 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
115 120 125

Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile

```
    130                 135                 140

Pro Ser Phe Ile Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser
145                 150                 155                 160

Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys
                165                 170                 175

Asn Ala Lys Lys Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu
            180                 185                 190

Glu Asp
```

<210> 1044
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 241; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486598"

<400> 1044

```
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1               5                   10                  15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20                  25                  30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35                  40                  45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
    50                  55                  60
```

```
Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65                  70                  75                  80


Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85                  90                  95


Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100                 105                 110


Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115                 120                 125


Leu Ile Arg Gln Arg His Ile Ser Pro Arg Arg
    130                 135


<210> 1045
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 242; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC012314.7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484394"

<400> 1045
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1               5                   10                  15


Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20                  25                  30


Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35                  40                  45


Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
```

```
    50                  55                  60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65                  70                  75                  80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85                  90                  95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100                 105                 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115                 120                 125

Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile
    130                 135                 140

Pro Ser Phe Ile Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser
145                 150                 155                 160

Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys
                165                 170                 175

Asn Ala Lys Lys Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu
            180                 185                 190

Glu Asp
```

<210> 1046
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 242; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486773"

<400> 1046
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1   5   10   15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20   25   30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35   40   45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
    50   55   60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65   70   75   80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85   90   95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100   105   110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115   120   125

Leu Ile Arg Gln Arg His Ile Ser Pro Arg Arg
    130   135

<210> 1047
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 243; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:

AC012314.9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482023"

<400> 1047

```
Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro
1               5                  10                  15

Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile
            20                  25                  30

Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe
        35                  40                  45

Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp
    50                  55                  60

Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg
65                  70                  75                  80

Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr
                85                  90                  95

Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr
            100                 105                 110

Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val
        115                 120                 125

Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile
    130                 135                 140

Pro Ser Phe Ile Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser
145                 150                 155                 160

Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys
                165                 170                 175

Asn Ala Lys Lys Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu
            180                 185                 190

Glu Asp
```

<210> 1048
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 243; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012314.9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486233"

<400> 1048

Met	Pro	Val	Ala	Arg	Ser	Trp	Val	Cys	Arg	Lys	Thr	Tyr	Val	Thr	Pro
1				5				10						15	
Arg	Arg	Pro	Phe	Glu	Lys	Ser	Arg	Leu	Asp	Gln	Glu	Leu	Lys	Leu	Ile
			20					25					30		
Gly	Glu	Tyr	Gly	Leu	Arg	Asn	Lys	Arg	Glu	Val	Trp	Arg	Val	Lys	Phe
		35					40					45			
Thr	Leu	Ala	Lys	Ile	Arg	Lys	Ala	Ala	Arg	Glu	Leu	Leu	Thr	Leu	Asp
	50					55					60				
Glu	Lys	Asp	Pro	Arg	Arg	Leu	Phe	Glu	Gly	Asn	Ala	Leu	Leu	Arg	Arg
65					70					75					80
Leu	Val	Arg	Ile	Gly	Val	Leu	Asp	Glu	Gly	Lys	Met	Lys	Leu	Asp	Tyr
				85					90					95	
Ile	Leu	Gly	Leu	Lys	Ile	Glu	Asp	Phe	Leu	Glu	Arg	Arg	Leu	Gln	Thr
			100					105					110		
Gln	Val	Phe	Lys	Leu	Gly	Leu	Ala	Lys	Ser	Ile	His	His	Ala	Arg	Val
		115					120					125			

Leu Ile Arg Gln Arg His Ile Ser Pro Arg Arg
130 135

<210> 1049
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 244; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC012363.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486995"

<400> 1049
Leu Ser Gly Asn Glu Ser Lys Gly His Ser Ser Leu Ser Leu
1 5 10

<210> 1050
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 245; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC013269.5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000386773"

<400> 1050
Met Thr Val Asn Lys Ile Met Val His Ala Asp Tyr Asn Glu Leu His
1 5 10 15

```
Arg Met Gly Ser Asp Ile Thr Leu Leu Gln Leu His His His Val Glu
            20                  25                  30

Phe Ser Ser His Ile Leu Pro Ala Cys Leu Pro Glu Pro Thr Thr Trp
        35                  40                  45

Leu Ala Pro Asp Ser Ser Cys Trp Ile Ser Gly Trp Gly Met Val Thr
    50                  55                  60

Glu Asp Val Phe Leu Pro Glu Pro Phe Gln Leu Gln Glu Ala Glu Val
65                  70                  75                  80

Gly Val Met Asp Asn Thr Val Cys Gly Ser Phe Phe Gln Pro Gln Tyr
                85                  90                  95

Pro Gly Gln Pro Ser Ser Ser Asp Tyr Thr Ile His Glu Asp Met Leu
            100                 105                 110

Cys Ala Gly Asp Leu Ile Thr Gly Lys Ala Ile Cys Arg Cys Gly Glu
        115                 120                 125

Leu Arg Pro Arg Glu Glu Val Tyr His Pro Ser Glu Thr Pro Gly Val
    130                 135                 140

Pro Ser Ser Ala His
145
```

<210> 1051
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 246; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC013286.1; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000487141"

<400> 1051
Met Ala Val Ser Glu Ser Ile Ala Ser Thr Pro Gln Asn His Tyr Thr
1   5   10   15

<210> 1052
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 247; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC015688.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463557"

<400> 1052
Ser Trp Ser Pro Val Ile Gln Arg Cys Ser Gln Pro Tyr Gly Phe Ser
1   5   10   15

Leu Leu Ile Ser Phe Phe Leu Lys Cys Val Ser Glu Thr Ser Gln Gln
            20   25   30

Pro Pro Arg Gln Lys Asn Thr Ala Cys Pro Ala Leu Gln Thr Arg Ser
        35   40   45

Thr Arg Pro Arg Phe Arg Leu Leu Ala Ile Asn Pro Thr Arg Glu Met
    50   55   60

Glu Leu His Leu Leu Phe Leu Lys Met Thr Pro Pro Thr Thr Lys Pro
65   70   75   80

Val Met Thr Asp Ser Lys Cys Leu His Val Tyr Phe Ser
                85   90

<210> 1053
<211> 66
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 247; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC015688.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000464452"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1053
Xaa Thr Ser Gln Gln Pro Pro Arg Gln Lys Asn Thr Ala Cys Pro Ala
1 5 10 15

Leu Gln Thr Arg Ser Thr Arg Pro Arg Phe Arg Leu Leu Ala Ile Asn
20 25 30

Pro Thr Arg Glu Met Glu Leu His Leu Leu Phe Leu Lys Met Thr Pro
35 40 45

Pro Thr Thr Lys Pro Val Met Thr Asp Ser Lys Cys Leu His Val Tyr
50 55 60

Phe Ser
65

<210> 1054
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 248; "

<220>
<221> source

<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC016142.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485447"

<400> 1054

Met	Thr	Leu	Asn	Glu	His	Ala	Ala	Phe	Lys	His	Leu	Phe	Asn	Lys	Ala
1				5				10					15		
His	Leu	Ala	Pro	Pro	Leu	Ile	His	Leu	Thr	Leu	Ser	Gly	His	Ser	Thr
		20					25					30			
Cys	Phe	Arg	Glu	His	Arg	Val	Gly	Asp	Lys	Val	Thr	Asp	Gln	Gln	Asp
	35					40					45				
Pro	Lys	Ala	Glu	Glu	Phe	Phe	Leu	Val	Gln	Asn	Lys	Met	Lys	Ser	Leu
50					55					60					
Pro	Cys	Leu	Leu	Leu	Ser	Thr	Gln	Thr	Arg	Gln	Pro	Ser	Asp	Phe	Ser
65				70					75					80	
Ile	Phe	Ser	Pro	Pro	Phe	Pro	Pro	Phe	Tyr	Ser	Thr	Lys	Pro	Pro	Leu
			85					90					95		
Ser	Ser	Trp	Pro	Ile	Pro	Asn	Glu	Pro	Leu	Gly	Thr	Pro	Pro	Arg	Arg
		100					105					110			
Gly	Arg	Gly	Arg	Ala	Glu	Gly	Leu	Leu	Thr	Ser	Gln				
	115					120									

<210> 1055
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 249; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC016549.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486279"

<400> 1055
Met Gly Ala Leu Ile Ile Ser Gly Ser Ser Ala Gly Pro Val Thr Lys
1 5 10 15

Gln Ala Ser Leu Pro Pro Trp Gly Leu Ser His Gly Arg Cys Gly Phe
20 25 30

Leu Leu Tyr Met Glu Met Thr Leu Cys Ser His Arg Thr Gln Ser Phe
35 40 45

Ser Glu Leu Ser Gln Ser Leu Met Arg Pro Gly Phe Leu Gln Met Pro
50 55 60

Tyr Ile Ser Cys Ala Lys Leu Ser Lys Ile Trp Phe Pro Ala Ser Lys
65 70 75 80

Pro Cys Leu Leu Ala Phe Leu Glu Val Phe Leu Leu Met Ser Arg Leu
85 90 95

Ser Leu Phe Ser Lys Met Ile Cys Phe Leu Phe Leu Ser Phe Leu Phe
100 105 110

Pro Pro His Ile Tyr Thr His Ala Ser
115 120

<210> 1056
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 250; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC016577.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485075"

<400> 1056
Met Asn Pro Ser Glu Met Gln Arg Lys Gly Pro Pro Arg Arg Trp Tyr
1 5 10 15

Leu Gln Val Tyr Pro Thr Ala Pro Lys Arg Gln Arg Pro Ser Arg Thr
20 25 30

Gly His Asp Asp Asp Gly Gly Phe Val Glu Lys Lys Arg Gly Lys Cys
35 40 45

Gly Glu Lys Gln Glu Arg Ser Asn Cys Tyr Cys Val Cys Val Glu Arg
50 55 60

Ser Arg His Arg Arg Leu His Phe Val Met Cys
65 70 75

<210> 1057
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480313"

<400> 1057
Met Ala Ala Val Arg Ala Leu Val Ala Ser Arg Leu Ala Ala Ala Ser
1 5 10 15

Ala Phe Thr Ser Leu Ser Pro Gly Gly Arg Thr Pro Ser Gln Arg Ala
20 25 30

```
Ala Leu His Leu Ser Val Pro Arg Pro Ala Ala Arg Val Ala Leu Val
        35                  40                  45

Leu Ser Gly Cys Gly Val Tyr Asp Gly Thr Glu Ile His Glu Ala Ser
    50                  55                  60

Ala Ile Leu Val His Leu Ser Arg Gly Gly Ala Glu Val Gln Ile Phe
65                  70                  75                  80

Ala Pro Asp Val Pro Gln Met His Val Ile Asp His Thr Lys Gly Gln
                85                  90                  95

Pro Ser Glu Gly Glu Ser Arg Asn Val Leu Thr Glu Ser Ala Arg Ile
            100                 105                 110

Ala Arg Gly Lys Ile Thr Asp Leu Ala Asn Leu Ser Ala Ala Asn His
        115                 120                 125

Asp Ala Ala Ile Phe Pro Gly Gly Phe Gly Ala Ala Lys Asn Leu Ser
    130                 135                 140

Thr Phe Ala Val Asp Gly Lys Asp Cys Lys Val Asn Lys Glu Val Glu
145                 150                 155                 160

Arg Val Leu Lys Glu Phe His Gln Ala Gly Lys Pro Ile Gly Leu Cys
                165                 170                 175

Cys Ile Ala Pro Val Leu Ala Ala Lys Val Leu Arg Gly Val Glu Val
            180                 185                 190

Thr Val Gly His Glu Gln Glu Glu Gly Gly Lys Trp Pro Tyr Ala Gly
        195                 200                 205

Thr Ala Glu Ala Ile Lys Ala Leu Gly Ala Lys His Cys Val Lys Glu
    210                 215                 220

Val Val Glu Ala His Val Asp Gln Lys Asn Lys Val Val Thr Thr Pro
225                 230                 235                 240

Ala Phe Met Cys Glu Thr Ala Leu His Tyr Ile His Asp Gly Ile Gly
                245                 250                 255
```

```
Ala Met Val Arg Lys Val Leu Glu Leu Thr Gly Lys
            260                 265


<210> 1058
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483086"

<400> 1058
Met His Val Ile Asp His Thr Lys Gly Gln Pro Ser Glu Gly Glu Ser
1               5                  10                  15


Arg Asn Val Leu Thr Glu Ser Ala Arg Ile Ala Arg Gly Lys Ile Thr
            20                  25                  30


Asp Leu Ala Asn Leu Ser Ala Ala Asn His Asp Ala Ala Ile Phe Pro
        35                  40                  45


Gly Gly Phe Gly Ala Ala Lys Asn Leu Ser Thr Phe Ala Val Asp Gly
    50                  55                  60


Lys Asp Cys Lys Val Asn Lys Glu Val Glu Arg Val Leu Lys Glu Phe
65                  70                  75                  80


His Gln Ala Gly Lys Pro Ile Gly Leu Cys Cys Ile Ala Pro Val Leu
                85                  90                  95


Ala Ala Lys Val Leu Arg Gly Val Glu Val Thr Val Gly His Glu Gln
            100                 105                 110


Glu Glu Gly Gly Lys Trp Pro Tyr Ala Gly Thr Ala Glu Ala Ile Lys
```

```
        115                 120                 125

Ala Leu Gly Ala Lys His Cys Val Lys Glu Val Val Glu Ala His Val
    130                 135                 140

Asp Gln Lys Asn Lys Val Val Thr Thr Pro Ala Phe Met Cys Glu Thr
145                 150                 155                 160

Ala Leu His Tyr Ile His Asp Gly Ile Gly Ala Met Val Arg Lys Val
                165                 170                 175

Leu Glu Leu Thr Gly Lys
            180


<210> 1059
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485058"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1059
Xaa Asp Gly Thr Glu Ile His Glu Ala Ser Ala Ile Leu Val His Leu
1               5                   10                  15

Ser Arg Gly Gly Ala Glu Val Gln Ile Phe Ala Pro Asp Val Pro Gln
            20                  25                  30

Met His Val Ile Asp His Thr Lys Gly Gln Pro Ser Glu Gly Glu Ser
```

```
        35                  40                  45

Arg Asn Val Leu Thr Glu Ser Ala Arg Ile Ala Arg Gly Lys Ile Thr
    50                  55                  60

Asp Leu Ala Asn Leu Ser Ala Ala Asn His Asp Ala Ala Ile Phe Pro
65                  70                  75                  80

Gly Gly Phe Gly Ala Ala Lys Asn Leu Gly Ser Pro Tyr Ser Asp Pro
                85                  90                  95

Ala Lys His Arg Ser Leu Gly Leu Gln Leu
            100                 105


<210> 1060
<211> 237
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485300"

<400> 1060
Met Ala Ala Val Arg Ala Leu Val Ala Ser Arg Leu Ala Ala Ala Ser
1               5                   10                  15

Ala Phe Thr Ser Leu Ser Pro Gly Gly Arg Thr Pro Ser Gln Arg Ala
            20                  25                  30

Ala Leu His Leu Ser Val Pro Arg Pro Ala Ala Arg Val Ala Leu Val
        35                  40                  45

Leu Ser Gly Cys Gly Val Tyr Asp Gly Thr Glu Ile His Glu Ala Ser
    50                  55                  60
```

```
Ala Ile Leu Val His Leu Ser Arg Gly Gly Ala Glu Val Gln Ile Phe
65                  70                  75                  80

Ala Pro Asp Val Pro Gln Met His Val Ile Asp His Thr Lys Gly Gln
                85                  90                  95

Pro Ser Glu Gly Glu Ser Arg Asn Val Leu Thr Glu Ser Ala Arg Ile
            100                 105                 110

Ala Arg Gly Lys Ile Thr Asp Leu Ala Asn Leu Ser Ala Ala Asn His
        115                 120                 125

Asp Ala Ala Ile Phe Pro Gly Gly Phe Gly Ala Ala Lys Asn Leu Leu
    130                 135                 140

Cys Cys Ile Ala Pro Val Leu Ala Ala Lys Val Leu Arg Gly Val Glu
145                 150                 155                 160

Val Thr Val Gly His Glu Gln Glu Glu Gly Gly Lys Trp Pro Tyr Ala
                165                 170                 175

Gly Thr Ala Glu Ala Ile Lys Ala Leu Gly Ala Lys His Cys Val Lys
            180                 185                 190

Glu Val Val Glu Ala His Val Asp Gln Lys Asn Lys Val Val Thr Thr
        195                 200                 205

Pro Ala Phe Met Cys Glu Thr Ala Leu His Tyr Ile His Asp Gly Ile
    210                 215                 220

Gly Ala Met Val Arg Lys Val Leu Glu Leu Thr Gly Lys
225                 230                 235


<210> 1061
<211> 224
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "

<220>
<221> source
<223> /note="Gene Symbol:; "
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<220>
<221> source
<223> /note="Gene Name:
AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485335"

<400> 1061

```
Pro Ser Gln Arg Ala Ala Leu His Leu Ser Val Pro Arg Pro Ala Ala
1               5                  10                  15

Arg Val Ala Leu Val Leu Ser Gly Cys Gly Val Tyr Asp Gly Thr Glu
            20                  25                  30

Ile His Glu Ala Ser Ala Ile Leu Val His Leu Ser Arg Gly Gly Ala
        35                  40                  45

Glu Val Gln Ile Phe Ala Pro Asp Val Pro Gln Met His Val Ile Asp
    50                  55                  60

His Thr Lys Gly Gln Pro Ser Glu Gly Glu Ser Arg Asn Val Leu Thr
65                  70                  75                  80

Glu Ser Ala Arg Ile Ala Arg Gly Lys Ile Thr Asp Leu Ala Asn Leu
                85                  90                  95

Ser Ala Ala Asn His Asp Ala Ala Ile Phe Pro Gly Gly Phe Gly Ala
            100                 105                 110

Ala Lys Asn Leu Ser Thr Phe Ala Val Asp Gly Lys Asp Cys Lys Val
        115                 120                 125

Asn Lys Glu Val Glu Arg Val Leu Lys Glu Phe His Gln Ala Gly Lys
    130                 135                 140

Pro Ile Gly His Ser Leu Lys Asp Leu Pro Gly His Cys Pro Gly Arg
145                 150                 155                 160

Pro Leu Lys Trp Ser Leu Arg Lys Arg Cys Arg Leu Arg Ala Pro Glu
                165                 170                 175

Gly Gly Pro Cys Cys Ser Arg Val Thr Ala Gly Val Lys Val Ser Pro
            180                 185                 190
```

```
Met Val Ser Thr Ser Gly Ser Arg Pro Cys Gln Arg Ser Val Pro Trp
        195                 200                 205


Met Ser Ala Gln Arg Glu Glu Pro Met Ala Leu Ser Ser Val Thr Asp
    210                 215                 220


<210> 1062
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485404"

<400> 1062
Met Ala Ala Val Arg Ala Leu Val Ala Ser Arg Leu Ala Ala Ala Ser
1               5                   10                  15


Ala Phe Thr Ser Leu Ser Pro Gly Gly Arg Thr Pro Ser Gln Arg Ala
            20                  25                  30


Ala Leu His Leu Ser Val Pro Arg Pro Ala Ala Arg Val Ala Leu Asp
        35                  40                  45


Pro Gly Ala Pro Glu Pro Trp Arg Gly
    50                  55


<210> 1063
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 251; "
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<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC016734.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485439"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1063
Xaa Asp Gly Thr Glu Ile His Glu Ala Ser Ala Ile Leu Val His Leu
1 5 10 15

Ser Arg Gly Gly Ala Glu Val Gln Ile Phe Ala Pro Asp Val Pro Gln
20 25 30

Met His Val Ile Asp His Thr Lys Gly Gln Pro Ser Glu Gly Glu Ser
35 40 45

Arg Asn Val Leu Thr Glu Ser Ala Arg Ile Ala Arg Gly Lys Ile Thr
50 55 60

Asp Leu Ala Asn Leu Ser Ala Ala Asn His Asp Ala Ala Ile Phe Pro
65 70 75 80

Gly Gly Phe Gly Ala Ala Lys Asn Leu Ser Thr Phe Ala Val Asp Gly
85 90 95

Lys Asp Cys Lys Val Asn Lys Glu Val Glu Arg Val Leu Lys Glu Phe
100 105 110

His Gln Ala Gly Lys Pro Ile Gly Gly Ser Pro Tyr Ser Asp Pro Ala
115 120 125

Lys His Arg Ser Leu Gly Leu Gln Leu
130 135

<210> 1064
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 252; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC016753.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486211"

<400> 1064
Ile Ile Ile Ile Ile Ile Ile Ile Lys Phe Ile Phe Ile Tyr Leu Phe
1 5 10 15

Ile Phe Phe Glu Thr Gly Ser His Cys
20 25

<210> 1065
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 253; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC017028.10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485328"

<400> 1065
Met Arg Ser Gln Gly Gln Gly Gly Pro Gly Ala Trp Arg Arg Met Glu
1 5 10 15

Ser Trp Ser Ala Glu Pro Ala Gly Pro Gly Gln Gly Arg Leu Gly Ser
20 25 30

Pro Cys Glu Ala Ala Glu Gln Ala Ser Phe Glu Lys Thr Val Ile Gly
35 40 45

Val Gly Gln Ala Arg Ala Ala Leu Ser Glu Glu Glu His Arg Val Trp
50 55 60

Glu Ala Ala Ala Gly Val Gly Gly Leu Glu Gln Trp Gly Cys Trp Glu
65 70 75 80

Ala Gly Val Thr Ser Gly Trp Gly
85

<210> 1066
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 254; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC017081.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485556"

<400> 1066
Met Val Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn
1 5 10 15

Lys Ala His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His
20 25 30

Ser Thr Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Gln
35 40 45

Gln Asp Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys

```
    50                  55                  60

Ser Leu Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp
65                  70                  75                  80

Phe Ser Ile Phe Ser Pro Pro Phe Pro Leu Phe Tyr Ser Thr Lys Pro
                85                  90                  95

Pro Leu Ser Ser Trp Pro Val Leu Asn Glu Leu Leu Gly Thr Pro Pro
            100                 105                 110

Arg Arg Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
        115                 120                 125


<210> 1067
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 255; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC018512.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485162"

<400> 1067
Met Ser Gln Lys Lys Lys Lys Lys Ser Gln Lys Lys Glu Lys Lys Lys
1               5                   10                  15


<210> 1068
<211> 551
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 256; "

<220>
<221> source
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<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC018755.18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000415200"

<400> 1068

```
Met Leu Pro Leu Leu Leu Leu Pro Leu Leu Trp Gly Gly Ser Leu Gln
1               5                  10                  15

Glu Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val Thr Val Gln
            20                  25                  30

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
        35                  40                  45

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
    50                  55                  60

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
65                  70                  75                  80

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
                85                  90                  95

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
            100                 105                 110

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
        115                 120                 125

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
    130                 135                 140

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
145                 150                 155                 160

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
                165                 170                 175

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
```

```
            180                 185                 190

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
        195                 200                 205

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr
    210                 215                 220

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
225                 230                 235                 240

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
                245                 250                 255

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
            260                 265                 270

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
        275                 280                 285

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
    290                 295                 300

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
305                 310                 315                 320

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
                325                 330                 335

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
            340                 345                 350

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
        355                 360                 365

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
    370                 375                 380

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
385                 390                 395                 400

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
                405                 410                 415
```

```
Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
            420                 425                 430

Gly Thr Gly Val Val Pro Ala Ala Leu Gly Gly Ala Gly Val Met Ala
        435                 440                 445

Leu Leu Cys Ile Cys Leu Cys Leu Ile Phe Phe Leu Ile Val Lys Ala
    450                 455                 460

Arg Arg Lys Gln Ala Ala Gly Arg Pro Glu Lys Met Asp Asp Glu Asp
465                 470                 475                 480

Pro Ile Met Gly Thr Ile Thr Ser Gly Ser Arg Lys Lys Pro Trp Pro
                485                 490                 495

Asp Ser Pro Gly Asp Gln Ala Ser Pro Pro Gly Asp Ala Pro Pro Leu
            500                 505                 510

Glu Glu Gln Lys Glu Leu His Tyr Ala Ser Leu Ser Phe Ser Glu Met
        515                 520                 525

Lys Ser Arg Glu Pro Lys Asp Gln Glu Ala Pro Ser Thr Thr Glu Tyr
    530                 535                 540

Ser Glu Ile Lys Thr Ser Lys
545                 550
```

<210> 1069
<211> 551
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 256; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC018755.18; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000470259"

<400> 1069
Met Leu Pro Leu Leu Leu Leu Pro Leu Leu Trp Gly Gly Ser Leu Gln
1 5 10 15

Glu Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val Thr Val Gln
20 25 30

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
35 40 45

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
50 55 60

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
65 70 75 80

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
85 90 95

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Ala Arg Met Glu Asp
100 105 110

Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly Arg Asp Val Lys Tyr
115 120 125

Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val Thr Ala Leu Ile Glu
130 135 140

Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu Ser Gly Arg Pro Thr
145 150 155 160

Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu Ala Gly Pro Pro Leu
165 170 175

Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro Leu Asp Pro Glu Thr
180 185 190

Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg Pro Glu Asp His Gly
195 200 205

Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly Ala Gln Val Thr Thr

```
    210                 215                 220

Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala Pro Gln Thr Ile Thr
225                 230                 235                 240

Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu Gln Asn Thr Ser Tyr
                245                 250                 255

Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu Leu Cys Asp Ala Pro
            260                 265                 270

Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln Gly Ser Pro Ala Leu
        275                 280                 285

Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu Glu Leu Arg Arg Val
    290                 295                 300

Arg Ser Ala Glu Glu Gly Gly Phe Thr Cys Arg Ala Gln His Pro Leu
305                 310                 315                 320

Gly Phe Leu Gln Ile Phe Leu Asn Leu Ser Val Tyr Ser Leu Pro Gln
                325                 330                 335

Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Arg
            340                 345                 350

Cys Ser Phe Arg Ala Arg Pro Ala Pro Ser Leu Cys Trp Arg Leu Glu
        355                 360                 365

Glu Lys Pro Leu Glu Gly Asn Ser Ser Gln Gly Ser Phe Lys Val Asn
    370                 375                 380

Ser Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ile Leu His Gly
385                 390                 395                 400

Gly Leu Ser Ser Asp Leu Lys Val Ser Cys Lys Ala Trp Asn Ile Tyr
                405                 410                 415

Gly Ser Gln Ser Gly Ser Val Leu Leu Leu Gln Gly Arg Ser Asn Leu
            420                 425                 430

Gly Thr Gly Val Val Pro Ala Ala Leu Gly Gly Ala Gly Val Met Ala
        435                 440                 445
```

```
Leu Leu Cys Ile Cys Leu Cys Leu Ile Phe Phe Leu Ile Val Lys Ala
    450                 455                 460

Arg Arg Lys Gln Ala Ala Gly Arg Pro Glu Lys Met Asp Asp Glu Asp
465                 470                 475                 480

Pro Ile Met Gly Thr Ile Thr Ser Gly Ser Arg Lys Lys Pro Trp Pro
                485                 490                 495

Asp Ser Pro Gly Asp Gln Ala Ser Pro Pro Gly Asp Ala Pro Pro Leu
            500                 505                 510

Glu Glu Gln Lys Glu Leu His Tyr Ala Ser Leu Ser Phe Ser Glu Met
        515                 520                 525

Lys Ser Arg Glu Pro Lys Asp Gln Glu Ala Pro Ser Thr Thr Glu Tyr
    530                 535                 540

Ser Glu Ile Lys Thr Ser Lys
545                 550
```

<210> 1070
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 257; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC018867.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487424"

<400> 1070

```
Ile Pro Pro Ala Leu Ala Ser Gln Ala Ala Gly Ser Thr Asp Ser Val
1               5                   10                  15
```

Ser Lys Lys Lys Lys Lys Ile Ile
20

<210> 1071
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 258; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC018902.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486897"

<400> 1071
Met Val Ile Leu Lys Ile Tyr Thr Glu Phe Ser Arg Val Trp Ile
1 5 10 15

<210> 1072
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 259; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC019206.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485336"

<400> 1072
Ser Arg Arg Arg Ser Lys Ser Ser Arg Arg Ser Ser Arg Arg Ser Ser
1 5 10 15

```
Arg Arg Ser Arg Ser Lys Arg Ser Arg Ser Arg Arg Arg Ser Lys Ser
            20                  25                  30

Ser Arg Arg Ser Ser Arg Arg Ser Arg Arg Arg Ser Arg Thr Arg Arg
        35                  40                  45

Ser Arg Ser Ser Ser Arg Arg Ser Ser Thr Asn Arg Ser Ser Ser Lys
    50                  55                  60


<210> 1073
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 260; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC021106.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485267"

<400> 1073
Met Lys Met Glu Leu Gly Arg Asp Val Cys Ser Ser Ala Leu Arg Ile
1               5                   10                  15

Met Lys Ala Thr Asn Ile Lys Lys Arg Ser Gly Gly Arg Asp Thr Val
            20                  25                  30

Ala Pro Gln Gly Met Asn Gln Leu Gly Lys Glu Lys Lys Glu Ser Leu
        35                  40                  45

Leu Ser Ser
    50


<210> 1074
<211> 167
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 261; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC022016.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489443"

<400> 1074

```
Met Gly Lys Asp Phe Met Thr Lys Thr Pro Lys Ala Met Ala Thr Lys
1               5                  10                  15

Ala Lys Ile Asp Lys Trp Asp Leu Ile Lys Leu Lys Ser Phe Cys Thr
            20                  25                  30

Ala Lys Glu Thr Thr Ile Arg Val Asn Arg Gln Pro Thr Glu Trp Glu
        35                  40                  45

Lys Ile Phe Thr Ile Tyr Pro Ser Asp Lys Gly Gln Ser His Tyr Trp
    50                  55                  60

Val Tyr Thr Gln Arg Ile Ile Asn His Ala Thr Ile Lys Thr His Ala
65                  70                  75                  80

His Val Cys Leu Leu Ser Ile Ile Lys Lys Gln Lys Gln Lys Gln Lys
                85                  90                  95

Gln Thr Ser Leu Pro Val Val Leu Ala Leu Trp Glu Ala Lys Val Gly
            100                 105                 110

Gly Leu Leu Glu Leu Arg Arg Leu Arg Pro Ala Trp Ala Lys Trp Lys
        115                 120                 125

Asn His Val Ser Thr Lys Asn Thr Lys Ile Ser Trp Ala Trp Trp Cys
    130                 135                 140

Val Pro Ile Val Pro Ala Thr Trp Glu Ala Glu Val Gly Arg Ser Pro
145                 150                 155                 160
```

Glu Pro Gln Glu Val Lys Val
165

<210> 1075
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 262; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC022210.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485425"

<400> 1075
Met Thr Leu Pro Arg Lys Gln Thr Leu Ser His Glu Ala Arg Lys Pro
1 5 10 15

Leu Ser

<210> 1076
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 263; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC022405.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485588"

<400> 1076
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1   5   10   15

His Leu Ala Pro Pro Leu Ile His Ser Thr Leu Ser Gly His Ser Thr
            20   25   30

Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Thr Asp Gln Gln Asp
        35   40   45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
    50   55   60

Pro Cys Leu Pro Leu Pro Thr Gln Thr Gln Gln Pro Ser Asp Phe Ser
65   70   75   80

Ile Phe Ser Pro Pro Phe Pro Ile Phe Tyr Ser Thr Lys Leu Pro Leu
                85   90   95

Ser Ser Trp Pro Val Leu Asn Glu Leu Leu Ser Thr Pro Pro Arg Arg
            100   105   110

Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
        115   120

<210> 1077
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 264; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC022819.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485910"

<400> 1077

Val Thr Arg Leu Cys Thr Arg Ile Ser Phe Ser Ile Leu Pro Lys Asn
1 5 10 15

Lys Asn Leu Phe Phe Asn Phe Thr Thr Leu His
20 25

<210> 1078
<211> 429
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 265; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC023491.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484693"

<400> 1078
Met Asp Ser Leu Trp Gly Pro Gly Ala Gly Ser His Pro Phe Gly Val
1 5 10 15

His Asn Thr Arg Leu Ser Pro Asp Leu Cys Pro Gly Lys Ile Val Leu
20 25 30

Arg Ala Leu Lys Glu Ser Gly Ala Gly Met Pro Glu Gln Asp Lys Asp
35 40 45

Pro Arg Val Gln Glu Asn Pro Gly Asp Gln Arg Arg Val Pro Glu Val
50 55 60

Thr Gly Asp Ala Pro Ser Ala Phe Arg Pro Leu Arg Asp Asn Arg Gly
65 70 75 80

Leu Ser Pro Phe Val Pro Gly Pro Gly Pro Leu Gln Thr Asp Leu His
85 90 95

Ala Gln Arg Ser Glu Ile Arg Tyr Asn Gln Thr Ser Gln Ile Ser Trp
100 105 110

```
Thr Ser Ser Cys Thr Asn Arg Asn Ala Ile Ser Ser Ser Tyr Ser Ser
        115                 120                 125

Met Gly Gly Leu Pro Gly Leu Lys Arg Arg Arg Gly Pro Ala Ser Ser
    130                 135                 140

His Cys Gln Leu Thr Leu Ser Ser Ser Lys Thr Val Ser Glu Asp Arg
145                 150                 155                 160

Pro Gln Ala Val Ser Ser Gly His Thr Gln Cys Glu Lys Ala Ala Asp
                165                 170                 175

Ile Ala Pro Gly Gln Thr Leu Ala Leu Arg Asn Asp Ser Ser Thr Ser
            180                 185                 190

Glu Ala Ser Arg Pro Ser Thr His Lys Phe Pro Leu Leu Pro Arg Arg
        195                 200                 205

Arg Gly Glu Pro Leu Met Leu Pro Pro Pro Leu Glu Leu Gly Tyr Arg
    210                 215                 220

Val Thr Val Glu Asp Leu Asp Arg Glu Lys Glu Ala Ala Phe Gln Arg
225                 230                 235                 240

Ile Asn Ser Ala Leu Gln Val Glu Asp Lys Ala Ile Ser Asp Cys Arg
                245                 250                 255

Pro Ser Arg Pro Ser His Thr Leu Ser Ser Leu Ala Thr Gly Thr Ser
            260                 265                 270

Gly Leu Pro Ala Ile Ser Lys Ala Pro Ser Met Asp Val Gln Gln Glu
        275                 280                 285

Thr His Lys Ser Gln Asp Cys Leu Gly Leu Leu Ala Pro Leu Ala Ser
    290                 295                 300

Ala Ala Gly Val Pro Ser Thr Ala Pro Met Ser Gly Lys Lys His Arg
305                 310                 315                 320

Pro Pro Gly Pro Leu Phe Ser Ser Ser Asp Pro Leu Pro Ala Thr Ser
                325                 330                 335
```

```
Ser His Ser Gln Asp Ser Ala Gln Val Thr Ser Leu Ile Pro Ala Pro
            340                 345                 350

Phe Pro Ala Ala Ser Met Asp Ala Gly Met Arg Arg Thr Arg Cys Gly
        355                 360                 365

Thr Ser Ala Pro Ala Ala Ala Ala Ala Ala Pro Pro Pro Ser Thr Leu
    370                 375                 380

Asn Pro Thr Leu Gly Ser Leu Leu Glu Trp Met Glu Ala Leu His Ile
385                 390                 395                 400

Ser Gly Pro Gln Pro Gln Leu Gln Gln Val Pro Arg Gly Gln Asn Gln
                405                 410                 415

Arg Ser Gln Thr Ser Arg Thr Ser Ser Cys Pro Lys Arg
            420                 425


<210> 1079
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 266; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC024060.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486286"

<400> 1079
Leu Lys Arg Leu Val Asp Gly Val Ser Leu Cys Arg Pro Gly Trp Ser
1               5                   10                  15

Ala Val Ala Arg Ser
            20


<210> 1080
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<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 267; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC024361.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485748"

<400> 1080
Glu Ser Val Leu Arg Arg His Leu Asn Cys Ser Pro Val Pro Pro Thr
1 5 10 15

Gly His

<210> 1081
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 268; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC024592.12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465499"

<400> 1081
Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
1 5 10 15

```
Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
            20                  25                  30

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
        35                  40                  45

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
    50                  55                  60

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
65                  70                  75                  80

Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
                85                  90                  95

Gly Gly Leu Thr Leu Gly Ala Arg Lys Thr Gly Phe His Arg Val Ser
            100                 105                 110

Gln Asp Gly Leu Asp Leu Leu Thr Ser
        115                 120


<210> 1082
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 268; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC024592.12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466639"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1082
```

```
Xaa Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr Asp
1               5                   10                  15

Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala Gly
            20                  25                  30

Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr Phe
        35                  40                  45

Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Asp Thr
    50                  55                  60

Gly Ser Glu Arg Pro Arg Gly Ser Cys Cys Ala Arg Leu Glu Ala Leu
65                  70                  75                  80

Ala Leu Pro Val Tyr Pro Ala Ala Ala Val Gly Ala Val Phe Gly Leu
                85                  90                  95

Thr Thr Cys Ile Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu
            100                 105                 110

Asn Tyr Phe Leu Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg
        115                 120                 125

Thr Thr Leu Thr His Gly Ser Pro Gly Pro Ser Gln Ala Thr Val Ala
    130                 135                 140

Val Ala Pro Leu Ser Gly Arg Ala Ala Val Ser Ala Ala Gly Gly Cys
145                 150                 155                 160

Val Phe Leu Leu Leu Pro Ala Cys Val
                165


<210> 1083
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 268; "

<220>
<221> source
<223> /note="Gene Symbol:; "
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<220>
<221> source
<223> /note="Gene Name:
AC024592.12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467210"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1083
Xaa Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr Asp
1 5 10 15

Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala Gly
20 25 30

Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr Phe
35 40 45

Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala Ala
50 55 60

Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val Arg
65 70 75 80

Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala Gly
85 90 95

Gly Leu Thr Leu Gly Ala Arg Thr Thr Leu Thr His Gly Ser Pro Gly
100 105 110

Pro Ser Gln Ala Thr Val Ala Val Ala Pro Leu Ser Gly Arg Ala Ala
115 120 125

Val Ser Ala Ala Gly Gly Cys Val Phe Leu Leu Leu Pro Ala Cys Val
130 135 140

<210> 1084
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 269; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC025263.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454833"

<400> 1084
Leu Gln Pro Ile Arg Phe Val Lys Ala Ser Ala Val Glu Cys Gly Gly
1 5 10 15

Pro Lys Lys Cys Ala Leu Thr Gly Gln Ser Lys Ser Cys Lys His Arg
20 25 30

Ile Lys Leu Gly Asp Ser Ser Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys
35 40 45

Arg Tyr Arg Ile Thr Ser Val Cys Asn Phe Phe Thr Tyr Ile Arg Tyr
50 55 60

Ile Gln Gln Gly Leu Val Lys Gln Gln Asp Val Leu
65 70 75

<210> 1085
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 270; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC026248.1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000485285"

<400> 1085
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1   5   10   15

His Leu Ala Pro Pro Leu Ile His Ser Thr Leu Ser Gly Tyr Ser Thr
            20   25   30

Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Thr Asp Gln Gln Asp
        35   40   45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
    50   55   60

Pro Cys Leu Pro Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65   70   75   80

Ile Phe Pro Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
                85   90   95

Ser Ser Trp Pro Val Leu Asn Glu Leu Leu Gly Thr Pro Pro Arg Arg
            100   105   110

Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
        115   120

<210> 1086
<211> 185
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 271; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC026369.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480683"

<400> 1086
Met Glu Ser Leu Leu Glu Asn Pro Val Arg Ala Val Leu Tyr Leu Lys
1 5 10 15

Glu Leu Thr Ala Ile Val Gln Asn Gln Gln Ser Leu Ile His Thr Gln
20 25 30

Arg Glu Arg Ile Asp Glu Leu Glu Arg Arg Leu Asp Glu Leu Ser Ala
35 40 45

Glu Asn Arg Ser Leu Trp Glu His Gln Gln Leu Leu Gln Ala Gln Pro
50 55 60

Pro Pro Gly Leu Val Pro Pro Ser Ser Ala Pro Leu Pro Ala Ala Pro
65 70 75 80

Ala Thr Ala Pro Ala Ala Ala Ala Arg Ala Gln Glu Pro Leu Gln Asp
85 90 95

Gln Gly Gln Arg Ser Ala Ala Ala Pro His Pro Ala Pro Asp Arg Pro
100 105 110

Pro Arg Gln His His Gly Gln Leu Leu Glu Gln Pro Gln Arg Gly Pro
115 120 125

Gly Ser Arg Ala His Thr Pro Gln Ser Pro His Lys His Leu Gly Thr
130 135 140

Gln Gly Ala Val Thr Asp Lys Glu Lys Glu Arg Pro Pro Ser Cys Cys
145 150 155 160

Ala Ala Ala Gly Ala Leu Leu Gln His Lys Ser Pro Ser Ala Leu Gly
165 170 175

Lys Gly Val Leu Ser Arg Arg Pro Glu
180 185

<210> 1087
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 272; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC026449.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485486"

<400> 1087
Lys Val Tyr Phe Cys Phe Ser Leu Leu His Asn Phe Leu Arg Lys Arg
1 5 10 15

Ser Trp Glu Ser Phe
20

<210> 1088
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 273; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC037459.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399696"

<400> 1088
Met Asp Ser Glu Gly Gly Ser Leu Leu Leu Asp Glu Asp Ser Glu Val
1 5 10 15

Phe Lys Met Leu Gln Glu Asn Arg Glu Gly Arg Ala Ala Pro Arg Gln
20 25 30

Ser Ser Ser Phe Arg Leu Leu Gln Glu Ala Leu Glu Ala Glu Glu Arg
35 40 45

```
Asp Gly Ala Gly Glu Gly Leu Ala Arg Gly Cys Ile Val Pro Gly Val
    50                  55                  60

Thr Ser Thr Tyr Arg Arg Ile Pro Asp Ala Ala His Gly Cys Ser Ser
65                  70                  75                  80

Trp Glu Arg Gly Asp Lys Phe Arg Gly Val Gly Arg Glu Ala Leu Phe
                85                  90                  95

Leu Lys Leu Ala Ser Arg Asp Ser Gly Val Glu Met Ala Val Gly Asp
            100                 105                 110

Ser Pro Leu Ala Ala Leu Pro Gly Leu Ser Gln Asp Ser Leu Asp Phe
        115                 120                 125

Glu Ser Ser Gly Ser Ser Glu Pro Pro Ala Gln Val Gly Arg Leu Leu
    130                 135                 140

Ala Ser Gln Lys Leu Gly Glu Val Leu Glu Arg Ser Arg Arg Leu Pro
145                 150                 155                 160

Thr Ala Pro Thr Ser Leu Ser Gly Gln His Arg Ser Leu Arg Leu Ala
                165                 170                 175

Ser Lys Pro Glu Arg Glu Val Pro Leu Gly Ala Gly Gln Gln Glu Ser
            180                 185                 190

Met Glu Ala Asp Thr Asp Leu Glu Ala Gly Leu Glu Glu Glu Ala Val
        195                 200                 205

Gly Gly Leu Gly Pro Gly Ala Trp Ala Cys Leu Pro Gly Gln Gly Leu
    210                 215                 220

Arg Tyr Leu Glu His Leu Cys Leu Val Leu Glu Gln Met Ala Arg Leu
225                 230                 235                 240

Gln Gln Leu Tyr Leu Gln Leu Arg Ile Gln Arg Pro Pro Gly Asp Pro
                245                 250                 255

Gly Glu Glu Glu Ser Thr Arg Ala Pro Leu Pro Ser Pro Leu His Thr
            260                 265                 270
```

Pro Gly Asn Arg Gly Gln Gly Pro Trp Glu Leu Leu Ser Gln Thr Glu
275 280 285

His Thr Gly
290

<210> 1089
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 273; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC037459.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428700"

<400> 1089
Met Asp Ser Glu Gly Gly Ser Leu Leu Leu Asp Glu Asp Ser Glu Val
1 5 10 15

Phe Lys Met Leu Gln Glu Asn Arg Glu Gly Arg Ala Ala Pro Arg Gln
20 25 30

Ser Ser Ser Phe Arg Leu Leu Gln Glu Ala Leu Glu Ala Glu Glu Arg
35 40 45

Gly Gly Thr Pro Ala Phe Leu Pro Ser Ser Leu Ser Pro Gln Ser Ser
50 55 60

Leu Pro Ala Ser Arg Ala Leu Ala Thr Pro Pro Lys Leu His Thr Cys
65 70 75 80

Glu Lys Cys Ser Thr Ser Ile Ala Asn Gln Ala Val Arg Ile Gln Glu
85 90 95

Gly Arg Tyr Arg His Pro Gly Cys Tyr Thr Cys Ala Asp Cys Gly Leu

100 105 110

Asn Leu Lys Met Arg Gly His Phe Trp Met Gly Leu Ala Arg Ala Trp
115 120 125

His Gly Ala Ala
130

<210> 1090
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 273; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC037459.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429988"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1090
Xaa Ala Val Leu Val Leu Pro Pro Ser Pro Gly Pro Arg Ser Ser Arg
1 5 10 15

Pro Ser Met Asp Ser Glu Gly Gly Ser Leu Leu Leu Asp Glu Asp Ser
20 25 30

Glu Val Phe Lys Met Leu Gln Glu Asn Arg Glu Gly Arg Ala Ala Pro
35 40 45

Arg Gln Ser Ser Ser Phe Arg Leu Leu Gln Glu Ala Leu Glu Ala Glu
50 55 60

Glu Arg Gly Gly Thr Pro Ala Phe Leu Pro Ser Ser Leu Ser Pro Gln

65 70 75 80

Ser Ser Leu Pro Ala Ser Arg Ala Leu Ala Thr Pro Pro Lys Leu His
85 90 95

Thr Cys Glu Lys Cys Ser Thr Ser Ile Ala Trp Gly Trp Arg Gly Pro
100 105 110

Gly Thr Gly Leu His Ser Ala Trp Ser His Gln His Leu Gln Thr Asp
115 120 125

Pro Arg Arg Cys Pro Arg Val Leu Ile Leu Gly Glu Arg
130 135 140

<210> 1091
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 274; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC037482.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459798"

<400> 1091
Met Val Ser Ser Cys Cys Gly Ser Val Cys Ser Asp Gln Gly Cys Gly
1 5 10 15

Gln Val Leu Cys Gln Glu Thr Cys Cys Arg Pro Ser Cys Cys Gln Thr
20 25 30

Thr Cys Cys Arg Thr Thr Cys Tyr Arg Pro Ser Cys Cys Val Ser Ser
35 40 45

Cys Cys Arg Pro Gln Cys Cys Gln Ser Val Cys Cys Gln Pro Thr Cys
50 55 60

```
Cys Arg Pro Ser Cys Cys Glu Thr Thr Cys Cys His Pro Arg Cys Cys
65                  70                  75                  80

Ile Ser Ser Cys Cys Arg Pro Ser Cys Cys Met Ser Ser Cys Cys Lys
                85                  90                  95

Pro Gln Cys Cys Gln Ser Val Cys Cys Gln Pro Thr Cys Cys His Pro
            100                 105                 110

Ser Cys Cys Ile Ser Ser Cys Cys Arg Pro Ser Cys Cys Val Ser Arg
        115                 120                 125

Cys Cys Arg Pro Gln Cys Cys Gln Ser Val Cys Cys Gln Pro Thr Cys
    130                 135                 140

Cys Arg Pro Ser Cys Cys Ile Ser Ser Cys Cys Arg Pro Ser Cys Cys
145                 150                 155                 160

Glu Ser Ser Cys Cys Arg Pro Cys Cys Cys Arg Pro Cys Cys Cys Leu
                165                 170                 175

Arg Pro Val Cys Gly Arg Val Ser Cys His Thr Thr Cys Tyr Arg Pro
            180                 185                 190

Thr Cys Val Ile Ser Thr Cys Pro Arg Pro Leu Cys Cys Ala Ser Ser
        195                 200                 205

Cys Cys
    210


<210> 1092
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 275; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
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AC055733.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485356"

<400> 1092
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1   5   10   15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
            20   25   30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
        35   40   45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
    50   55   60

Pro Cys Leu Leu Leu Ser Ile Gln Thr Arg Gln Pro Cys Asp Phe Ser
65   70   75   80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
                85   90   95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
            100   105   110

Gly Gly Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
        115   120

<210> 1093
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 276; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC055866.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486664"

<400> 1093
Gly Asp Phe Leu Pro Pro Gly Gln Val Val Leu
1   5   10

<210> 1094
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 277; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC063956.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485465"

<400> 1094
Ile Lys Phe Arg Leu Phe Ala Ile Ser Leu Ile Leu Met Leu Ser Val
1   5   10   15

Thr

<210> 1095
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC063956.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488950"

<400> 1095
Ile Lys Phe Arg Leu Phe Ala Ile Ser Leu Ile Leu Met Leu Ser Val
1   5   10   15

Thr

<210> 1096
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 279; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC064829.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485106"

<400> 1096
Thr His Leu His Arg Gly Leu Phe Leu Cys Gln Ala Ala Gly Asn Cys
1   5   10   15

Arg Ile Gln Asp Ile Ser Val Val Arg Ser His Trp Arg Lys Arg Phe
            20   25   30

Leu Asn Ser Glu Val Val Ala Glu Asn Cys Phe Ser Asp Phe Ile Pro
        35   40   45

Glu Arg Gly Cys Val Gln Glu Ser Gly Pro Met Glu Ile Gly Leu Leu
    50   55   60

Ser Gly Lys Val Glu Gly Pro His Pro Pro Leu Thr Arg Leu Tyr Pro
65   70   75   80

```
Leu Pro Tyr Leu Ile Leu Phe Leu Leu Thr Leu Cys Val Pro Lys
                85                  90                  95


<210> 1097
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 279; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC064829.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485522"

<400> 1097
Met Gln Ser Gln Arg Gly Leu Leu Leu Cys Gln Ala Thr Gly Thr Cys
1               5                   10                  15


Gly Ile Cys Ala Val Ser Val Val Gly Ser Leu Trp Arg Arg Arg Cys
            20                  25                  30


Gln Asp Cys Glu Val Val Ala Glu Asn Cys Phe Ser Asp Phe Ile Pro
        35                  40                  45


Glu Arg Gly Cys Val Gln Glu Ser Gly Pro Met Glu Ile Gly Leu Leu
    50                  55                  60


Ser Ala Leu His Gly Leu Ser Gly Lys Gly Arg His His Asp Lys Gly
65                  70                  75                  80


Lys Ser Lys Ile Lys Gln Cys Ser His Met Ser Asn Trp Pro Leu Lys
                85                  90                  95


Gly Ala Gly Lys Val Glu Gly Pro His Pro Pro Leu Thr Arg Leu Tyr
            100                 105                 110


Pro Leu Pro Tyr Leu Ile Leu Phe Leu Leu Thr Leu Cys Val Pro Lys
        115                 120                 125
```

<210> 1098
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 280; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC066615.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453665"

<400> 1098

Met	Thr	Leu	Asn	Glu	His	Ala	Ala	Phe	Lys	His	Leu	Phe	Asn	Lys	Ala
1				5				10						15	
His	Leu	Ala	Pro	Pro	Leu	Ile	His	Leu	Thr	Leu	Ser	Gly	His	Ser	Thr
			20					25					30		
Cys	Phe	Arg	Glu	His	Arg	Val	Gly	Asp	Lys	Val	Thr	Asp	Gln	Gln	Asp
		35					40					45			
Pro	Lys	Ala	Glu	Glu	Phe	Phe	Leu	Val	Gln	Asn	Lys	Met	Lys	Ser	Leu
	50					55					60				
Pro	Cys	Leu	Leu	Leu	Ser	Thr	Gln	Thr	Arg	Gln	Pro	Ser	Asp	Phe	Ser
65					70					75					80
Ile	Phe	Ser	Pro	Pro	Phe	Pro	Pro	Phe	Tyr	Ser	Thr	Lys	Pro	Pro	Leu
				85					90					95	
Ser	Ser	Trp	Pro	Ile	Pro	Asn	Glu	Pro	Leu	Gly	Thr	Pro	Pro	Arg	Arg
			100					105					110		
Gly	Cys	Gly	Arg	Ala	Glu	Gly	Leu	Leu	Thr	Ser	Gln				
		115					120								

<210> 1099
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 281; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC068533.7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396527"

<400> 1099

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Met Asp Ala Thr Ser Glu Arg Asp Phe Val Ala Glu Phe Leu Phe Trp
1               5                  10                  15

Ala Ser Leu Cys Met Thr His Leu Ser Arg Met Ala Glu Asp Leu Ile
            20                  25                  30

Leu Tyr Cys Thr Lys Glu Phe Ser Phe Val Gln Leu Ser Asp Ala Tyr
        35                  40                  45

Ser Thr Gly Ser Ser Leu Met Pro Gln Lys Lys Asn Pro Asp Ser Leu
    50                  55                  60

Glu Leu Ile Arg Ser Lys Ala Gly Arg Val Phe Gly Arg Cys Ala Gly
65                  70                  75                  80

Leu Leu Met Thr Leu Lys Gly Leu Pro Ser Thr Tyr Asn Lys Asp Leu
                85                  90                  95

Gln Glu Asp Lys Glu Ala Val Phe Glu Val Ser Asp Thr Met Ser Ala
            100                 105                 110

Val Leu Gln Val Ala Thr Gly Val Ile Ser Thr Leu Gln Ile His Gln
        115                 120                 125

Glu Asn Met Gly Gln Ala Leu Ser Pro Asp Met Leu Ala Thr Asp Leu
    130                 135                 140
```

```
Ala Tyr Tyr Leu Val Arg Lys Gly Met Pro Phe Arg Gln Ala His Glu
145                 150                 155                 160

Ala Ser Gly Lys Ala Val Phe Met Ala Glu Thr Lys Gly Val Ala Leu
                165                 170                 175

Asn Gln Leu Ser Leu Gln Glu Leu Gln Thr Ile Arg Lys Asp Ala Asn
            180                 185                 190

Ser Ala Leu Leu Ser Asn Tyr Glu Val Phe Gln Leu Leu Thr Asp Leu
        195                 200                 205

Lys Glu Gln Arg Lys Glu Ser Gly Lys Asn Lys His Ser Ser Gly Gln
    210                 215                 220

Gln Asn Leu Asn Thr Ile Thr Tyr Glu Thr Leu Lys Tyr Ile Ser Lys
225                 230                 235                 240

Thr Pro Cys Arg His Gln Ser Pro Glu Ile Val Arg Glu Phe Leu Thr
                245                 250                 255

Ala Leu Lys Ser His Lys Leu Thr Lys Ala Glu Lys Leu Gln Leu Leu
            260                 265                 270

Asn His Arg Pro Val Thr Ala Val Glu Ile Gln Leu Met Val Glu Glu
        275                 280                 285

Ser Glu Glu Arg Leu Thr Glu Glu Gln Ile Glu Ala Leu Leu His Thr
    290                 295                 300

Val Thr Ser
305


<210> 1100
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 282; "

<220>
<221> source
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<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC069063.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485481"

<400> 1100
Met Thr His Ile Tyr Ser Asn Phe Cys Phe Asn Lys Ser Val Phe Ala
1 5 10 15

Phe Asp Leu Ile Pro Met
20

<210> 1101
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 283; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC069063.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485237"

<400> 1101
Met Ile Pro Leu Tyr Pro Ser Phe Asn Phe Asn Lys Ser His Phe Ala
1 5 10 15

Phe Gln Ile Leu Pro Ile Ala Thr Asn Ile Leu Phe Phe Ser Gly Val
20 25 30

Ala Glu Leu Ile
35

<210> 1102
<211> 227

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 284; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC069368.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397942"

<400> 1102
Met Glu Glu Glu Gly Val Lys Glu Ala Gly Glu Lys Pro Arg Gly Ala
1 5 10 15

Gln Met Val Asp Lys Ala Gly Trp Ile Lys Lys Ser Ser Gly Gly Leu
20 25 30

Leu Gly Phe Trp Lys Asp Arg Tyr Leu Leu Leu Cys Gln Ala Gln Leu
35 40 45

Leu Val Tyr Glu Asn Glu Asp Asp Gln Lys Cys Val Glu Thr Val Glu
50 55 60

Leu Gly Ser Tyr Glu Lys Cys Gln Asp Leu Arg Ala Leu Leu Lys Arg
65 70 75 80

Lys His Arg Phe Ile Leu Leu Arg Ser Pro Gly Asn Lys Val Ser Asp
85 90 95

Ile Lys Phe Gln Ala Pro Thr Gly Glu Glu Lys Glu Ser Trp Ile Lys
100 105 110

Ala Leu Asn Glu Gly Ile Asn Arg Gly Lys Asn Lys Ala Phe Asp Glu
115 120 125

Val Lys Val Asp Lys Ser Cys Ala Leu Glu His Val Thr Arg Asp Arg
130 135 140

```
Val Arg Gly Gly Gln Arg Arg Arg Pro Pro Thr Arg Val His Leu Lys
145                 150                 155                 160

Glu Phe Gly Met Asn Ala Leu Leu Leu Ser Ala Trp Phe Gly His Leu
                165                 170                 175

Arg Ile Leu Gln Ile Leu Val Asn Ser Gly Ala Lys Ile His Cys Glu
            180                 185                 190

Ser Lys Glu Gly Asn Thr Ala Leu His Leu Ala Ala Gly Arg Gly His
        195                 200                 205

Met Ala Val Leu Gln Arg Leu Val Asp Ile Gly Leu Asp Leu Glu Glu
    210                 215                 220

Gln Asn Ala
225
```

<210> 1103
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 285; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC069499.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486986"

<400> 1103
```
Ala Lys Ser Ser Cys Leu Lys Ala Leu Leu Ile Arg Val Ser His Tyr
1               5                   10                  15
```

<210> 1104
<211> 41
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 286; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC073072.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486755"

<400> 1104
Trp Leu Met Pro Val Ile Ser Ala Leu Trp Glu Ala Lys Val Gly Gly
1 5 10 15

Ser Pro Glu Ile Cys Ser Phe Ser Gly Val Gln Asp Gln Pro Gly Gln
20 25 30

His Gly Glu Thr Gln Ser Leu Gln Lys
35 40

<210> 1105
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 287; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC073130.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486045"

<400> 1105
Leu Glu Gln Glu Ser Glu Val Lys Lys Met Gly Lys Gly His Glu Gln
1 5 10 15

<210> 1106

<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 288; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC073333.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485072"

<400> 1106

Met	Val	Met	Thr	Leu	Asn	Glu	His	Ala	Ala	Phe	Lys	His	Leu	Phe	Asn
1				5				10						15	

Lys	Ala	His	Leu	Ala	Pro	Pro	Leu	Ile	His	Leu	Thr	Leu	Ser	Gly	His
			20					25					30		

Ser	Thr	Cys	Phe	Arg	Glu	His	Arg	Val	Gly	Gly	Lys	Val	Ile	Asp	Gln
		35					40					45			

Gln	Asp	Pro	Lys	Ala	Glu	Glu	Phe	Phe	Leu	Val	Gln	Asn	Lys	Met	Lys
	50					55					60				

Ser	Leu	Pro	Cys	Leu	Leu	Leu	Ser	Thr	Gln	Thr	Gln	Gln	Pro	Ser	Asp
65				70					75						80

Phe	Ser	Ile	Phe	Ser	Pro	Pro	Phe	Pro	Leu	Phe	Tyr	Ser	Thr	Lys	Pro
				85					90					95	

Pro	Leu	Ser	Ser	Trp	Pro	Val	Leu	Asn	Glu	Leu	Leu	Gly	Thr	Pro	Pro
			100					105					110		

Arg	Arg	Gly	Gly	Gly	Arg	Ala	Glu	Gly	Leu	Leu	Thr	Ser	Gln		
		115					120					125			

<210> 1107
<211> 62
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 289; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC073610.5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443189"

<400> 1107
Asn Lys Gln Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp
1 5 10 15

Lys Leu Gly Leu His Ser Leu Arg His Arg Asn Trp Tyr Ile Gln Ala
20 25 30

Thr Cys Ala Thr Ser Gly Asp Gly Leu Tyr Glu Gly Leu Asp Trp Leu
35 40 45

Ala Asn Gln Leu Lys Asn Lys Asn Gly Cys Ser Gly Ala Val
50 55 60

<210> 1108
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 290; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC073657.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485571"

<400> 1108
Lys Asn Gln Ser Phe Phe Phe Leu Arg Arg Ser Phe Ala Leu Ser Pro
1   5   10   15

Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala His Cys Lys Leu Cys Leu
            20   25   30

Pro Gly Ser Arg His Ser Pro Ala Pro Ala Thr Arg Glu Ala Glu Ala
        35   40   45

Arg Glu Ser Leu Glu Pro Gly Arg Trp Arg Leu Gln
    50   55   60

<210> 1109
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 291; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC074033.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486275"

<400> 1109
Ser Gly Ser Asn Phe Asp Pro Phe Leu Gln Lys Leu Leu Lys Ile
1   5   10   15

<210> 1110
<211> 215
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 292; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC079355.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484537"

<400> 1110
Thr Ala Ser Gly Arg Trp Ala Ser Pro Gly Pro Ala Trp Ala Ser Arg
1 5 10 15

Arg Pro Leu Gln Ala Gln Val Val Leu Lys Ser Ala Ser Pro Gly Pro
20 25 30

Ala Pro Ala Ser Gln Gln Ala Ser Ser Phe Gly Ser Ala Pro Ala Gln
35 40 45

Leu Pro Pro Ala Phe Val Asp Pro Glu Leu Ser Pro Ala Lys Leu Leu
50 55 60

Ser Pro Thr Ser Cys Leu Pro Val Ala Cys Thr Gly Pro Gly Leu Ala
65 70 75 80

Gly Glu Gln Pro Leu Gln Ala Pro Leu Leu Pro Pro Arg Gly Val Ser
85 90 95

Arg Pro Ser Ser Arg Leu Thr Ala Ala Ser Arg Asp Gln Val Pro Ala
100 105 110

Cys Leu Pro Ala Ala Cys Val Arg Pro Ser Ser Ser Val Thr Val Ala
115 120 125

Cys Gly Pro Thr His Ala Ser Gly Thr Leu Ser Arg Gly Val Ser Pro
130 135 140

Cys Leu Thr Leu Ala Ser Leu Thr Leu Arg Glu Val Ser Val Ser Pro
145 150 155 160

Cys Leu Thr Leu Ala Ser Leu Thr Leu Arg Glu Val Ser Val Ser Pro
165 170 175

Cys Leu Thr Leu Ala Ser Leu Thr Leu Arg Glu Val Leu Pro His Ala
180 185 190

Gly Leu Leu Arg Pro Ser Ser Cys Leu Cys Trp Leu Leu Leu Ala Gln
195 200 205

Pro Leu Pro Val Gly Gly Leu
210 215

<210> 1111
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 293; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC079907.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486880"

<400> 1111
Asn Arg Phe Ser Leu Ile Val Asp His Glu Thr Gly Ser Cys Ser Val
1 5 10 15

Thr Gln Ala Gly Val
20

<210> 1112
<211> 598
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 294; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:

AC084219.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467018"

<400> 1112

```
Met Ile Asp Ser Gly Glu Lys Lys Pro Gly Arg Arg Ala Glu Glu Ala
1               5                  10                  15

Val Thr Phe Lys Asp Val Ala Val Ile Phe Thr Glu Glu Glu Leu Gly
            20                  25                  30

Leu Leu Asp Pro Ala Gln Arg Lys Leu Tyr Arg Asp Val Met Leu Glu
        35                  40                  45

Asn Phe Arg Asn Leu Leu Ser Val Gly His Gln Pro Phe His Gly Asp
    50                  55                  60

Thr Phe His Phe Leu Arg Glu Glu Lys Phe Trp Val Met Gly Thr Thr
65                  70                  75                  80

Ser Gln Arg Glu Gly Asn Leu Gly Thr Ile Leu Leu Ser Leu Glu Leu
                85                  90                  95

Cys His Ser Gly Leu Cys Lys Phe Pro Lys Val Gly Gly Lys Met Thr
            100                 105                 110

Met Ser Lys Glu Ala Val Thr Phe Lys Asp Val Ala Val Val Phe Thr
        115                 120                 125

Glu Glu Glu Leu Gly Leu Leu Asp Leu Ala Gln Arg Lys Leu Tyr Arg
    130                 135                 140

Asp Val Met Leu Glu Asn Phe Arg Asn Leu Leu Ser Val Gly His Gln
145                 150                 155                 160

Pro Phe His Arg Asp Thr Phe His Phe Leu Arg Glu Glu Lys Phe Trp
                165                 170                 175

Met Met Asp Ile Ala Thr Gln Arg Glu Gly Asn Ser Gly Gly Lys Ile
            180                 185                 190

Gln Pro Glu Met Lys Thr Phe Pro Glu Ala Gly Pro His Glu Gly Trp
        195                 200                 205
```

```
Ser Cys Gln Gln Ile Trp Glu Glu Ile Ala Ser Asp Leu Thr Arg Pro
    210                 215                 220

Gln Asp Ser Thr Ile Lys Ser Ser Gln Phe Phe Glu Gln Gly Asp Ala
225                 230                 235                 240

His Ser Gln Val Glu Glu Gly Leu Ser Ile Met His Thr Gly Gln Lys
                245                 250                 255

Pro Ser Asn Cys Gly Lys Cys Lys Gln Ser Phe Ser Asp Met Ser Ile
            260                 265                 270

Phe Asp Leu Pro Gln Gln Ile Arg Ser Ala Glu Lys Ser His Ser Cys
        275                 280                 285

Asp Glu Cys Gly Lys Ser Phe Cys Tyr Ile Ser Ala Leu His Ile His
    290                 295                 300

Gln Arg Val His Leu Gly Glu Lys Leu Phe Lys Cys Asp Val Cys Gly
305                 310                 315                 320

Lys Glu Phe Ser Gln Ser Leu His Leu Gln Thr His Gln Arg Val His
                325                 330                 335

Thr Gly Glu Lys Pro Phe Lys Cys Glu Gln Cys Gly Arg Gly Phe Arg
            340                 345                 350

Cys Arg Ser Ala Leu Thr Val His Cys Lys Leu His Met Gly Glu Lys
        355                 360                 365

His Tyr Asn Cys Glu Ala Cys Gly Arg Ala Phe Ile His Asp Phe Gln
    370                 375                 380

Leu Gln Lys His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Lys Cys
385                 390                 395                 400

Glu Ile Cys Ser Val Ser Phe Arg Leu Arg Ser Ser Leu Asn Arg His
                405                 410                 415

Cys Val Val His Thr Gly Lys Lys Pro Asn Ser Thr Gly Glu Tyr Gly
            420                 425                 430
```

```
Lys Gly Phe Ile Arg Arg Leu Asp Leu Cys Lys His Gln Thr Ile His
        435                 440                 445

Thr Gly Glu Lys Pro Tyr Asn Cys Lys Glu Cys Gly Lys Ser Phe Arg
    450                 455                 460

Arg Ser Ser Tyr Leu Leu Ile His Gln Arg Val His Thr Gly Glu Lys
465                 470                 475                 480

Pro Tyr Lys Cys Asp Lys Cys Gly Lys Ser Tyr Ile Thr Lys Ser Gly
                485                 490                 495

Leu Asp Leu His His Arg Ala His Thr Gly Glu Arg Pro Tyr Asn Cys
            500                 505                 510

Asp Asp Cys Gly Lys Ser Phe Arg Gln Ala Ser Ser Ile Leu Asn His
        515                 520                 525

Lys Arg Leu His Cys Arg Lys Lys Pro Phe Lys Cys Glu Asp Cys Gly
    530                 535                 540

Lys Lys Leu Val Tyr Arg Ser Tyr Arg Lys Asp Gln Gln Lys Asn His
545                 550                 555                 560

Ser Gly Glu Asn Pro Ser Lys Cys Glu Asp Cys Gly Lys Arg Tyr Lys
                565                 570                 575

Arg Arg Leu Asn Leu Asp Ile Ile Leu Ser Leu Phe Leu Asn Asp Thr
            580                 585                 590

His Asn Ser Val Phe Ser
        595


<210> 1113
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 295; "

<220>
<221> source
<223> /note="Gene Symbol:; "
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<220>
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<223> /note="Gene Name:
AC087350.1; "

<220>
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<223> /note="ENSP ID: ENSP00000487350"

<400> 1113
Phe Leu Val Leu Lys Lys Phe Lys Gly Leu Thr Phe Thr Gln Ser Lys
1 5 10 15

Cys Phe Ser Lys Val Met Leu Tyr Pro Gly Pro Ser Tyr Tyr Ile Val
20 25 30

<210> 1114
<211> 19
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 296; "

<220>
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<223> /note="Gene Symbol:; "

<220>
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<223> /note="Gene Name:
AC087392.1; "

<220>
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<223> /note="ENSP ID: ENSP00000486177"

<400> 1114
Cys Ser Thr Val Arg Leu Glu Cys Thr Gly Met Ile Ser Ala His Cys
1 5 10 15

Asn Leu Cys

<210> 1115
<211> 21
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 297; "

<220>
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<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC087651.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487442"

<400> 1115
Arg Ala Leu Arg Pro Ser Val Leu Pro Gly Ser Thr Val Arg Ile Lys
1 5 10 15

Pro Glu Leu Gly Gly
20

<210> 1116
<211> 21
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 298; "

<220>
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<220>
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<223> /note="Gene Name:
AC087651.2; "

<220>
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<223> /note="ENSP ID: ENSP00000486689"

<400> 1116
Gln Met Gln Lys Ala Val Gln Ser Ser Leu Lys Arg Trp Gly Phe Thr
1 5 10 15

Ile Leu Ala Arg Leu
20

<210> 1117
<211> 174

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 299; "

<220>
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<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC087762.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485301"

<400> 1117
Met Leu Cys Pro Cys Leu Gly Thr Ala Ser Phe Pro Leu Pro Ile Trp
1 5 10 15

Leu Pro Ala Ala Pro Cys Val Pro Thr Pro Pro Ala Pro Val Phe Gly
20 25 30

Trp Pro Pro Leu Pro Ala Glu Pro Val Pro Leu Arg Ser Cys Gln Gln
35 40 45

Trp Gly Cys Ala Arg Pro Pro Pro Val Leu Gln Gly Ala Gly Phe Leu
50 55 60

Leu Arg Pro Ser Arg Val Ser Ser Ser Ser Ala Pro Cys Thr Arg Ser
65 70 75 80

Ala Asp Leu Thr Glu Ser Ala Pro Leu Leu Gln Leu Ala Leu Ala Ser
85 90 95

Cys Leu Pro Leu Ser Asp Pro Val Val Phe Cys Leu Leu Gly Leu Pro
100 105 110

Pro Gly Leu Ala Ala Val Ser Leu Pro Gln Leu Val Phe Trp Gly Ile
115 120 125

Ser Asn Leu Pro Glu Leu Pro Leu Pro Ile Trp Ser Pro Asp Leu Gly
130 135 140

Ser Thr Thr Pro Leu Gln Asn Ser Pro Pro Ser Thr Pro Pro Trp Gly
145 150 155 160

Leu Gln Ala Pro Ser Lys Glu Gln Gln Asp Ser Pro Ser Gln
165 170

<210> 1118
<211> 57
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
AC090154.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485600"

<400> 1118
Gly Trp Ala Arg Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Thr
1 5 10 15

Glu Ala Gly Gly Ser Pro Glu Val Arg Ser Ser Arg Pro Ala Trp Pro
20 25 30

Thr Trp Arg Asn Pro Val Ser Thr Lys Met Thr Lys Leu Leu Gln Ile
35 40 45

Tyr Glu Leu Met Leu Glu Tyr Gln Ala
50 55

<210> 1119
<211> 25
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 301; "

<220>

<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC090498.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485567"

<400> 1119
Met Arg Ala Lys Trp Arg Lys Lys Arg Met Arg Arg Leu Lys Arg Lys
1 5 10 15

Arg Arg Lys Met Arg Gln Arg Ser Lys
20 25

<210> 1120
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 302; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC090958.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487458"

<400> 1120
Met Ala Leu Gln Thr Leu Gln Ser Ser Trp Val Thr Phe Arg Lys Ile
1 5 10 15

Leu Ser His Phe Pro Glu Glu Leu Ser Leu Ala Phe Val Tyr Gly Ser
20 25 30

Gly Val Tyr Arg Gln Ala Gly Pro Ser Ser Asp Gln Lys Ser Tyr Leu
35 40 45

Thr Ala Ala Ser Arg Thr Cys Trp Leu Pro Tyr Pro Gln Ser Thr Phe

50 55 60

Leu Gln His Gly Ser Leu Pro Phe Pro Val Leu Pro Pro Val Leu Pro
65 70 75 80

Ala Ser Leu Phe Asn Ser Arg Val Leu Gln Asp Ser Asp Leu Ser Ser
85 90 95

Leu Gly Glu Phe Leu Pro Pro Val Pro Leu Ile
100 105

<210> 1121
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 303; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC091180.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486343"

<400> 1121
Ser Lys Val Glu Gln Asn Thr Thr Pro Ser Pro His Pro Pro Gln Pro
1 5 10 15

Glu

<210> 1122
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 304; "

<220>
<221> source

<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC091304.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484734"

<400> 1122
Met Arg Ala Lys Trp Arg Lys Lys Arg Met Arg Arg Leu Lys Arg Lys
1 5 10 15

Arg Arg Lys Met Arg Gln Arg Ser Lys
20 25

<210> 1123
<211> 46
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 305; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC092159.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485157"

<400> 1123
Met Ala Val Thr Thr Phe Arg Arg Asn Ile Pro Ile Lys Thr Gln Gln
1 5 10 15

Ile Trp Lys Thr Glu His Met Lys Gln Lys Tyr Leu Lys Ile Phe Arg
20 25 30

Asn Leu Glu Asn Leu Asn Tyr Ile Leu Arg His Arg Met Ser
35 40 45

<210> 1124
<211> 16

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 306; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC092384.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486761"

<400> 1124
Ala Asp Gly Asp Arg Gln Leu Leu Gln Gln Lys Val Arg Ser Phe Pro
1 5 10 15

<210> 1125
<211> 306
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 307; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC092718.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485105"

<400> 1125
Met Gly Glu Asp Ser Pro Val Ala Met Phe Ser Trp Tyr Leu Asp Asn
1 5 10 15

Thr Pro Thr Glu Gln Ala Glu Pro Leu Leu Asp Ala Cys Arg Leu Arg
20 25 30

Gly Phe Trp Pro Arg Ser Leu Thr Leu Leu Gln Ser Asn Thr Ser Thr

```
        35                  40                  45

Leu Leu Leu Asn Ser Ser Phe Leu Gln Ser Arg Gly Glu Val Ile Arg
    50                  55                  60

Ile Arg Ala Thr Ala Leu Thr Arg His Ala Tyr Gly Glu Asp Thr Tyr
65                  70                  75                  80

Val Ile Ser Thr Val Pro Pro Arg Glu Val Pro Ala Cys Thr Ile Ala
                85                  90                  95

Pro Glu Glu Gly Thr Val Leu Thr Ser Phe Ala Ile Phe Cys Asn Ala
            100                 105                 110

Ser Thr Ala Leu Gly Pro Leu Glu Phe Cys Phe Cys Leu Glu Ser Gly
        115                 120                 125

Ser Cys Leu His Cys Gly Pro Glu Pro Ala Leu Pro Ser Val Tyr Leu
    130                 135                 140

Pro Leu Gly Glu Glu Asn Asn Asp Phe Val Leu Thr Val Val Ile Ser
145                 150                 155                 160

Ala Thr Asn Arg Ala Gly Asp Thr Gln Gln Thr Gln Ala Met Ala Lys
                165                 170                 175

Val Ala Leu Gly Asp Thr Cys Val Glu Asp Val Ala Phe Gln Ala Ala
            180                 185                 190

Val Ser Glu Lys Ile Pro Thr Ala Leu Gln Gly Glu Gly Gly Pro Glu
        195                 200                 205

Gln Leu Leu Gln Leu Ala Lys Ala Val Ser Ser Met Leu Asn Gln Glu
    210                 215                 220

His Glu Ser Gln Gly Ser Gly Gln Ser Leu Ser Ile Asp Val Arg Gln
225                 230                 235                 240

Lys Val Arg Glu His Val Leu Gly Ser Leu Ser Ala Val Thr Thr Gly
                245                 250                 255

Leu Glu Asp Val Gln Arg Val Gln Glu Leu Ala Glu Val Leu Arg Glu
            260                 265                 270
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Val Thr Cys Arg Ser Lys Glu Leu Thr Pro Ser Ala Gln Gly Ser Cys
275 280 285

Met Gly Asp Ser Trp Glu Gly Ala Pro Pro Ala Ala His Val Ser His
290 295 300

Ala Arg
305

<210> 1126
<211> 522
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 308; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC092835.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478941"

<400> 1126
Met Glu Pro Glu Gly Arg Gly Ser Leu Phe Glu Asp Ser Asp Leu Leu
1 5 10 15

His Ala Gly Asn Pro Lys Glu Asn Asp Val Thr Ala Val Leu Leu Thr
20 25 30

Pro Gly Ser Gln Glu Leu Met Ile Arg Asp Met Ala Glu Ala Leu Thr
35 40 45

Gln Trp Arg Gln Leu Asn Ser Pro Gln Gly Asp Val Pro Glu Lys Pro
50 55 60

Arg Asn Leu Val Leu Leu Gly Leu Pro Ile Ser Thr Pro Asp Val Ile
65 70 75 80

```
Ser Gln Leu Glu His Glu Glu Glu Leu Glu Arg Glu Val Ser Lys Ala
                85                  90                  95

Ala Ser Gln Lys His Trp Glu Thr Ile Pro Glu Ser Lys Glu Leu Thr
            100                 105                 110

Pro Glu Lys Asp Ile Ser Glu Glu Glu Ser Ala Pro Gly Val Leu Ile
        115                 120                 125

Val Arg Phe Ser Lys Glu Ser Ser Ser Glu Cys Glu Asp Ser Leu Glu
    130                 135                 140

Ser Gln Gln Glu Asn His Glu Lys His Leu Ile Gln Glu Ala Val Thr
145                 150                 155                 160

Glu Lys Ser Ser Arg Glu Arg Ser Tyr Gln Ser Asp Glu Phe Arg Arg
                165                 170                 175

Asn Cys Thr Gln Arg Ser Leu Leu Val Gln Gln Gln Gly Glu Arg Leu
            180                 185                 190

His His Cys Asp Ser Phe Lys Asn Asn Leu Lys Gln Asn Ser Asp Ile
        195                 200                 205

Ile Arg His Glu Arg Ile Cys Ala Gly Lys Lys Pro Trp Lys Cys Asn
    210                 215                 220

Glu Cys Glu Lys Ala Phe Ser Tyr Tyr Ser Ala Phe Val Leu His Gln
225                 230                 235                 240

Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys
                245                 250                 255

Ala Phe Ser Gln Ser Ile His Leu Thr Leu His Gln Arg Ile His Thr
            260                 265                 270

Gly Glu Lys Pro Tyr Glu Cys His Glu Cys Gly Lys Ala Phe Ser His
        275                 280                 285

Arg Ser Ala Leu Ile Arg His His Ile Ile His Thr Gly Glu Lys Pro
    290                 295                 300

Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser Tyr Leu
```

305 310 315 320

Thr Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asn
325 330 335

Glu Cys Gly Lys Ala Phe Ser Gln Ser Thr Phe Leu Thr Gln His Gln
340 345 350

Val Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys
355 360 365

Ala Phe Ser Asp Arg Ser Gly Leu Ile Gln His Gln Arg Thr His Thr
370 375 380

Gly Glu Arg Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Gly Tyr
385 390 395 400

Cys Ser Ala Leu Thr Gln His Gln Arg Thr His Thr Gly Glu Lys Pro
405 410 415

Tyr Lys Cys Asn Asp Cys Ala Lys Ala Phe Ser Asp Arg Ser Ala Leu
420 425 430

Ile Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Lys
435 440 445

Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Ser Leu Thr Lys His Gln
450 455 460

Lys Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys
465 470 475 480

Ala Phe Ser Gln Ser Ser Ser Leu Ser Gln His Gln Lys Thr His Ala
485 490 495

Gly Val Lys Thr Lys Lys Tyr Val Gln Ala Leu Ser Glu His Leu Thr
500 505 510

Phe Gly Gln His Lys Arg Ile His Thr Gly
515 520

<210> 1127
<211> 123

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 308; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC092835.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482715"

<400> 1127
Met Glu Pro Glu Gly Arg Gly Ser Leu Phe Glu Asp Ser Asp Leu Leu
1 5 10 15

His Ala Gly Asn Pro Lys Glu Asn Asp Val Thr Ala Val Leu Leu Thr
20 25 30

Pro Gly Ser Gln Glu Leu Met Ile Arg Asp Met Ala Glu Ala Leu Thr
35 40 45

Gln Trp Arg Gln Leu Asn Ser Pro Gln Gly Asp Val Pro Glu Lys Pro
50 55 60

Arg Asn Leu Val Leu Leu Gly Leu Pro Ile Ser Thr Pro Asp Val Ile
65 70 75 80

Ser Gln Leu Glu His Glu Glu Glu Leu Glu Arg Glu Val Ser Lys Ala
85 90 95

Ala Ser Gln Lys Arg Asn Ser Leu Gly Asp Asn Ser Pro Leu Lys Asn
100 105 110

Val Pro Phe Phe Trp Arg Lys Glu Gly Thr Phe
115 120

<210> 1128
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 309; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC092881.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485076"

<400> 1128
Met Gln Leu Glu Tyr Lys Ser Met Phe Ile Gly Phe Tyr Ser Tyr His
1 5 10 15

Ser Met Tyr Ser Ile His Val Asn Tyr Trp Met Lys Ser Pro Ile Ile
20 25 30

Tyr Ile Phe Gly Tyr Asn His Thr Ile Leu Glu Leu Lys Thr Ile Gln
35 40 45

Val Ser Val Pro Ala Phe Ser Gly Tyr Leu Met Ala Leu His Asn His
50 55 60

Phe His Pro Asn Leu Ala Lys Ser Lys Phe Lys His Phe Cys Ile Tyr
65 70 75 80

Ser Lys Thr Asn Ser Leu Ser Cys Leu Ile Ser Val Thr Leu Thr Ser
85 90 95

Arg Glu Gly Thr Leu Pro Ser Ile Ser Leu Pro Pro Leu Thr Phe Leu
100 105 110

Thr Ile Lys Asn Ile Gln
115

<210> 1129
<211> 20
<212> PRT
<213> Homo sapiens

<220>

<221> source
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<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC100821.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487589"

<400> 1129
Glu Leu Met Gln Glu Val Lys Asn Ile Ser Ile Lys Leu Glu Asn Leu
1 5 10 15

Arg Trp Tyr Pro
20

<210> 1130
<211> 300
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 311; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104057.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485196"

<400> 1130
Met Arg Gly Pro Asp Gln Met Glu Ile Arg Gly Gly Pro Tyr Leu Leu
1 5 10 15

Leu Gly Glu Val Val Gly His Ser Ala Leu Gly Ala Gln Pro Ala Gln
20 25 30

Ala Ala Asn Gly Asp Ala Asp Glu Leu Leu Glu Leu Ser Ala Leu Leu

```
        35                  40                  45

Gln Pro Arg Ala Gly Arg Gly Pro Cys Ala Thr Leu Ser Gly Arg Cys
    50                  55                  60

Ile Thr Pro Ala Thr Ala Leu Leu Leu Leu Ser His Arg Leu Arg Ala
65                  70                  75                  80

Gln Cys Arg Pro Met Gln Ala Thr Ala Ala Glu Ala Gly Ser Pro Gly
                85                  90                  95

Leu Gly Arg Leu Gly Lys Glu Pro Pro Ser Arg Glu Ser Trp Thr Gly
            100                 105                 110

Ser Ala Pro Arg Arg Cys Pro Cys Gln Asp Ala Ser Arg Ala Gly Ser
        115                 120                 125

Gly Val Cys Arg Ser Arg Pro Gln Ser Arg Gly Gly Gly Ser Arg Lys
    130                 135                 140

Pro Arg Arg Gln Lys Ala Ala Ala Thr Gly Gln Lys Ala Ala Ala Ala
145                 150                 155                 160

Gln Ala Lys Ser Leu Gly Gly Gly Gly Lys Lys Pro Arg Arg Gln Lys
                165                 170                 175

Cys Ala Ala Gly Gln Lys Ala Ala Ala Glu Glu Ser Arg Arg Gly Gly
            180                 185                 190

Gly Lys Lys Pro Arg Arg Gly Gly Gln Lys Ala Val Gly Ala Gly Ala
        195                 200                 205

Lys Lys Pro Gln Lys Ala Ala Ala Ala Gly Thr Lys Thr Pro Arg Arg
    210                 215                 220

Arg Arg Gln Lys Ala Ala Lys Ala Ala Val Trp Gly Gln Lys Ala Ala
225                 230                 235                 240

Ala Gly Glu Ser Leu Thr Pro Asn Ser Leu Ala Ser Val Ser Phe Ser
                245                 250                 255

Arg Pro Met Phe Leu Arg His Tyr Pro Phe Ser Ser Cys Glu Cys Lys
            260                 265                 270
```

Ser His Lys His Gly Ser Thr Phe Asp His Phe Asn Cys Leu Thr Phe
275 280 285

His Val Thr Arg Pro Ser Thr Ile Glu Ser Met Tyr
290 295 300

<210> 1131
<211> 301
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 312; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104073.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485644"

<400> 1131
Met Arg Gly Pro Asp Gln Met Glu Ile Arg Gly Gly Pro Tyr Leu Leu
1 5 10 15

Leu Gly Glu Val Val Gly His Ser Ala Leu Gly Ala Gln Pro Ala Gln
20 25 30

Ala Ala Asn Gly Asp Ala Asp Glu Leu Leu Glu Leu Ser Ala Leu Leu
35 40 45

Gln Pro Arg Ala Gly Arg Gly Pro Cys Ala Thr Leu Ser Gly Arg Cys
50 55 60

Ile Thr Pro Ala Thr Ala Leu Leu Leu Leu Ser His Arg Leu Arg Ala
65 70 75 80

Gln Cys Arg Ser Met Gln Ala Thr Ala Ala Glu Ala Gly Ser Pro Gly
85 90 95

```
Leu Trp Arg Leu Gly Lys Glu Pro Pro Ser Arg Glu Ser Trp Thr Gly
            100                 105                 110

Ser Ala Pro Arg Arg Cys Pro Cys Gln Asp Ala Ser Arg Ala Gly Ser
        115                 120                 125

Gly Val Cys Arg Ser Arg Pro Gln Ser Arg Gly Gly Gly Ser Arg Lys
    130                 135                 140

Pro Arg Arg Gln Lys Ala Ala Ala Thr Gly Gln Lys Ala Ala Ala Ala
145                 150                 155                 160

Gln Ala Lys Ser Leu Gly Gly Gly Gly Lys Lys Pro Arg Arg Gln Lys
                165                 170                 175

Cys Ala Ala Ala Gly Gln Lys Ala Ala Ala Glu Glu Ser Arg Arg Gly
            180                 185                 190

Gly Gly Lys Lys Pro Arg Arg Gly Gly Gln Lys Ala Val Gly Ala Gly
        195                 200                 205

Ala Lys Lys Pro Gln Lys Ala Ala Ala Ala Gly Thr Lys Thr Pro Arg
    210                 215                 220

Gln Arg Arg Gln Lys Ala Ala Lys Ala Ala Val Trp Gly Gln Lys Ala
225                 230                 235                 240

Ala Ala Gly Glu Ser Leu Thr Pro Asn Ser Leu Ala Ser Val Ser Phe
                245                 250                 255

Ser Arg Pro Met Phe Leu Arg His Tyr Pro Phe Ser Ser Cys Glu Cys
            260                 265                 270

Lys Ser His Lys His Gly Ser Thr Phe Asp His Phe Asn Cys Leu Thr
        275                 280                 285

Phe His Val Thr Arg Pro Ser Thr Ile Glu Ser Met Tyr
    290                 295                 300
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<210> 1132
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 313; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104389.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485458"

<400> 1132
Met Asp Cys Gln Asn Gly His Gln His Ile Ser Gln Glu Leu Glu Val
1 5 10 15

Leu Arg Ile His Met Gln Leu Val Thr Val Gln Phe Thr Gln Leu Gly
20 25 30

Lys Gly Ala Leu Glu Ile Ile Gln Val Leu Tyr Gly Ile Ser Gln Gly
35 40 45

Ser Gln His Leu Leu Ala Met Cys Leu Asp Phe Gly Val Ala His Asp
50 55 60

Gly Arg Gly Arg Gly Gln Val Ala Lys Ala Val Lys Glu Pro Leu Gly
65 70 75 80

Pro Trp Val Asp Asn Gln Glu Pro Pro Ser Gln Gly Phe Ser Ser Ser
85 90 95

Ile Phe His Ile His Leu Ala Pro Gln Ala Cys Asp Ser Ser Leu Val
100 105 110

Leu Leu Cys Glu Met Thr His Gly Val Trp Thr Arg Ser Leu Leu Ile
115 120 125

Thr Ser Asp Val Pro Glu Ala Ser Val
130 135

<210> 1133
<211> 137
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 314; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104389.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485381"

<400> 1133

Met	Asp	Cys	Gln	Asn	Gly	His	Gln	His	Ile	Ser	Gln	Glu	Leu	Glu	Val
1				5				10						15	
Leu	Arg	Ile	His	Met	Gln	Leu	Val	Thr	Val	Gln	Phe	Thr	Gln	Leu	Gly
			20					25					30		
Lys	Gly	Ala	Leu	Glu	Ile	Ile	Gln	Val	Leu	Cys	Gly	Ile	Ser	Gln	Gly
		35					40					45			
Ser	Gln	His	Leu	Leu	Ala	Met	Cys	Leu	Asp	Phe	Gly	Val	Ala	His	Asp
	50					55					60				
Gly	Arg	Gly	Arg	Gly	Gln	Val	Ala	Lys	Ala	Val	Lys	Glu	Pro	Leu	Gly
65					70					75					80
Pro	Trp	Val	Asp	Asn	Gln	Glu	Pro	Pro	Ser	Gln	Gly	Phe	Ser	Ser	Ser
				85					90					95	
Ile	Phe	His	Ile	His	Leu	Ala	Pro	Gln	Ala	Cys	Asp	Ser	Ser	Leu	Val
			100					105					110		
Leu	Leu	Cys	Glu	Met	Thr	His	Gly	Val	Trp	Thr	Arg	Ser	Leu	Leu	Ile
		115					120					125			
Thr	Ser	Asp	Val	Pro	Glu	Ala	Ser	Val							
	130					135									

<210> 1134

<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 315; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104532.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468419"

<400> 1134
Met Ser Ala Pro Pro Ala Leu Gln Ile Arg Glu Ala Asn Ala His Leu
1 5 10 15

Ala Ala Val His Arg Arg Ala Ala Glu Leu Glu Ala Arg Leu Asp Ala
20 25 30

Ala Glu Arg Thr Val His Ala Gln Ala Glu Arg Leu Ala Leu His Asp
35 40 45

Gln Gln Leu Arg Ala Ala Leu Asp Glu Leu Gly Arg Ala Lys Asp Arg
50 55 60

Gly Thr Phe His
65

<210> 1135
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 316; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC104534.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470059"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1135

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Xaa Met Val Tyr Gly Leu Asp Gln Ser Lys Met Asn Cys Asp Arg Val
1               5                  10                  15

Phe Asn Val Phe Cys Leu Tyr Gly Asn Val Glu Lys Val Lys Phe Met
            20                  25                  30

Lys Ser Lys Pro Gly Ala Ala Met Val Glu Met Ala Asp Gly Tyr Ala
        35                  40                  45

Val Asp Arg Ala Ile Thr His Leu Asn Asn Asn Phe Met Phe Gly Gln
    50                  55                  60

Lys Leu Asn Val Cys Val Ser Lys Gln Pro Ala Ile Met Pro Gly Gln
65                  70                  75                  80

Ser Tyr Gly Leu Glu Asp Gly Ser Cys Ser Tyr Lys Asp Phe Ser Glu
                85                  90                  95

Ser Arg Asn Asn Arg Phe Ser Thr Pro Glu Gln Ala Ala Lys Asn Arg
            100                 105                 110

Ile Gln His Pro Ser Asn Val Leu His Phe Phe Asn Ala Pro Leu Glu
        115                 120                 125

Val Thr Glu Glu Asn Phe Phe Glu Ile Cys Asp Glu Leu Gly Val Lys
    130                 135                 140

Arg Pro Ser Ser Val Lys Val Phe Ser Gly Lys Ser Glu Arg Ser Ser
145                 150                 155                 160

Ser Gly Leu Leu Glu Trp Glu Ser Lys Ser Asp Ala Leu Glu Thr Leu
                165                 170                 175
```

```
Gly Phe Leu Asn His Tyr Gln Met Lys Asn Pro Arg Leu Thr Gly Ser
            180                 185                 190

Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg Leu Thr Gly Ser Ser Ala
        195                 200                 205

Gln Glu Glu Ala Ser Gly Val Ala Leu Gly Glu Ala Pro Asp His Ser
    210                 215                 220

Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln Lys His Val Leu His Val
225                 230                 235                 240

Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala Met Asn Lys Val Phe Trp
                245                 250                 255

Arg Glu Met Val Glu Cys Phe Asn Lys Ile Ser Arg Asp Ala Asp Cys
            260                 265                 270

Arg Ala Val Val Ile Ser Gly Ala Gly Lys Met Phe Thr Ala Gly Ile
        275                 280                 285

Asp Leu Met Asp Met Ala Ser Asp Ile Leu Gln Pro Lys Gly Asp Asp
    290                 295                 300

Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp Ile Ile Thr Arg Tyr Gln
305                 310                 315                 320

Glu
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<210> 1136
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 316; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:

AC104534.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471066"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1136
Xaa Met Val Tyr Gly Leu Asp Gln Ser Lys Met Asn Cys Asp Arg Val
1 5 10 15

Phe Asn Val Phe Cys Leu Tyr Gly Asn Val Glu Lys Ile Cys Asp Glu
20 25 30

Leu Gly Val Lys Arg Pro Ser Ser Val Lys Val Phe Ser Gly Lys Ser
35 40 45

Glu Arg Ser Ser Ser Gly Leu Leu Glu Trp Glu Ser Lys Ser Asp Ala
50 55 60

Leu Glu Thr Leu Gly Phe Leu Asn His Tyr Gln Met Lys Asn Pro Ser
65 70 75 80

Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu Gln Pro Lys Gly Asp
85 90 95

Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp Ile Ile Thr Arg Tyr
100 105 110

Gln Glu

<210> 1137
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 316; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104534.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489000"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1137
Xaa Met Val Tyr Gly Leu Asp Gln Ser Lys Met Asn Cys Asp Arg Val
1 5 10 15

Phe Asn Val Phe Cys Leu Tyr Gly Asn Val Glu Lys Ile Cys Asp Glu
20 25 30

Leu Gly Val Lys Arg Pro Ser Ser Val Lys Val Phe Ser Gly Lys Ser
35 40 45

Glu Arg Ser Ser Ser Gly Leu Leu Glu Trp Glu Ser Lys Ser Asp Ala
50 55 60

Leu Glu Thr Leu Gly Phe Leu Asn His Tyr Gln Met Lys Asn Pro Ser
65 70 75 80

Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu Gln Pro Lys Gly Asp
85 90 95

Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp Ile Ile Thr Arg Tyr
100 105 110

Gln Glu

<210> 1138
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 316; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104534.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489028"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1138
Xaa Met Val Tyr Gly Leu Asp Gln Ser Lys Met Asn Cys Asp Arg Val
1 5 10 15

Phe Asn Val Phe Cys Leu Tyr Gly Asn Val Glu Lys Val Lys Phe Met
20 25 30

Lys Ser Lys Pro Gly Ala Ala Met Val Glu Met Ala Asp Gly Tyr Ala
35 40 45

Val Asp Arg Ala Ile Thr His Leu Asn Asn Asn Phe Met Phe Gly Gln
50 55 60

Lys Leu Asn Val Cys Val Ser Lys Gln Pro Ala Ile Met Pro Gly Gln
65 70 75 80

Ser Tyr Gly Leu Glu Asp Gly Ser Cys Ser Tyr Lys Asp Phe Ser Glu
85 90 95

Ser Arg Asn Asn Arg Phe Ser Thr Pro Glu Gln Ala Ala Lys Asn Arg
100 105 110

Ile Gln His Pro Ser Asn Val Leu His Phe Phe Asn Ala Pro Leu Glu
115 120 125

Val Thr Glu Glu Asn Phe Phe Glu Ile Cys Asp Glu Leu Gly Val Lys
130 135 140

```
Arg Pro Ser Ser Val Lys Val Phe Ser Gly Lys Ser Glu Arg Ser Ser
145                 150                 155                 160

Ser Gly Leu Leu Glu Trp Glu Ser Lys Ser Asp Ala Leu Glu Thr Leu
                165                 170                 175

Gly Phe Leu Asn His Tyr Gln Met Lys Asn Pro Arg Leu Thr Gly Ser
            180                 185                 190

Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg Leu Thr Gly Ser Ser Ala
        195                 200                 205

Gln Glu Glu Ala Ser Gly Val Ala Leu Gly Glu Ala Pro Asp His Ser
    210                 215                 220

Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln Lys His Val Leu His Val
225                 230                 235                 240

Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala Met Asn Lys Val Phe Trp
                245                 250                 255

Arg Glu Met Val Glu Cys Phe Asn Lys Ile Ser Arg Asp Ala Asp Cys
            260                 265                 270

Arg Ala Val Val Ile Ser Gly Ala Gly Lys Met Phe Thr Ala Gly Ile
        275                 280                 285

Asp Leu Met Asp Met Ala Ser Asp Ile Leu Gln Pro Lys Gly Asp Asp
    290                 295                 300

Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp Ile Ile Thr Arg Tyr Gln
305                 310                 315                 320

Glu
```

<210> 1139
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 317; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104581.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487284"

<400> 1139
Leu Trp Thr Arg Ser Leu Tyr Leu Phe Gly Arg Asn Gly Val Cys Leu
1 5 10 15

<210> 1140
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 318; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104650.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487144"

<400> 1140
Gln Asn Leu Pro Ser Thr Val Ser Gln Ala Pro Leu Pro Tyr Gly Arg
1 5 10 15

Gly Pro Cys Arg Pro Gln Gly Gly Gly Ser Val Arg
20 25

<210> 1141
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 319; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC104981.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485383"

<400> 1141
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 1142
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 320; "

<220>

<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC105009.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486401"

<400> 1142
Glu Ile Ser Pro Gly Ala Met Asp Arg Val Ile Arg Gln Phe His Tyr
1 5 10 15

Phe Gln Thr Asn
20

<210> 1143
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 321; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC105052.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485271"

<400> 1143
Met Arg Gln Glu Val Glu Gly Arg Gly Arg Gly Ser His Glu Leu Ile
1 5 10 15

Ile Thr Asp Lys Arg Cys Gly Val Cys Gly Gly Ser Leu Ser Cys Ile
20 25 30

Val Tyr Leu Cys Ile Ser Leu Asn Phe Ser Arg Ile Lys Lys Leu Lys
35 40 45

Lys Tyr Thr Trp Pro Gly Pro Thr Arg Asp Ser Pro Asn Ala Ser Leu

```
    50                  55                  60

Gln Pro Gly Arg Ala Lys Phe Ala Phe Ser His Ala Ser His Thr Pro
65                  70                  75                  80

Leu His Ser Gln Leu Gly Ala Leu Gln Thr Gly Lys Pro Gln Ala Leu
                85                  90                  95

Leu Ala Ser Ala Asn Pro Leu Ser Arg Ser Met Gly Pro Pro Asp His
            100                 105                 110

His Leu Thr Thr Leu Ile Leu Ile Ser Leu Tyr Thr Pro Phe Pro Gly
        115                 120                 125

Leu Leu Ser Ser Gly Cys Phe Ser Leu Thr Leu Thr Leu Pro Leu Asp
    130                 135                 140

His Gly Gly Leu Gly Asn Arg Cys Leu Pro Arg Cys Trp Arg Tyr Arg
145                 150                 155                 160


<210> 1144
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 322; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC107081.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487138"

<400> 1144
Lys Gly Ile Leu Lys Thr Glu Ser Cys Ser Val Thr Gln Asp Arg Val
1               5                   10                  15

Gln Trp His Tyr Leu Gly Ser Leu Gln Ala Gln Ala Gly Leu Glu Leu
            20                  25                  30
```

Leu Gly Ser Ser Asp Pro Pro Ala Leu Gly Ser
35 40

<210> 1145
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 323; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC108925.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485456"

<400> 1145
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln

115 120

<210> 1146
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 324; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC108938.5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000473841"

<400> 1146
Met Ala Phe Ser Gly Arg Ala Arg Pro Cys Ile Ile Pro Glu Asn Glu
1 5 10 15

Glu Ile Pro Arg Ala Ala Leu Asn Thr Val His Glu Ala Asn Gly Thr
20 25 30

Glu Asp Glu Arg Ala Val Ser Lys Leu Gln Arg Arg His Ser Asp Val
35 40 45

Lys Val Tyr Lys Glu Phe Cys Asp Phe Tyr Ala Lys Phe Asn Met Ala
50 55 60

Asn Ala Leu Ala Ser Ala Thr Cys Glu Arg Cys Lys Gly Gly Phe Ala
65 70 75 80

Pro Ala Glu Thr Ile Val Asn Ser Asn Gly Glu Leu Tyr His Glu Gln
85 90 95

Cys Phe Val Cys Ala Gln Cys Phe Gln Gln Phe Pro Glu Gly Leu Phe
100 105 110

Tyr Glu Phe Glu Gly Arg Lys Tyr Cys Glu His Asp Phe Gln Met Leu
115 120 125

```
Phe Ala Pro Cys Cys His Gln Cys Gly Glu Phe Ile Ile Gly Arg Val
    130                 135                 140

Ile Lys Ala Met Asn Asn Ser Trp His Pro Glu Cys Phe Arg Cys Asp
145                 150                 155                 160

Leu Cys Gln Glu Val Leu Ala Asp Ile Gly Phe Val Lys Asn Ala Gly
                165                 170                 175

Arg His Leu Cys Arg Pro Cys His Asn Arg Glu Lys Ala Arg Gly Leu
            180                 185                 190

Gly Lys Tyr Ile Cys Gln Lys Cys His Ala Ile Ile Asp Glu Gln Pro
        195                 200                 205

Leu Ile Phe Lys Asn Asp Pro Tyr His Pro Asp His Phe Asn Cys Ala
    210                 215                 220

Asn Cys Gly Gln Glu Gly Ser Asp Cys Arg Cys Thr Gly Ala Glu Arg
225                 230                 235                 240

Gly Ala Ile Leu Pro Ala Met Pro
                245


<210> 1147
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 325; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC109344.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485520"

<400> 1147
Met Ser Pro Leu Ile Met Gly Leu Asp Val Asn Pro Asp Ala Cys Leu
```

```
1               5                   10                  15

Thr Ala Leu Leu Asp Ile Cys Lys Leu Leu Glu Ala Val Cys Pro Ser
            20                  25                  30

Ser Pro Thr Ser Ser Gly His Glu Ile Pro Thr Gln Leu Leu Gly Lys
        35                  40                  45

Asp Leu Gln Ser Ser Leu Cys Pro Pro Phe Pro Leu Ala Trp Ala Leu
    50                  55                  60

Leu Leu Pro Thr Pro Leu Leu Ser Phe His Pro Glu Gly Cys Ala Pro
65                  70                  75                  80

Ser His Ser His Cys Leu Ala Cys His Leu Ser Leu His Pro Val Gln
                85                  90                  95

Thr Ser Ser Ser Gly Leu Leu Ala His Gln Pro Val Met Gly Trp Met
            100                 105                 110

Pro Lys Cys Arg Ala Lys Leu Met His Leu Leu Leu Met Ser Phe Ser
        115                 120                 125

Val Cys Leu Met Thr Ser Gly Asp Pro Ser Ser Ser Ala Arg Gln Pro
    130                 135                 140

Arg Ser Pro Thr Leu Ala Ser Ala Tyr Leu Pro Ser His Gly Arg Gln
145                 150                 155                 160

His Pro Gln Ser Arg Glu Val Cys Ala Ser Gly Thr Trp Asn Met Gln
                165                 170                 175

Gly Phe Ala Asp Arg Ala Pro Cys Tyr Phe Leu Cys Pro Ser His Ser
            180                 185                 190

Leu Gln Asn Pro His Cys Ser Pro Val Thr Thr Cys Ala Leu Leu Ile
        195                 200                 205

Pro Ser Ala Pro Ile Ser His Ser Pro Ala Ile Leu Thr Pro Ser Ala
    210                 215                 220

Thr Phe Leu Ile Pro
225
```

<210> 1148
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 326; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC109486.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485453"

<400> 1148

Met	Thr	Leu	Asn	Glu	His	Ala	Ala	Phe	Lys	His	Leu	Phe	Asn	Lys	Ala
1				5				10						15	

His	Leu	Ala	Pro	Pro	Leu	Ile	His	Leu	Thr	Leu	Ser	Gly	His	Ser	Thr
			20					25					30		

Cys	Phe	Arg	Glu	His	Arg	Val	Gly	Gly	Lys	Val	Thr	Asp	Gln	Gln	Asp
		35					40					45			

Pro	Lys	Ala	Glu	Glu	Phe	Phe	Leu	Val	Gln	Asn	Lys	Met	Lys	Ser	Leu
	50					55					60				

Pro	Cys	Leu	Pro	Leu	Ser	Thr	Gln	Thr	Gln	Gln	Pro	Ser	Asp	Phe	Ser
65					70					75					80

Ile	Phe	Ser	Pro	Pro	Phe	Pro	Pro	Phe	Tyr	Ser	Thr	Lys	Pro	Pro	Leu
				85					90					95	

Ser	Ser	Trp	Pro	Val	Leu	Asn	Glu	Leu	Leu	Gly	Thr	Pro	Pro	Arg	Trp
			100					105					110		

Gly	Gly	Gly	Arg	Ala	Glu	Gly	Leu	Leu	Thr	Ser	Gln				
			115					120							

<210> 1149
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 327; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC109829.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403181"

<400> 1149

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Met Ala Pro Ile Trp Gly Met Asp Val Pro Leu Pro Ser Asp Ile Ser
1               5                  10                  15

Leu Leu Leu Leu Phe Val Phe Phe Ile Trp Arg Leu Trp Thr Leu Phe
            20                  25                  30

Ser Arg Asn Arg Ser Trp Lys Gln Val Ala Ala Lys Ile Asn Ser Glu
        35                  40                  45

Thr Ser Lys Gln His Arg Leu Lys Lys Ile Gln Lys Leu Thr Gly Gln
    50                  55                  60

Arg Asp Pro Ile Leu Tyr Ser Ser Ala Gln Asp Pro Gln Trp Glu Glu
65                  70                  75                  80

Asn Leu Arg Met Ala Cys Thr Glu Ala Asn Leu Thr Cys Val Ser Glu
                85                  90                  95

Leu Pro Val Gly Trp Thr Gln Glu Tyr Ile Leu Trp Ser Met Glu Arg
            100                 105                 110

Ser Leu Gln Gln Ile Phe Arg Tyr Leu Glu Ser Ala Arg Ser Arg Leu
        115                 120                 125

Val Glu Gln Asp Leu Pro Glu Ser Gln Asp Met Ile Ser Ser Ser Thr
    130                 135                 140
```

```
Thr Ser Val Leu Val Ala Gln Lys Thr Val Leu Cys Cys Cys Asp Tyr
145                 150                 155                 160

Lys Lys Ala Lys His Ser Thr Asp His Ser Ile Ser Phe Ser Ser Ser
                165                 170                 175

Cys Asn Asp Ser Ser Leu Ser His Leu Pro Val Phe Ser Glu Gly Thr
            180                 185                 190

Thr Trp Glu Phe Arg Ser His Ser Leu Pro Ile Ser His Lys Lys Gln
        195                 200                 205

Ser Ser Val Phe Arg Asn Gln Gly Arg Thr Leu Pro Leu Phe Gln Leu
    210                 215                 220

Ser Glu Pro Gln Lys Ser Lys Ile Phe Gln Asn Leu Ala Asp Leu Ser
225                 230                 235                 240

Pro Leu Gln Pro Gln Ser Ser Phe Ile Asn Ser Ile Ser Glu Pro Leu
                245                 250                 255

Asn Ile Cys Lys Gln
            260


<210> 1150
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 328; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC109829.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485639"

<400> 1150
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Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1 5 10 15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
20 25 30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
35 40 45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
50 55 60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65 70 75 80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
85 90 95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
100 105 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
115 120

<210> 1151
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 329; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC110602.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487518"

<400> 1151
Ile Arg Glu Ala Gly Ser Ser Asp Ser Pro Thr Ser Pro Ser Arg Val
1 5 10 15

Ala Gly Asn Ile Ile Leu Thr Pro Gln Ala Cys Met Phe Val Lys Gln
20 25 30

Leu Tyr Leu Ser
35

<210> 1152
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 330; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC110615.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485507"

<400> 1152
Met Glu Asn Leu Pro Gly Ser Tyr Phe Ile Leu Phe Leu Phe Phe Lys
1 5 10 15

Ser Ala Ser Arg Ser Ala Asn Cys Phe Ser Arg Lys Glu Arg Leu Phe
20 25 30

Phe Asp Arg Thr Phe Trp Leu Tyr Arg Ile Ile Ile Lys Phe Phe Cys
35 40 45

Phe Phe Phe Ser Leu Phe Val Glu Leu Glu Asn Gly Phe Val Leu Val
50 55 60

Phe Phe Leu Thr Asn Ser Phe Arg Ser Val Phe Pro Ala Ile Ala Val
65 70 75 80

Ala Ser Leu Val Ser Leu Ser Asp Phe Gly Phe Leu
85 90

<210> 1153
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 331; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC112719.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487114"

<400> 1153
Ser Ser Val Arg Val Phe Asn Ser Asp Pro Glu Gln Pro Ser Lys Ile
1 5 10 15

Gly Ala Ile Val Ile Tyr Ile Leu Gln Lys Arg Lys Gln Ala
20 25 30

<210> 1154
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 332; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC118758.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469705"

<400> 1154
Met Ala Ser Gly Arg Trp Ala Pro Pro Gly Pro Ala Trp Ala Ser Gln
1 5 10 15

```
Arg Pro Leu Gln Thr Gln Val Val Leu Lys Ser Ala Ser Pro Gly Pro
            20                  25                  30

Ala Pro Ala Ser Arg Gln Ala Ile Cys Phe Gly Ser Ala Pro Ala Gln
        35                  40                  45

Leu Pro Leu Ala Phe Gly Gly Pro Lys Leu Ser Pro Ala Lys Leu Phe
    50                  55                  60

Arg Pro Thr Ser Cys Leu Pro Val Ala Cys Thr Gly Pro Ala Leu Ala
65                  70                  75                  80

Gly Glu Gln Pro Leu Gln Ala Pro Leu Leu Pro Pro Arg Gly Leu Ser
                85                  90                  95

Arg Pro Ser Ser Arg Pro Thr Val Ala Ser Trp Gly Gln Val Pro Ala
            100                 105                 110

Cys Leu Pro Ala Ala Arg Glu Arg Pro Ser Ser Ser Leu Thr Val Ala
        115                 120                 125

Cys Leu Gly Pro Thr Arg Val Ser Gly Thr Leu Ser Arg Gly Val Ser
    130                 135                 140

Pro Cys Leu Thr Leu Ala Ser Leu Met Leu Arg Glu
145                 150                 155


<210> 1155
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 333; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC123512.1; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000485642"

<400> 1155
Met Asn Val Cys Cys Ser Ser His Pro Val Asn Glu Lys Val Trp Lys
1   5   10   15

Pro Ser Ser Arg Lys Trp Ser Ser Lys Val Trp Ser Met Asp Glu Phe
            20   25   30

Asp Leu Gln Thr Ala Cys Tyr Trp Phe Met Thr Arg Ser Thr Asn Cys
        35   40   45

Ile Leu Arg Ala Gln Ile Ser Arg Glu Gln Cys Asn Leu Ser Gln Lys
    50   55   60

Asp Asp Tyr Val Tyr Ala Leu Ser Cys Leu Phe Pro Cys Leu Thr Gln
65   70   75   80

Arg Arg His Lys Glu Lys Val Ser Ser Ala Trp Ile Asn Trp Arg Leu
                85   90   95

<210> 1156
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 334; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC123512.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485548"

<400> 1156
Met Asn Val Cys Cys Ser Ser His Pro Val Asn Glu Lys Val Trp Lys
1   5   10   15

Pro Ser Ser Arg Lys Trp Ser Ser Lys Val Trp Ser Met Asp Glu Phe
            20   25   30

Asp Leu Gln Thr Ala Cys Tyr Trp Phe Met Thr Arg Ser Thr Asn Cys
35 40 45

Ile Leu Arg Ala Gln Ile Ser Arg Glu Gln Cys Asn Leu Ser Gln Lys
50 55 60

Asp Asp Tyr Val Tyr Ala Leu Ser Cys Val Cys Met Cys Met Tyr Ile
65 70 75 80

Arg Tyr Phe His Ala
85

<210> 1157
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 335; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC124312.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485422"

<400> 1157
Met Glu Pro Ile Tyr Arg Val Leu Ser Arg Lys Lys Ile Ser Ile Thr
1 5 10 15

Asn Leu Leu Thr Thr Asp Phe His Cys Cys Tyr Glu Asn Thr Met Gly
20 25 30

Thr Lys Lys Ser Ser Ala Met Lys Lys Asn Glu Pro Lys Asn Asn Lys
35 40 45

Asp Val Ala Leu Gly Ser Leu Pro Asn His Lys Glu Leu Ser Thr Ser
50 55 60

Gly Glu Gln Gly Asn Pro Glu Pro Ala Leu Lys Asp Lys Pro Gly His

65 70 75 80

Thr Glu Ala Gly Tyr Arg Leu Thr Leu Leu Cys His Leu His Ile His
85 90 95

Pro Val Leu Gln Thr Leu Cys Val Leu Pro Ser Leu Thr Lys Arg Ser
100 105 110

Pro Ser His Lys Glu Ser Pro Leu His Arg Ser Thr Tyr Cys Pro Val
115 120 125

Thr Pro Phe Asp Pro Lys Trp Thr Pro Ser
130 135

<210> 1158
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 336; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC126407.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486685"

<400> 1158
Ala Pro Pro Ala Ala Pro Arg Ser Ala Leu Ala Glu Ser Gly Ala Ala
1 5 10 15

Asp Ser Pro Glu Gly Ser Gln Thr Gly Arg Ser Gly Pro Asp Thr Pro
20 25 30

<210> 1159
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 337; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC129492.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485311"

<400> 1159

Met	Gln	Pro	Thr	Leu	Ser	Ala	Val	Ser	Ser	Cys	Thr	Ala	Pro	Pro	Arg
1				5				10						15	
Pro	Arg	Ser	Arg	Arg	Ser	Thr	Arg	Pro	Pro	Ser	Ser	Arg	Leu	Asn	Arg
			20					25					30		
Ser	Arg	Ser	Arg	Ser	Thr	Ser	Gly	Ser	Ile	Gly	Gly	Met	Ala	Gly	Val
		35					40					45			
Gly	Val	Gly	Ala	Gly	Ala	Gly	Gln	Gly	Arg	Ala	Gly	Ala	Glu	Gly	Gly
	50					55					60				
Gly	Gly	Gly	Ala	Pro	Leu	Arg	Arg	Ile	Leu	Ser	Cys	Arg	Leu	Leu	Ala
65					70					75					80
Thr	Lys	Trp	Val	Arg	Ser	Pro	Trp	Arg	Leu	Thr	Val	Pro	Ser	Ser	Ser
				85					90					95	
Arg	Gly	Leu	Glu	Met	Val	Ala	Arg	Arg	Pro	Pro	Pro	Ala	Pro	Asp	Ser
			100					105					110		
Ala	Leu	Pro	Glu	Asp	Pro	Ala	Pro	Pro	His	Ala	Ser	Leu	Ser	Pro	Ser
		115					120					125			
Arg	Leu	Arg	Leu	Ser											
	130														

<210> 1160
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 338; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC130310.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484037"

<400> 1160
Met Gly Leu Gln Gln Gln Thr Gly Thr Gln Gln Leu Glu Pro His Pro
1 5 10 15

Pro Gln Pro Glu Pro Gln Pro Pro Leu Asp Pro Pro Gln Glu Pro Gln
20 25 30

Pro Pro Leu Glu Pro Pro Gln Glu Pro Gln Pro Pro Leu Asp Pro Pro
35 40 45

Gln Glu His Ser Pro Pro Cys Ser Leu His Arg Ser His Ser Pro Pro
50 55 60

Trp Ser Pro Gln Lys Ser His Ser Pro Leu Cys His Ser Trp Ser Arg
65 70 75 80

Asn Arg Leu Ala His Gly Ser Thr Arg Ala Cys Ser Ser Arg Arg Ala
85 90 95

His Ser Ser Trp Ser Gln Asn Leu His Ser Gln Ser His Ser Pro His
100 105 110

Ser Arg Ser His Ser Pro His Ser Arg Ser His Ser Pro His Ser Trp
115 120 125

Ser His Ser Leu Arg Ser Ser Arg Asn Ser Pro Trp Phe Trp Trp Ile
130 135 140

Glu Gly Gly Ala Gly Arg Gly Ala Gly Glu Arg Glu Val Gln Val Trp
145 150 155 160

Ser Ser Leu Ser Leu Asp Pro Leu Tyr Pro Cys Pro Gly Ser Cys Val
165 170 175

Arg Leu Gly Thr His Phe Leu Val Pro Val Cys Ala Ile Phe Arg Ala
180 185 190

Pro Phe Ser Cys Phe Leu
195

<210> 1161
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 339; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC131263.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487024"

<400> 1161
Asp Arg Val Ser Leu Cys Cys Pro Gly Trp Asn Val Val Val Leu Ser
1 5 10 15

Gln Leu Thr Ala Ala Ser Ala Ser Ala Gly Leu Lys Leu Leu Thr Ser
20 25 30

Gly Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Ile Gly Val
35 40 45

Ser His His Ala Arg Leu Thr Cys Lys
50 55

<210> 1162
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 340; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC133551.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479378"

<400> 1162
Met Arg Ala Ser Pro Cys Ile Ser Gln Pro Ala Ala Ser Trp His Pro
1 5 10 15

Arg Pro Ser Ala Leu Arg Pro Thr Ala Gly Ser Gly Pro Asp Thr Arg
20 25 30

Thr Pro Gly Thr Val Glu Asp Gly Ser Ala Pro Cys Pro Ala Phe Arg
35 40 45

Ser Pro Ala Val Ser Pro Cys Gly Glu Glu Pro Cys Cys Phe Gln Ile
50 55 60

Ser Pro Ala Glu Glu Thr Leu Glu Leu Gly Arg Leu Val Ser Pro Gly
65 70 75 80

Cys His Lys Ser Ser Ala Pro Gln Glu Arg Arg Leu Asp Pro Arg Ala
85 90 95

Arg Cys Val Val His Ile
100

<210> 1163
<211> 581
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 341; "

<220>
<221> source

<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC136352.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478796"

<400> 1163

```
Met Val Ala Glu Val Cys Ser Met Pro Ala Ala Ser Ala Val Lys Lys
1               5                  10                  15

Pro Phe Asp Leu Arg Ser Lys Met Gly Lys Trp Cys His His Arg Phe
            20                  25                  30

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Met Gly Thr Ser Gly Asp
        35                  40                  45

His Asp Asp Ser Phe Met Lys Thr Leu Arg Ser Lys Met Gly Lys Cys
    50                  55                  60

Cys His His Cys Phe Pro Cys Cys Arg Gly Ser Gly Thr Ser Asn Val
65                  70                  75                  80

Gly Thr Ser Gly Asp His Asp Asn Ser Phe Met Lys Thr Leu Arg Ser
                85                  90                  95

Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
            100                 105                 110

Gly Lys Ser Asn Val Gly Thr Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115                 120                 125

Met Glu Pro Arg Tyr His Val Arg Arg Glu Asp Leu Asp Lys Leu His
    130                 135                 140

Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145                 150                 155                 160

Leu Arg Asp Thr Asp Met Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala
                165                 170                 175

Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Gln Leu Leu
```

```
            180                 185                 190

Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195                 200                 205

Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Val Leu Met
    210                 215                 220

Leu Leu Glu His Gly Ala Asp Gly Asn Ile Gln Asp Glu Tyr Gly Asn
225                 230                 235                 240

Thr Ala Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
                245                 250                 255

Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys Cys Gly
            260                 265                 270

Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Glu Val Val
        275                 280                 285

Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290                 295                 300

Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305                 310                 315                 320

Val Asn Leu Leu Leu Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu
                325                 330                 335

Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340                 345                 350

Ile Cys Glu Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355                 360                 365

Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
    370                 375                 380

Glu Glu Ser Gln Arg Leu Lys Val Ser Glu Asn Ser Gln Pro Glu Lys
385                 390                 395                 400

Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Cys Asp Arg Glu Val Glu
                405                 410                 415
```

```
Glu Glu Ile Lys Lys His Gly Ser Asn Pro Val Gly Leu Pro Glu Asn
            420                 425                 430

Leu Thr Asn Gly Ala Ser Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
        435                 440                 445

Gln Arg Lys Ser Arg Lys Pro Glu Asn Gln Gln Phe Pro Asp Thr Glu
    450                 455                 460

Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Leu
465                 470                 475                 480

Ser Glu Glu Gln Asn Thr Gly Ile Ser Gln Asp Glu Ile Leu Thr Asn
                485                 490                 495

Lys Gln Lys Gln Ile Glu Val Ala Glu Lys Glu Met Asn Ser Glu Leu
            500                 505                 510

Ser Leu Ser His Lys Lys Glu Glu Asp Leu Leu Arg Glu Asn Ser Met
        515                 520                 525

Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Glu Thr Lys
    530                 535                 540

His Gln Asn Gln Leu Arg Glu Asn Lys Ile Leu Glu Glu Ile Glu Ser
545                 550                 555                 560

Val Lys Glu Lys Leu Leu Lys Ala Ile Gln Leu Asn Glu Glu Ala Leu
                565                 570                 575

Thr Lys Thr Ser Ile
            580
```

<210> 1164
<211> 381
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 341; "

<220>
<221> source

<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC136352.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479796"

<400> 1164

```
Met Val Ala Glu Val Cys Ser Met Pro Ala Ala Ser Ala Val Lys Lys
1               5                  10                  15

Pro Phe Asp Leu Arg Ser Lys Met Gly Lys Trp Cys His His Arg Phe
            20                  25                  30

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Met Gly Thr Ser Gly Asp
        35                  40                  45

His Asp Asp Ser Phe Met Lys Thr Leu Arg Ser Lys Met Gly Lys Cys
    50                  55                  60

Cys His His Cys Phe Pro Cys Cys Arg Gly Ser Gly Thr Ser Asn Val
65                  70                  75                  80

Gly Thr Ser Gly Asp His Asp Asn Ser Phe Met Lys Thr Leu Arg Ser
                85                  90                  95

Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
            100                 105                 110

Gly Lys Ser Asn Val Gly Thr Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115                 120                 125

Met Glu Pro Arg Tyr His Val Arg Arg Glu Asp Leu Asp Lys Leu His
    130                 135                 140

Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145                 150                 155                 160

Leu Arg Asp Thr Asp Met Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala
                165                 170                 175

Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Gln Leu Leu
```

```
            180                 185                 190

Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195                 200                 205

Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Val Leu Met
    210                 215                 220

Leu Leu Glu His Gly Ala Asp Gly Asn Ile Gln Asp Glu Tyr Gly Asn
225                 230                 235                 240

Thr Ala Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
                245                 250                 255

Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys Cys Gly
            260                 265                 270

Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Glu Val Val
        275                 280                 285

Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290                 295                 300

Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305                 310                 315                 320

Val Asn Leu Leu Leu Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu
                325                 330                 335

Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340                 345                 350

Ile Cys Glu Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355                 360                 365

Ser Ser Glu Asn Ser Asn Pro Gly Lys Glu Ala Glu Glu
    370                 375                 380
```

<210> 1165
<211> 199
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 342; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC136352.5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482263"

<400> 1165

```
Met Ala Leu Leu Leu Arg Phe Val Leu Leu Cys Arg Val Ala Asp Phe
1               5                  10                  15

Ile Arg Gly Trp Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
            20                  25                  30

Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu Ser Pro Glu
        35                  40                  45

Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser Pro Ala Asp Asn
    50                  55                  60

Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
65                  70                  75                  80

Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg Val His Phe Lys Ser Asn
                85                  90                  95

Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Phe Gln Leu
            100                 105                 110

Ser Asp Ile Gly Thr Asp Gln Cys Lys Val Lys Arg Ala Pro Gly Val
        115                 120                 125

Ala Asn Arg Lys Ile Gln Leu Val Val Leu Gly Lys Met Cys Arg Leu
    130                 135                 140

Gln Arg Ala Ala Arg Pro Leu Pro Glu Ala Thr Ala Val Ile Ile His
145                 150                 155                 160
```

```
Pro Trp Asp Pro Tyr Leu Leu Pro Thr Trp Lys Asp Ile Pro Arg Leu
                165                 170                 175

Ser Ile Asn Lys Tyr Gln Val Lys Thr Leu Asn Ala Leu Leu Arg Val
            180                 185                 190

Arg Leu Ser His Leu Leu Arg
        195


<210> 1166
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 343; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC136612.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482038"

<400> 1166
Met Arg Ala Ser Pro Cys Ile Ser Gln Pro Ala Ala Ser Trp His Pro
1               5                   10                  15

Arg Pro Ser Ala Leu Arg Pro Thr Ala Gly Ser Gly Pro Asp Thr Arg
            20                  25                  30

Thr Pro Gly Thr Val Glu Asp Gly Ser Ala Pro Cys Pro Ala Phe Arg
        35                  40                  45

Ser Pro Ala Val Ser Pro Cys Gly Glu Glu Pro Cys Cys Phe Gln Ile
    50                  55                  60

Ser Pro Ala Glu Glu Thr Leu Glu Leu Gly Arg Leu Val Ser Pro Gly
65                  70                  75                  80

Asn Cys Asp Thr Leu Ser Pro Arg Ala Ala Gly Phe Tyr Ala Cys His
                85                  90                  95
```

```
Val Arg Ser Leu Ile Pro Cys Arg Ser Thr Lys Gly Arg Trp Pro Leu
            100                 105                 110

Thr Ala Ser Ala Ala Gly Leu Ser Ser Phe Ser Gly
        115                 120


<210> 1167
<211> 635
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 344; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC136616.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480079"

<400> 1167
Met Ala Lys Lys Ser Ala Glu Asn Gly Ile Cys Ser Val Ser Gly Asp
1               5                   10                  15

Gln Lys Lys Gly Pro Leu Ile Ala Pro Gly Pro Asp Gly Ala Arg Ala
            20                  25                  30

Lys Gly Asp Gly Pro Ala Gly Leu Gly Thr Pro Gly Gly Gly Leu Ala
        35                  40                  45

Val Pro Ala Arg Ala Thr Trp Thr Arg Gln Met Asp Phe Ile Met Ser
    50                  55                  60

Cys Val Gly Phe Ala Val Asp Leu Gly Asn Val Trp Arg Phe Pro Tyr
65                  70                  75                  80

Leu Cys Tyr Lys Asn Gly Gly Gly Val Phe Leu Ile Pro Cys Ile Leu
                85                  90                  95
```

```
Ile Ala Leu Val Gly Gly Ile Pro Ile Phe Phe Leu Glu Ile Ser Leu
            100                 105                 110

Gly Gln Phe Met Lys Ala Gly Ser Ile Asn Val Trp Asn Ile Cys Pro
        115                 120                 125

Leu Phe Lys Gly Leu Gly Tyr Ala Ser Met Val Ile Val Phe Tyr Cys
    130                 135                 140

Asn Thr Tyr Tyr Ile Met Val Leu Ala Trp Gly Phe Tyr Tyr Leu Val
145                 150                 155                 160

Lys Ser Phe Thr Thr Thr Leu Pro Trp Ala Thr Cys Gly His Thr Trp
                165                 170                 175

Asn Thr Pro Asp Cys Val Glu Ile Phe Arg His Glu Asp Cys Ala Ser
            180                 185                 190

Ala Ser Leu Ala Asn Leu Thr Cys Asp Gln Leu Ala Asp Arg Arg Ser
        195                 200                 205

Pro Val Ile Glu Phe Trp Glu Asn Lys Val Leu Arg Leu Ser Gly Gly
    210                 215                 220

Leu Glu Val Pro Gly Ala Leu Asn Trp Glu Val Thr Leu Cys Leu Leu
225                 230                 235                 240

Ala Cys Trp Val Leu Val Tyr Phe Cys Val Lys Gly Val Lys Ser Met
                245                 250                 255

Gly Lys Ile Val Tyr Phe Thr Ala Thr Phe Pro Tyr Val Val Leu Val
            260                 265                 270

Val Leu Leu Val Leu Gly Val Leu Leu Pro Gly Thr Leu Asp Ser Ile
        275                 280                 285

Ile Tyr Tyr Leu Lys Pro Asp Trp Ser Lys Leu Gly Ser Pro Gln Val
    290                 295                 300

Trp Ile Asp Val Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile Gly Leu
305                 310                 315                 320

Gly Ala Leu Thr Ala Leu Gly Ser Tyr Asn Arg Phe Asn Asn Asn Cys
```

325 330 335

Tyr Lys Asp Ala Ile Ile Leu Ala Val Ile Asn Ser Gly Thr Ser Phe
340 345 350

Phe Ala Gly Phe Val Val Phe Ser Ile Leu Gly Phe Met Ala Ala Glu
355 360 365

Gln Gly Met His Ile Ser Lys Val Ala Glu Ser Gly Pro Gly Leu Ala
370 375 380

Phe Ile Ala Tyr Pro Gln Ala Val Thr Leu Met Pro Val Ala Pro Leu
385 390 395 400

Trp Ala Ala Leu Phe Phe Phe Met Leu Leu Leu Leu Gly Leu Asp Ser
405 410 415

Gln Phe Val Gly Val Glu Gly Phe Ile Thr Gly Leu Leu Asn Leu Leu
420 425 430

Pro Ala Ser Tyr Tyr Phe Cys Phe Gln Arg Glu Ile Ser Val Ala Leu
435 440 445

Cys Cys Ala Leu Arg Phe Val Ile Asp Leu Ser Met Val Thr Asp Gly
450 455 460

Gly Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ser Ala Ser Gly Thr
465 470 475 480

Thr Leu Leu Trp Gln Ala Phe Trp Glu Cys Val Val Val Ala Trp Val
485 490 495

Tyr Gly Ala Asp Arg Phe Thr Asp Asp Ile Ala Cys Met Ile Gly Tyr
500 505 510

Arg Pro Cys Pro Trp Met Lys Trp Cys Trp Ser Phe Phe Thr Pro Leu
515 520 525

Val Cys Met Gly Ile Phe Ile Phe Asn Val Val Tyr Tyr Glu Pro Leu
530 535 540

Val Tyr Asn Asn Thr Asn Val Tyr Pro Trp Trp Gly Glu Ala Met Gly
545 550 555 560

```
Trp Ala Phe Val Leu Ser Ser Met Leu Cys Met Pro Leu His Leu Leu
                565                 570                 575

Gly Cys Leu Leu Arg Ala Lys Gly Thr Met Ala Glu Cys Trp Lys His
            580                 585                 590

Leu Thr Gln Thr Ile Trp Gly Leu His His Leu Glu Tyr Arg Ala Gln
        595                 600                 605

Asp Ala Asp Val Arg Gly Leu Thr Thr Leu Thr Pro Val Ser Glu Ser
    610                 615                 620

Ser Lys Val Val Val Val Glu Ser Val Met Gly
625                 630                 635


<210> 1168
<211> 520
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 344; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC136616.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482251"

<400> 1168
Met Lys Ala Gly Ser Ile Asn Val Trp Asn Ile Cys Pro Leu Phe Lys
1               5                   10                  15

Gly Leu Gly Tyr Ala Ser Met Val Ile Val Phe Tyr Cys Asn Thr Tyr
            20                  25                  30

Tyr Ile Met Val Leu Ala Trp Gly Phe Tyr Tyr Leu Val Lys Ser Phe
        35                  40                  45
```

```
Thr Thr Thr Leu Pro Trp Ala Thr Cys Gly His Thr Trp Asn Thr Pro
    50                  55                  60

Asp Cys Val Glu Ile Phe Arg His Glu Asp Cys Ala Ser Ala Ser Leu
65                  70                  75                  80

Ala Asn Leu Thr Cys Asp Gln Leu Ala Asp Arg Arg Ser Pro Val Ile
                85                  90                  95

Glu Phe Trp Glu Asn Lys Val Leu Arg Leu Ser Gly Gly Leu Glu Val
            100                 105                 110

Pro Gly Ala Leu Asn Trp Glu Val Thr Leu Cys Leu Leu Ala Cys Trp
        115                 120                 125

Val Leu Val Tyr Phe Cys Val Lys Gly Val Lys Ser Met Gly Lys Ile
    130                 135                 140

Val Tyr Phe Thr Ala Thr Phe Pro Tyr Val Val Leu Val Val Leu Leu
145                 150                 155                 160

Val Leu Gly Val Leu Leu Pro Gly Thr Leu Asp Ser Ile Ile Tyr Tyr
                165                 170                 175

Leu Lys Pro Asp Trp Ser Lys Leu Gly Ser Pro Gln Val Trp Ile Asp
            180                 185                 190

Val Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile Gly Leu Gly Ala Leu
        195                 200                 205

Thr Ala Leu Gly Ser Tyr Asn Arg Phe Asn Asn Asn Cys Tyr Lys Asp
    210                 215                 220

Ala Ile Ile Leu Ala Val Ile Asn Ser Gly Thr Ser Phe Phe Ala Gly
225                 230                 235                 240

Phe Val Val Phe Ser Ile Leu Gly Phe Met Ala Ala Glu Gln Gly Met
                245                 250                 255

His Ile Ser Lys Val Ala Glu Ser Gly Pro Gly Leu Ala Phe Ile Ala
            260                 265                 270

Tyr Pro Gln Ala Val Thr Leu Met Pro Val Ala Pro Leu Trp Ala Ala
```

```
        275                 280                 285

Leu Phe Phe Phe Met Leu Leu Leu Leu Gly Leu Asp Ser Gln Phe Val
    290                 295                 300

Gly Val Glu Gly Phe Ile Thr Gly Leu Leu Asn Leu Leu Pro Ala Ser
305                 310                 315                 320

Tyr Tyr Phe Cys Phe Gln Arg Glu Ile Ser Val Ala Leu Cys Cys Ala
                325                 330                 335

Leu Arg Phe Val Ile Asp Leu Ser Met Val Thr Asp Gly Gly Met Tyr
            340                 345                 350

Val Phe Gln Leu Phe Asp Tyr Tyr Ser Ala Ser Gly Thr Thr Leu Leu
        355                 360                 365

Trp Gln Ala Phe Trp Glu Cys Val Val Val Ala Trp Val Tyr Gly Ala
    370                 375                 380

Asp Arg Phe Thr Asp Asp Ile Ala Cys Met Ile Gly Tyr Arg Pro Cys
385                 390                 395                 400

Pro Trp Met Lys Trp Cys Trp Ser Phe Phe Thr Pro Leu Val Cys Met
                405                 410                 415

Gly Ile Phe Ile Phe Asn Val Val Tyr Tyr Glu Pro Leu Val Tyr Asn
            420                 425                 430

Asn Thr Asn Val Tyr Pro Trp Trp Gly Glu Ala Met Gly Trp Ala Phe
        435                 440                 445

Val Leu Ser Ser Met Leu Cys Met Pro Leu His Leu Leu Gly Cys Leu
    450                 455                 460

Leu Arg Ala Lys Gly Thr Met Ala Glu Cys Trp Lys His Leu Thr Gln
465                 470                 475                 480

Thr Ile Trp Gly Leu His His Leu Glu Tyr Arg Ala Gln Asp Ala Asp
                485                 490                 495

Val Arg Gly Leu Thr Thr Leu Thr Pro Val Ser Glu Ser Ser Lys Val
            500                 505                 510
```

Val Val Val Glu Ser Val Met Gly
515 520

<210> 1169
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 345; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC136616.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479675"

<400> 1169
Ala Ile Leu Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Ala
1 5 10 15

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
20 25 30

Ser Gly Phe Thr Cys Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala
35 40 45

Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Asn
50 55 60

Gly Gly Thr Thr Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile
65 70 75 80

Ser Arg Val Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
85 90 95

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr Gly Gly Gly Val
100 105 110

<210> 1170
<211> 75
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 345; "

<220>
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<220>
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<223> /note="Gene Name:
AC136616.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484138"

<400> 1170
Ala Ser Gly Phe Thr Cys Ser Asn Ala Trp Met Ser Trp Val Arg Gln
1 5 10 15

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Lys Ser Thr Gly
20 25 30

Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
35 40 45

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
50 55 60

Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala Arg
65 70 75

<210> 1171
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 346; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>

<221> source
<223> /note="Gene Name:
AC136616.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479119"

<400> 1171
Gln Val Gln Leu Leu Gln Pro Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile His Cys Val Arg Gln Ala Pro Gly Gly Phe Glu Arg Met Gly
35 40 45

Gly Ile Tyr Ser Gly Asn Gly Lys Thr Gly Tyr Ala Gln Lys Phe Gln
50 55 60

Gly Arg Val Thr Met Thr Arg Asp Met Ser Thr Ser Thr Ala Tyr Met
65 70 75 80

Glu Leu Ser Ser Gln Arg Ser Glu Asp Ile Asp Val Tyr Tyr Cys
85 90 95

<210> 1172
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 347; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC138028.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487195"

<400> 1172
Leu Thr Pro Val Gly Glu Ala Phe Gly Asp Cys Ser Pro Ser Ile Pro

1 5 10 15

Pro Pro Trp Pro Arg Pro Thr Arg
20

<210> 1173
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 348; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC138969.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000330634"

<400> 1173
Met Ala Ala Val Glu His Arg His Ser Ser Gly Leu Pro Tyr Trp Pro
1 5 10 15

Tyr Leu Thr Ala Glu Thr Leu Lys Asn Arg Met Gly His Gln Pro Pro
20 25 30

Pro Pro Thr Gln Gln His Ser Ile Ile Asp Asn Ser Leu Ser Leu Lys
35 40 45

Thr Pro Ser Glu Cys Val Leu Tyr Pro Leu Pro Pro Ser Ala Asp Asp
50 55 60

Asn Leu Lys Thr Pro Pro Glu Cys Leu Leu Thr Pro Leu Pro Pro Ser
65 70 75 80

Ala Leu Pro Ser Ala Asp Asp Asn Leu Lys Thr Pro Ala Glu Cys Leu
85 90 95

Leu Tyr Pro Leu Pro Pro Ser Ala Asp Asp Asn Leu Lys Thr Pro Pro
100 105 110

Glu Cys Leu Leu Thr Pro Leu Pro Pro Ser Ala Pro Pro Ser Ala Asp
        115   120   125

Asp Asn Leu Lys Thr Pro Pro Glu Cys Val Cys Ser Leu Pro Phe His
    130   135   140

Pro Gln Arg Met Ile Ile Ser Arg Asn
145   150

<210> 1174
<211> 369
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 348; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC138969.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370908"

<400> 1174
Met Phe Cys Cys Leu Gly Tyr Glu Trp Leu Ser Gly Gly Cys Lys Thr
1   5   10   15

Trp His Ser Ala Trp Val Ile Asn Thr Leu Ala Asp His Arg His Arg
            20   25   30

Gly Thr Asp Phe Gly Gly Ser Pro Trp Leu Leu Ile Ile Thr Val Phe
        35   40   45

Leu Arg Ser Tyr Lys Phe Ala Ile Ser Leu Cys Thr Ser Tyr Leu Cys
    50   55   60

Val Ser Phe Leu Lys Thr Ile Phe Pro Ser Gln Asn Gly His Asp Gly
65   70   75   80

Ser Thr Asp Val Gln Gln Arg Ala Arg Arg Ser Asn Cys Arg Arg Gln

```
                85                  90                  95

Glu Gly Ile Lys Ile Val Leu Glu Asp Ile Phe Thr Leu Trp Arg Gln
            100                 105                 110

Val Glu Thr Lys Val Arg Ala Lys Ile Arg Lys Met Lys Val Thr Thr
        115                 120                 125

Lys Val Asn Arg His Asp Lys Ile Asn Gly Lys Arg Lys Thr Ala Lys
    130                 135                 140

Glu His Leu Arg Lys Leu Ser Met Lys Glu Arg Glu His Gly Glu Lys
145                 150                 155                 160

Glu Arg Gln Val Ser Glu Ala Glu Glu Asn Gly Lys Leu Asp Met Lys
                165                 170                 175

Glu Ile His Thr Tyr Met Glu Met Phe Gln Arg Ala Gln Ala Leu Arg
            180                 185                 190

Arg Arg Ala Glu Asp Tyr Tyr Arg Cys Lys Ile Thr Pro Ser Ala Arg
        195                 200                 205

Lys Pro Leu Cys Asn Arg Val Arg Met Ala Ala Val Glu His Arg His
    210                 215                 220

Ser Ser Gly Leu Pro Tyr Trp Pro Tyr Leu Thr Ala Glu Thr Leu Lys
225                 230                 235                 240

Asn Arg Met Gly His Gln Pro Pro Pro Pro Thr Gln Gln His Ser Ile
                245                 250                 255

Ile Asp Asn Ser Leu Ser Leu Lys Thr Pro Ser Glu Cys Val Leu Tyr
            260                 265                 270

Pro Leu Pro Pro Ser Ala Asp Asp Asn Leu Lys Thr Pro Pro Glu Cys
        275                 280                 285

Leu Leu Thr Pro Leu Pro Pro Ser Ala Leu Pro Ser Ala Asp Asp Asn
    290                 295                 300

Leu Lys Thr Pro Ala Glu Cys Leu Leu Tyr Pro Leu Pro Pro Ser Ala
305                 310                 315                 320
```

Asp Asp Asn Leu Lys Thr Pro Pro Glu Cys Leu Leu Thr Pro Leu Pro
325 330 335

Pro Ser Ala Pro Pro Ser Ala Asp Asp Asn Leu Lys Thr Pro Pro Glu
340 345 350

Cys Val Cys Ser Leu Pro Phe His Pro Gln Arg Met Ile Ile Ser Arg
355 360 365

Asn

<210> 1175
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 348; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC138969.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435610"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1175
Xaa Arg His Arg Gly Thr Asp Phe Gly Gly Ser Pro Trp Leu Leu Ile
1 5 10 15

Ile Thr Val Phe Leu Arg Ser Tyr Lys Phe Ala Ile Ser Leu Cys Thr
20 25 30

Ser Tyr Leu Cys Val Ser Phe Leu Lys Thr Ile Phe Pro Ser Gln Asn
35 40 45

```
Gly His Asp Gly Ser Thr Asp Val Gln Gln Arg Ala Arg Arg Ser Asn
    50                  55                  60

Cys Arg Arg Gln Glu Gly Ile Lys Ile Val Leu Glu Asp Ile Phe Thr
65                  70                  75                  80

Leu Trp Arg Gln Val Glu Thr Lys Val Arg Ala Lys Ile Arg Lys Met
                85                  90                  95

Lys Val Thr Thr Lys Val Asn Arg His Asp Lys Ile Asn Gly Lys Arg
            100                 105                 110

Lys Thr Ala Lys Glu His Leu Arg Lys Leu Ser Met Lys Glu Arg Glu
        115                 120                 125

His Gly Glu Lys Glu Arg Gln Val Ser Glu Ala Glu Glu Asn Gly Lys
    130                 135                 140

Leu Asp Met Lys Glu Ile His Thr Tyr Met Glu Met Phe Gln Arg Ala
145                 150                 155                 160

Gln Ala Leu Arg Arg Arg Ala Glu Asp Tyr Tyr Arg Cys Lys Ile Thr
                165                 170                 175

Pro Ser Ala Arg Lys Pro Leu Cys Asn Arg Val Ser Leu Leu Val Phe
            180                 185                 190

Leu Ala Phe Gly His Ser Leu Pro Gly Gln Asp Met Asp Thr Phe Phe
        195                 200                 205

Ser Leu Arg Leu Cys Ala Gln Ala Leu Gln Arg Glu Met Ala Glu Arg
    210                 215                 220

Lys Ala Ala Tyr Lys His His Ser Pro Ile Pro Val Gly Asn Cys Val
225                 230                 235                 240

Ala Gln Lys His Leu His Pro His Pro Val Gly Pro Pro Ser Asn Ile
                245                 250                 255

Leu Ser Ile Arg Gly Ser Val Phe Val Ile Ala Asn Gly Pro
            260                 265                 270
```

<210> 1176
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 348; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC138969.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436257"

<400> 1176
Ala Lys Ile Arg Lys Met Lys Val Thr Thr Lys Val Asn Arg His Asp
1 5 10 15

Lys Ile Asn Gly Lys Arg Lys Thr Ala Lys Glu His Leu Arg Lys Leu
20 25 30

Ser Met Lys Glu Arg Glu His Gly Glu Lys Glu Arg Gln Val Ser Glu
35 40 45

Ala Glu Glu Asn Gly Lys Leu Asp Met Lys Glu Ile His Thr Tyr Met
50 55 60

Glu Met Phe Gln Arg Ala Gln Ala Leu Arg Arg Arg Ala Glu Asp Tyr
65 70 75 80

Tyr Arg Cys Lys Ile Thr Pro Ser Ala Arg Lys Pro Leu Cys Asn Arg
85 90 95

Cys Thr Tyr Asn Leu Val Leu Pro Gly Ser Glu Lys Lys Tyr Tyr Ser
100 105 110

His Ala

<210> 1177

<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 348; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC138969.4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000441983"

<400> 1177

Met	Phe	Cys	Cys	Leu	Gly	Tyr	Glu	Trp	Leu	Ser	Gly	Gly	Cys	Lys	Thr
1				5				10						15	

Trp	His	Ser	Ala	Trp	Val	Ile	Asn	Thr	Leu	Ala	Asp	His	Arg	His	Arg
			20					25					30		

Gly	Thr	Asp	Phe	Gly	Gly	Ser	Pro	Trp	Leu	Leu	Ile	Ile	Thr	Val	Phe
		35					40					45			

Leu	Arg	Ser	Tyr	Lys	Phe	Ala	Ile	Ser	Leu	Cys	Thr	Ser	Tyr	Leu	Cys
	50					55					60				

Val	Ser	Phe	Leu	Lys	Thr	Ile	Phe	Pro	Ser	Gln	Asn	Gly	His	Asp	Gly
65					70					75					80

Ser	Thr	Asp	Val	Gln	Gln	Arg	Ala	Arg	Arg	Ser	Asn	Cys	Arg	Arg	Gln
				85					90					95	

Glu	Gly	Ile	Lys	Ile	Val	Leu	Glu	Asp	Ile	Phe	Thr	Leu	Trp	Arg	Gln
			100					105					110		

Val	Glu	Thr	Lys	Val	Arg	Ala	Lys	Ile	Arg	Lys	Met	Lys	Val	Thr	Thr
		115					120					125			

Lys	Val	Asn	Arg	His	Asp	Lys	Ile	Asn	Gly	Lys	Arg	Lys	Thr	Ala	Lys
	130					135					140				

```
Glu His Leu Arg Lys Leu Ser Met Lys Glu Arg Glu His Gly Glu Lys
145                 150                 155                 160

Glu Arg Gln Val Ser Glu Ala Glu Glu Asn Gly Lys Leu Asp Met Lys
                165                 170                 175

Glu Ile His Thr Tyr Met Glu Met Phe Gln Arg Ala Gln Ala Leu Arg
            180                 185                 190

Arg Arg Ala Glu Asp Tyr Tyr Arg Cys Lys Ile Thr Pro Ser Ala Arg
        195                 200                 205

Lys Pro Leu Cys Asn Arg Cys Thr Tyr Asn Leu Val Leu Pro Gly Ser
    210                 215                 220

Glu Lys Lys Tyr Tyr Ser His Ala
225                 230


<210> 1178
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 349; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC141272.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478725"

<400> 1178
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn His
            20                  25                  30

Tyr Thr Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

35 40 45

Ser Tyr Ile Ser Gly Asn Ser Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

<210> 1179
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 350; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC142525.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485802"

<400> 1179
Gln Arg Ser Pro Arg Trp Glu Asp Ser Tyr Pro Ser Ala Trp Glu Gly
1 5 10 15

Phe Lys Glu Asn Gln Thr Gly Ser Leu
20 25

<210> 1180
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 351; "

<220>
<221> source

<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC145212.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478910"

<400> 1180
Met Phe Pro Val Ser Ser Gly Cys Phe Gln Glu Gln Gln Glu Thr Asn
1 5 10 15

Lys Ser Leu Pro Arg Ser Ala Ser Thr Pro Glu Thr Arg Thr Lys Phe
20 25 30

Thr Gln Asp Asn Leu Cys His Ala Gln Arg Glu Arg Leu Asp Ser Ala
35 40 45

Asn Leu Trp Val Leu Val Asp Cys Ile Leu Arg Asp Thr Ser Glu Asp
50 55 60

Leu Gly Leu Gln Cys Asp Ala Val Asn Leu Ala Phe Gly Arg Arg Cys
65 70 75 80

Glu Glu Leu Glu Asp Ala Arg His Lys Leu Gln His His Leu His Lys
85 90 95

Met Leu Arg Glu Ile Thr Asp Gln Glu His Asn Val Val Ala Leu Lys
100 105 110

Glu Ala Ile Lys Asp Lys Glu Glu Pro Leu His Ile Ala Gln Thr Arg
115 120 125

Leu

<210> 1181
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 352; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC156455.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486263"

<400> 1181
Met Thr Ala Leu Phe Pro Gly Leu Ala Pro Glu Thr Glu Gln Pro Asp
1 5 10 15

Ile His Thr Pro Arg Arg Gln Leu Glu Val Pro Pro Gly Asn Gln Asn
20 25 30

His Pro Gln Arg Arg Pro Pro Asp Thr Asp Ile
35 40

<210> 1182
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 353; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC171558.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480318"

<400> 1182
Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
1 5 10 15

Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
20 25 30

```
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
        35                  40                  45

Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
    50                  55                  60

Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65                  70                  75                  80

Met Leu Val Asp Phe Phe Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
                85                  90                  95

Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
            100                 105                 110

Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
        115                 120                 125

Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
    130                 135                 140

Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145                 150                 155                 160

Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
                165                 170                 175

Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
            180                 185                 190

Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
        195                 200                 205

Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
    210                 215                 220

Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Met Cys
225                 230                 235                 240

Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
                245                 250                 255

Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
```

260 265 270

Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
275 280 285

Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
290 295 300

His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
305 310 315

<210> 1183
<211> 313
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 354; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC171558.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484075"

<400> 1183
Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
1 5 10 15

Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
20 25 30

Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
35 40 45

Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
50 55 60

Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
65 70 75 80

```
Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
                85                  90                  95

Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
            100                 105                 110

Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
        115                 120                 125

Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
    130                 135                 140

Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
145                 150                 155                 160

Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
                165                 170                 175

Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
            180                 185                 190

Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
        195                 200                 205

Val Cys Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
    210                 215                 220

Leu Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
225                 230                 235                 240

Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
                245                 250                 255

Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
            260                 265                 270

Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
        275                 280                 285

Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
    290                 295                 300
```

```
Thr Lys Tyr Ile Leu Cys Lys Glu Lys
305                 310


<210> 1184
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 355; "

<220>
<221> source
<223> /note="Gene Symbol: CYP2D6; "

<220>
<221> source
<223> /note="Gene Name:
      AC208162.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486407"

<400> 1184
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Val Ile Val Ala Ile Phe
1               5                  10                  15


Leu Leu Leu Val Asp Leu Met His Arg Arg Gln Arg Trp Ala Ala Arg
            20                  25                  30


Tyr Ser Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
        35                  40                  45


Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
    50                  55                  60


Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65                  70                  75                  80


Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Leu Val Thr His Gly Glu
                85                  90                  95


Asp Thr Ala Asp Arg Pro Pro Val Pro Ile Thr Gln Ile Leu Gly Phe
            100                 105                 110


Gly Pro Arg Ser Gln Gly Val Phe Leu Ala Arg Tyr Gly Pro Ala Trp
        115                 120                 125
```

```
Arg Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu
    130                 135                 140

Gly Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu
145                 150                 155                 160

Cys Ala Ala Phe Ala Asn His Ser Gly Arg Pro Phe Arg Pro Asn Gly
                165                 170                 175

Leu Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly
            180                 185                 190

Arg Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu
        195                 200                 205

Ala Gln Glu Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu
    210                 215                 220

Asn Ala Val Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val
225                 230                 235                 240

Leu Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr
                245                 250                 255

Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr
            260                 265                 270

Glu Ala Phe Leu Ala Glu Met Glu Lys Ala Lys Gly Asn Pro Glu Ser
        275                 280                 285

Ser Phe Asn Asp Glu Asn Leu Arg Ile Val Val Ala Asp Leu Phe Ser
    290                 295                 300

Ala Gly Met Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu
305                 310                 315                 320

Met Ile Leu His Pro Asp Val Gln Arg Arg Val Gln Gln Glu Ile Asp
                325                 330                 335

Asp Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His
            340                 345                 350
```

```
Met Pro Tyr Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp
        355                 360                 365

Ile Val Pro Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val
    370                 375                 380

Gln Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser
385                 390                 395                 400

Ser Val Leu Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His
                405                 410                 415

Pro Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala
            420                 425                 430

Phe Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu
        435                 440                 445

Ala Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe
    450                 455                 460

Ser Phe Ser Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val
465                 470                 475                 480

Val Ser Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro
                485                 490                 495

Arg
```

<210> 1185
<211> 446
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 355; "

<220>
<221> source
<223> /note="Gene Symbol: CYP2D6; "

<220>
<221> source
<223> /note="Gene Name:

AC208162.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487524"

<400> 1185
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Val Ile Val Ala Ile Phe
1 5 10 15

Leu Leu Leu Val Asp Leu Met His Arg Arg Gln Arg Trp Ala Ala Arg
20 25 30

Tyr Ser Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
35 40 45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
50 55 60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65 70 75 80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Leu Val Thr His Gly Glu
85 90 95

Asp Thr Ala Asp Arg Pro Pro Val Pro Ile Thr Gln Ile Leu Gly Phe
100 105 110

Gly Pro Arg Ser Gln Gly Arg Pro Phe Arg Pro Asn Gly Leu Leu Asp
115 120 125

Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg Arg Phe
130 135 140

Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala Gln Glu
145 150 155 160

Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn Ala Val
165 170 175

Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val Leu Arg Phe
180 185 190

Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu His Arg
195 200 205

Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu Ala Phe
210 215 220

Leu Ala Glu Met Glu Lys Ala Lys Gly Asn Pro Glu Ser Ser Phe Asn
225 230 235 240

Asp Glu Asn Leu Arg Ile Val Val Ala Asp Leu Phe Ser Ala Gly Met
245 250 255

Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu Met Ile Leu
260 265 270

His Pro Asp Val Gln Arg Arg Val Gln Gln Glu Ile Asp Asp Val Ile
275 280 285

Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met Pro Tyr
290 295 300

Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Val Pro
305 310 315 320

Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val Gln Gly Phe
325 330 335

Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser Val Leu
340 345 350

Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His Pro Glu His
355 360 365

Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe Leu Pro
370 375 380

Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala Arg Met
385 390 395 400

Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser Phe Ser
405 410 415

Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val Val Ser Phe
420 425 430

```
Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
        435                 440                 445


<210> 1186
<211> 176
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 356; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC213203.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478882"

<400> 1186
Met Gly Asn His Glu Leu Met Thr Ser Trp Leu Leu Asp Val Arg Lys
1               5                   10                  15


Asn Leu Gln Ser Gln Arg Glu Leu Ser Lys Phe Cys Pro Glu Gln Thr
            20                  25                  30


Glu Gly Trp Arg Cys His Arg Leu Arg Trp Glu Asn Gly Arg Cys His
        35                  40                  45


Arg Leu Gln Gly Lys Val Gly Asp Gln Leu Arg Ala Pro Glu Pro Ser
    50                  55                  60


Trp Lys Glu Phe Pro Ile Gln Pro Ala Ser Val Ser Ala Ser Val Leu
65                  70                  75                  80


Phe Leu Met Thr Leu Arg Val Leu Ala Ser Gly Ser Phe Met Met Gln
                85                  90                  95


Arg Val Pro Pro Ser His Pro Gly Arg Leu Arg Ala Pro Ala Ser Ser
            100                 105                 110


Trp Gln Pro Gly Ala Arg Leu Arg Ile Trp Arg Pro Thr Thr Gly Trp
```

```
        115                 120                 125

Ser Leu Ala Ala Thr Ser Gln Arg Arg Ile Ser Ser Pro Val Val Ser
    130                 135                 140

Cys Gly Arg Val Ala Val Thr Arg Ser Arg Thr Arg Asp Ser Trp Pro
145                 150                 155                 160

Trp Cys Pro Ser Arg Ser Pro Arg Cys Val Ala Cys Arg Leu Phe Phe
                165                 170                 175


<210> 1187
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 357; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC231657.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485675"

<400> 1187
Met Glu Pro Arg Thr Gly Gly Ala Ala Asn Pro Lys Gly Ser Arg Gly
1               5                   10                  15

Arg Pro Gly Pro Leu Pro Pro Ala Cys Pro Ser Ala Leu Pro Leu Leu
            20                  25                  30

Ala Arg Leu Asp Ala Arg Pro Leu Ala Ala Arg Ala Ala Val Asp Val
        35                  40                  45

Ala Ala Leu Val His Arg Ala Gly Ala Thr Leu Arg Leu Arg Arg Lys
    50                  55                  60

Glu Ala Phe Ile Val Leu Gly Cys Lys Asp Asn Asn Val Met Asp Ser
65                  70                  75                  80
```

Arg Leu Pro His

<210> 1188
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 358; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC233755.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478289"

<400> 1188
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
35 40 45

Ser Ser Gly Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn
65 70 75 80

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg

115

<210> 1189
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 359; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC233755.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481152"

<400> 1189
Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys

<210> 1190
<211> 101
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 360; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC234582.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485039"

<400> 1190
Ala Gly Gly Ala Val Glu Pro Gly Ala Gly Leu Leu Ser Gly Ala Glu
1 5 10 15

Val Thr Pro Trp Ala Ala Gly Ala Val Glu Pro Gly Ala Gly Leu Leu
20 25 30

Ser Gly Ala Glu Val Thr Pro Trp Ala Gly Gly Ala Val Glu Pro Gly
35 40 45

Ala Gly Leu Val Ser Gly Ala Glu Val Thr Pro Trp Ala Gly Gly Ala
50 55 60

Val Glu Pro Gly Ala Gly Leu Val Ser Gly Ala Glu Val Thr Pro Trp
65 70 75 80

Ala Trp Gly Ala Val Glu Pro Gly Ala Gly Leu Val Ser Gly Ala Glu
85 90 95

Val Thr Pro Trp Ala
100

<210> 1191
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 361; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC234582.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485187"

<400> 1191
Ala Gly Gly Ala Val Glu Pro Gly Ala Gly Leu Val Ser Gly Ala Glu
1 5 10 15

Val Thr Pro Trp Ala Ala Gly Ala Val Glu Pro Gly Asp Gly Leu Val
20 25 30

Ser Gly Ala Glu Val Thr Pro Trp Ala Gly Gly Ala Val Glu Pro Gly
35 40 45

Ala Gly Leu Val Ser Gly Ala Glu Val Thr Pro Trp Ala Gly Gly Ala
50 55 60

Val Glu Pro Gly Ala Gly Leu Val Ser Gly Ala Glu Val Thr Pro Trp
65 70 75 80

Ala Gly Gly Ala Val Glu Pro Gly Ala Gly Leu Val Ser Gly Ala Glu
85 90 95

Val Thr Pro Trp Ala
100

<210> 1192
<211> 446
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 362; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source

<223> /note="Gene Name:
AC236040.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475794"

<400> 1192

```
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Val Ile Val Ala Ile Phe
1               5                  10                  15

Leu Leu Leu Val Asp Leu Met His Arg Arg Gln Arg Trp Ala Ala Arg
            20                  25                  30

Tyr Ser Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
        35                  40                  45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
    50                  55                  60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65                  70                  75                  80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Leu Val Thr His Gly Glu
                85                  90                  95

Asp Thr Ala Asp Arg Pro Pro Val Pro Ile Thr Gln Ile Leu Gly Phe
            100                 105                 110

Gly Pro Arg Ser Gln Gly Arg Pro Phe Arg Pro Asn Gly Leu Leu Asp
        115                 120                 125

Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg Arg Phe
    130                 135                 140

Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala Gln Glu
145                 150                 155                 160

Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn Ala Val
                165                 170                 175

Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val Leu Arg Phe
            180                 185                 190

Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu His Arg
```

```
        195                 200                 205

Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu Ala Phe
    210                 215                 220

Leu Ala Glu Met Glu Lys Ala Lys Gly Asn Pro Glu Ser Ser Phe Asn
225                 230                 235                 240

Asp Glu Asn Leu Arg Ile Val Val Ala Asp Leu Phe Ser Ala Gly Met
                245                 250                 255

Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu Met Ile Leu
            260                 265                 270

His Pro Asp Val Gln Arg Arg Val Gln Gln Glu Ile Asp Asp Val Ile
        275                 280                 285

Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met Pro Tyr
    290                 295                 300

Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Val Pro
305                 310                 315                 320

Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val Gln Gly Phe
                325                 330                 335

Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser Val Leu
            340                 345                 350

Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His Pro Glu His
        355                 360                 365

Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe Leu Pro
    370                 375                 380

Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala Arg Met
385                 390                 395                 400

Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser Phe Ser
                405                 410                 415

Val Pro Thr Gly Gln Pro Arg Pro Ser His His Gly Val Phe Ala Phe
            420                 425                 430
```

Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
435 440 445

<210> 1193
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 362; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC236040.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000476060"

<400> 1193
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Val Ile Val Ala Ile Phe
1 5 10 15

Leu Leu Leu Val Asp Leu Met His Arg Arg Gln Arg Trp Ala Ala Arg
20 25 30

Tyr Ser Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
35 40 45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
50 55 60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65 70 75 80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Leu Val Thr His Gly Glu
85 90 95

Asp Thr Ala Asp Arg Pro Pro Val Pro Ile Thr Gln Ile Leu Gly Phe
100 105 110

```
Gly Pro Arg Ser Gln Gly Val Phe Leu Ala Arg Tyr Gly Pro Ala Trp
        115                 120                 125

Arg Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu
    130                 135                 140

Gly Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu
145                 150                 155                 160

Cys Ala Ala Phe Ala Asn His Ser Gly Arg Pro Phe Arg Pro Asn Gly
                165                 170                 175

Leu Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly
            180                 185                 190

Arg Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu
        195                 200                 205

Ala Gln Glu Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu
    210                 215                 220

Asn Ala Val Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val
225                 230                 235                 240

Leu Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr
                245                 250                 255

Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr
            260                 265                 270

Glu Ala Phe Leu Ala Glu Met Glu Lys Ala Lys Gly Asn Pro Glu Ser
        275                 280                 285

Ser Phe Asn Asp Glu Asn Leu Arg Ile Val Val Ala Asp Leu Phe Ser
    290                 295                 300

Ala Gly Met Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu
305                 310                 315                 320

Met Ile Leu His Pro Asp Val Gln Arg Arg Val Gln Gln Glu Ile Asp
                325                 330                 335

Asp Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His
```

```
            340                 345                 350

Met Pro Tyr Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp
        355                 360                 365

Ile Val Pro Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val
    370                 375                 380

Gln Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser
385                 390                 395                 400

Ser Val Leu Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His
                405                 410                 415

Pro Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala
            420                 425                 430

Phe Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu
        435                 440                 445

Ala Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe
    450                 455                 460

Ser Phe Ser Val Pro Thr Gly Gln Pro Arg Pro Ser His His Gly Val
465                 470                 475                 480

Phe Ala Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro
                485                 490                 495

Arg
```

<210> 1194
<211> 299
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 363; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>

<221> source
<223> /note="Gene Name:
AC240274.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478612"

<400> 1194

```
Met Val Val Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn
1               5                  10                  15

Ile Leu Glu Met Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys
            20                  25                  30

Gln Gln Phe Arg Asn Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala
        35                  40                  45

Cys Phe Leu Ala Asn Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys
    50                  55                  60

Asp Leu Ile Lys Ser Val Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu
65                  70                  75                  80

Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys
                85                  90                  95

Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys
            100                 105                 110

Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Gln His Leu Gln
        115                 120                 125

Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu
    130                 135                 140

Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln Gln Leu Phe Gln
145                 150                 155                 160

Lys Leu Ser Pro Glu Asn Asp Asn Asp His Asp Glu Asp Val Gln Val
                165                 170                 175

Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ala Pro Arg Glu Met Gln
            180                 185                 190
```

```
Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala
        195                 200                 205

Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn Gln Pro His
    210                 215                 220

Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu
225                 230                 235                 240

Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
                245                 250                 255

Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
            260                 265                 270

Ser Pro Arg Thr Ser Val Gly Ser Ser Glu Lys Gly Gly Pro Arg Gly
        275                 280                 285

Asn Arg Ser Gln Ala Gln Gln Gly Ala Ala Gly
    290                 295


<210> 1195
<211> 672
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 363; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC240274.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478665"

<400> 1195
Met Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Thr Asn
1               5                   10                  15

Ile Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys
            20                  25                  30
```

```
Gln Gln Phe Arg Asn Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala
        35                  40                  45

Gly Phe Leu Ala Asn Arg Gln Lys Lys Tyr Lys Tyr Glu Glu Cys Lys
    50                  55                  60

Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu
65                  70                  75                  80

Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys
                85                  90                  95

Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys
            100                 105                 110

Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Gln His Leu Gln
        115                 120                 125

Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu
    130                 135                 140

Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln
145                 150                 155                 160

Lys Leu Ser Pro Glu Asn Asp Asn Asp His Asp Glu Asp Val Gln Val
                165                 170                 175

Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ala Pro Arg Glu Met Gln
            180                 185                 190

Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala
        195                 200                 205

Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn Gln Pro His
    210                 215                 220

Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu
225                 230                 235                 240

Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
                245                 250                 255
```

```
Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
            260                 265                 270

Ser Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu
        275                 280                 285

Ser Trp Asp Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu
    290                 295                 300

Ala Ser Tyr Gln Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln
305                 310                 315                 320

Gln Val Cys Met Ala Val Asp Ile Gly Gly His Arg Trp Asp Gln Val
                325                 330                 335

Lys Lys Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu
            340                 345                 350

Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys
        355                 360                 365

Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro
    370                 375                 380

Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly Trp Ala
385                 390                 395                 400

Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln
                405                 410                 415

Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu
            420                 425                 430

Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser
        435                 440                 445

Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val
    450                 455                 460

Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg
465                 470                 475                 480
```

```
Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro
                485                 490                 495

Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln
            500                 505                 510

Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln
        515                 520                 525

Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu
    530                 535                 540

Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly
545                 550                 555                 560

Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg
                565                 570                 575

Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg
            580                 585                 590

Leu Ser Gly Met Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
        595                 600                 605

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
    610                 615                 620

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
625                 630                 635                 640

His Ile Ser Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met
                645                 650                 655

Gly Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
            660                 665                 670


<210> 1196
<211> 791
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 363; "
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<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC240274.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480818"

<400> 1196
Met Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Thr Asn
1 5 10 15

Ile Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys
20 25 30

Gln Gln Phe Arg Asn Leu Lys Glu Met Phe Cys Asn Ser Thr Gly Arg
35 40 45

Leu Pro Gly Gln Pro Thr Glu Glu Ile Gln Gln Tyr Lys Val Leu Val
50 55 60

His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu
65 70 75 80

Gly Arg Asp Ala Ser Arg Ser Leu Asn Gln His Leu Gln Ala Leu Leu
85 90 95

Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln
100 105 110

Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu Ser
115 120 125

Pro Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu Glu Ala
130 135 140

Glu Lys Val Leu Glu Ser Ser Ala Pro Arg Glu Val Gln Lys Ala Glu
145 150 155 160

Glu Ser Lys Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys
165 170 175

```
Ser Asn Ser His Gly Pro Cys Asp Ser Asn Gln Pro His Lys Asn Ile
            180                 185                 190

Asn Ile Thr Phe Glu Glu Asp Lys Val Asn Ser Thr Leu Val Val Asp
        195                 200                 205

Arg Glu Ser Ser His Asp Glu Cys Gln Asp Ala Val Asn Ile Leu Pro
    210                 215                 220

Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
225                 230                 235                 240

Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu Met
                245                 250                 255

Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe Arg
            260                 265                 270

Asn Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Cys Phe Leu Ala
        275                 280                 285

Asn Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys
    290                 295                 300

Ser Val Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu
305                 310                 315                 320

Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu Val His
                325                 330                 335

Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu Gly
            340                 345                 350

Arg Asp Ala Ser Arg Ser Leu Asn Gln His Leu Gln Ala Leu Leu Thr
        355                 360                 365

Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln Leu
    370                 375                 380

Ala Glu Gly Cys Arg Leu Ala Gln Gln Leu Phe Gln Lys Leu Ser Pro
385                 390                 395                 400
```

```
Glu Asn Asp Asn Asp His Asp Glu Asp Val Gln Val Glu Val Ala Glu
                405                 410                 415

Lys Val Gln Lys Ser Ser Ala Pro Arg Glu Met Gln Lys Ala Glu Glu
            420                 425                 430

Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys Ser
        435                 440                 445

Asn Ser His Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr Lys
    450                 455                 460

Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser Ser
465                 470                 475                 480

Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu
                485                 490                 495

Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn
            500                 505                 510

Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu
        515                 520                 525

Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Gln
    530                 535                 540

Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met
545                 550                 555                 560

Ala Val Asp Ile Gly Gly His Arg Trp Asp Gln Val Lys Lys Glu Asp
                565                 570                 575

Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys
            580                 585                 590

Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro
        595                 600                 605

Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala
    610                 615                 620

Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp
```

625 630 635 640

Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys
645 650 655

Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu
660 665 670

Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu
675 680 685

Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu
690 695 700

Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp
705 710 715 720

Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg
725 730 735

Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp
740 745 750

Val Ile Gln Leu Leu Pro Val Val Leu Asn Ser Leu Thr Pro Ala Cys
755 760 765

Pro Met Glu Val Pro Phe Met His Trp Arg Lys Asn Met Leu Ala Phe
770 775 780

Leu Leu Thr Trp Glu Lys Leu
785 790

<210> 1197
<211> 603
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 363; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>

<221> source
<223> /note="Gene Name:
AC240274.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484923"

<400> 1197

```
Val Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln
1               5                  10                  15

Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu Val His Ser
            20                  25                  30

Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu Gly Arg
        35                  40                  45

Asp Ala Ser Arg Ser Leu Asn Gln His Leu Gln Ala Leu Leu Thr Pro
    50                  55                  60

Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln Leu Ala
65                  70                  75                  80

Glu Gly Cys Arg Leu Ala Gln Gln Leu Phe Gln Lys Leu Ser Pro Glu
                85                  90                  95

Asn Asp Asn Asp His Asp Glu Asp Val Gln Val Glu Val Ala Glu Lys
            100                 105                 110

Val Gln Lys Ser Ser Ala Pro Arg Glu Met Gln Lys Ala Glu Glu Lys
        115                 120                 125

Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys Ser Asn
    130                 135                 140

Ser His Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr Lys Ile
145                 150                 155                 160

Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser
                165                 170                 175

His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu Ser
            180                 185                 190
```

```
Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn Leu
        195                 200                 205

Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu Gly
    210                 215                 220

Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Gln Ser
225                 230                 235                 240

Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met Ala
                245                 250                 255

Val Asp Ile Gly Gly His Arg Trp Asp Gln Val Lys Lys Glu Asp Gln
            260                 265                 270

Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly
        275                 280                 285

Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser
    290                 295                 300

Gly Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe
305                 310                 315                 320

Tyr Ile Leu Glu Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu
                325                 330                 335

Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro
            340                 345                 350

Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln
        355                 360                 365

Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu
    370                 375                 380

Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu
385                 390                 395                 400

Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln
                405                 410                 415

Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu
```

```
            420                 425                 430

Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg
        435                 440                 445

Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu
    450                 455                 460

Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe
465                 470                 475                 480

Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg
                485                 490                 495

Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu
            500                 505                 510

Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Gly Met Leu
        515                 520                 525

Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys
    530                 535                 540

Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro Asp Ser Phe Gln His
545                 550                 555                 560

Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala
                565                 570                 575

Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His
            580                 585                 590

Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
        595                 600


<210> 1198
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 364; "

<220>
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<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC241377.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486219"

<400> 1198

```
Met Arg Arg Ala Pro Asp Trp Val Gln Arg Gln Ala Ala Pro Gly Ser
1               5                  10                  15

Lys Cys Arg Val Pro Trp Gln Arg Arg Glu Phe Pro Ser Arg Gly Gly
            20                  25                  30

Arg Lys Gln Pro Gln Pro Gly Ser Arg Gln Arg Lys Gln Asn Pro Ile
        35                  40                  45

Ser Leu Pro Gly Glu Gln Asn Gly Arg Lys Ala Thr Pro Gln Ala Gly
    50                  55                  60

Ala Leu Gly Ala Leu Gly Ile Arg Gly Ile Pro Ser Leu Cys Gln Ser
65                  70                  75                  80

Glu Gly Thr Arg Trp Ser Arg Arg Gly Arg Arg Trp Ala Glu Arg Cys
                85                  90                  95

Pro Pro Gly Val Leu Gly Ala Gly Arg Ser Leu Arg Ala Gln Arg Ser
            100                 105                 110

Arg Leu His Ser Arg Pro Pro Pro Leu Ser Pro Leu Arg Lys Pro Gly
        115                 120                 125

Gly Ser Asn Gln Pro Arg Ser Ala Ala Ala Ala Gly Thr His Glu Ala
    130                 135                 140

Cys Leu Gln Ala Ser Gly Thr Thr Arg Gly Trp Lys Tyr His Ala Leu
145                 150                 155                 160

Pro Leu Arg Leu Asp Pro Arg Ser Gly His Ala Gly Ser Ala Leu Lys
                165                 170                 175
```

```
Ala Gly Ser Cys Pro Arg Leu Gly Gly Gly Gly Arg Gly Arg Gly Glu
            180                 185                 190

Ala Gly Ala Pro Ser Arg Phe Trp Leu Pro Arg Ser Leu Gln Gln Leu
        195                 200                 205

Leu Pro Asn Glu Pro Arg Asn Ala Asp Val Gln Thr Leu His Pro Thr
    210                 215                 220

Pro Ser His Thr Arg Arg Gly Gln Arg Thr Gly Lys Gly Ala Leu Gly
225                 230                 235                 240

Pro Arg Phe Trp Lys Ser Lys Asn Ser Pro Ala Asn Arg Gln Ser Ser
                245                 250                 255

Ala Leu Asp Phe Trp Ile Thr Thr Ser Ile Ser Phe
            260                 265


<210> 1199
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 365; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC241585.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486699"

<400> 1199
Met Arg Arg Ala Pro Asp Trp Val Gln Arg Gln Ala Ala Pro Gly Ser
1               5                   10                  15

Lys Cys Arg Val Pro Trp Gln Arg Arg Glu Phe Pro Gly Arg Gly Gly
            20                  25                  30

Arg Lys Gln Pro Gln Pro Gly Ser Arg Gln Arg Lys Gln Asn Pro Ile
        35                  40                  45
```

```
Ser Leu Pro Gly Glu Gln Asn Gly Arg Lys Ala Thr Pro Gln Ala Gly
    50                  55                  60

Ala Leu Gly Ala Leu Gly Ile Arg Gly Ile Pro Ser Leu Cys Gln Ser
65                  70                  75                  80

Glu Gly Thr Arg Trp Ser Arg Arg Gly Arg Arg Trp Ala Glu Arg Cys
                85                  90                  95

Pro Pro Gly Val Leu Gly Ala Gly Arg Ser Leu Arg Ala Gln Arg Ser
            100                 105                 110

Arg Leu His Ser Arg Pro Pro Pro Leu Ser Pro Leu Arg Lys Pro Gly
        115                 120                 125

Gly Ser Asn Gln Pro Arg Cys Ala Ala Ala Ala Gly Thr Gln Glu Ala
    130                 135                 140

Cys Leu Gln Ala Ser Gly Thr Thr Arg Gly Trp Lys Tyr His Ala Leu
145                 150                 155                 160

Pro Leu Arg Leu Asp Pro Arg Ser Gly His Ala Gly Ser Ala Leu Lys
                165                 170                 175

Ala Gly Ser Cys Pro Arg Leu Gly Gly Gly Gly Arg Gly Arg Gly Glu
            180                 185                 190

Ala Gly Ala Pro Ser Arg Phe Trp Leu Pro Arg Ser Leu Gln Gln Leu
        195                 200                 205

Leu Pro Asn Glu Pro Arg Asn Ala Asp Val Gln Thr Leu His Pro Thr
    210                 215                 220

Pro Ser His Thr Arg Arg Gly Gln Arg Thr Gly Lys Gly Ala Leu Gly
225                 230                 235                 240

Pro Arg Phe Trp Lys Ser Lys Asn Ser Pro Ala Asn Arg Gln Ser Ser
                245                 250                 255

Ala Leu Asp Phe Trp Ile Thr Thr Ser Ile Ser Phe
            260                 265
```

<210> 1200
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 366; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC242988.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485440"

<400> 1200
Ile Tyr Asn Val Lys Ser Thr Arg Arg Leu Asp Leu Arg Glu Tyr Lys
1 5 10 15

Asn Asp Arg Asp Pro Glu Lys Gly Cys
20 25

<210> 1201
<211> 267
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 367; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC243687.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482099"

<400> 1201
Met Trp Asp Gln Arg Leu Val Lys Leu Ala Leu Leu Gln His Leu Arg
1 5 10 15

```
Ala Phe Tyr Gly Ile Lys Val Lys Gly Val Arg Gly Gln Cys Asp Arg
            20                  25                  30

Arg Arg His Glu Thr Ala Ala Thr Glu Ile Gly Gly Lys Ile Phe Gly
        35                  40                  45

Val Pro Phe Asn Ala Leu Pro His Ser Ala Val Pro Glu Tyr Gly His
    50                  55                  60

Ile Pro Ser Phe Leu Val Asp Ala Cys Thr Ser Leu Glu Glu His Ile
65                  70                  75                  80

His Thr Glu Gly Leu Phe Arg Lys Ser Gly Ser Val Ile Arg Leu Lys
                85                  90                  95

Ala Leu Lys Asn Lys Val Asp His Gly Glu Gly Cys Leu Ser Ser Ala
            100                 105                 110

Pro Pro Cys Asp Ile Ala Gly Leu Leu Lys Gln Phe Phe Arg Glu Leu
        115                 120                 125

Pro Glu Pro Ile Leu Pro Ala Asp Leu His Glu Ala Leu Leu Lys Ala
    130                 135                 140

Gln Gln Leu Gly Thr Glu Glu Lys Asn Lys Ala Ile Leu Leu Leu Ser
145                 150                 155                 160

Cys Leu Leu Ala Asp His Thr Val His Val Leu Arg Tyr Phe Phe Asn
                165                 170                 175

Phe Leu Arg Asn Val Ser Leu Arg Ser Ser Glu Asn Lys Met Asp Ser
            180                 185                 190

Ser Asn Leu Ala Val Ile Phe Ala Pro Asn Leu Leu Gln Thr Ser Glu
        195                 200                 205

Gly His Glu Lys Met Ser Ser Asn Ala Glu Lys Lys Gly Val Tyr Gln
    210                 215                 220

Thr Leu Ser Trp Lys Arg Tyr Gln Pro Cys Trp Val Leu Met Val Ser
225                 230                 235                 240
```

Val Leu Leu His His Trp Lys Ala Leu Lys Lys Val Asn Met Lys Leu
245 250 255

Leu Val Asn Ile Arg Glu Arg Glu Asp Asn Val
260 265

<210> 1202
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 368; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC243756.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000464619"

<400> 1202
Met Val Asn Ser Val Val Phe Phe Asp Ile Thr Val Asp Gly Lys Pro
1 5 10 15

Leu Gly Arg Ile Ser Ile Lys Leu Phe Ala Asp Lys Ile Pro Lys Thr
20 25 30

Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Arg Tyr
35 40 45

Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly
50 55 60

Gly Asp Phe Thr Arg Pro Asn Gly Thr Asp Asp Lys Ser Ile Tyr Gly
65 70 75 80

Glu Lys Phe Asp Asp Glu Asn Leu Ile Arg Lys His Thr Gly Ser Gly
85 90 95

Ile Leu Ser Met Val Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Leu

100 105 110

Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Ala
115 120 125

Phe Gly Lys Val Lys Glu Arg Val Asn Ile Val Glu Ala Met Glu His
130 135 140

Phe Gly Tyr Arg Asn Ser Lys Thr Ser Lys Lys Ile Thr Ile Ala Asp
145 150 155 160

Cys Gly Gln Phe

<210> 1203
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 369; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC243790.2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481534"

<400> 1203
Phe Thr Gln Thr Tyr Arg Arg Ser Arg Gln His Glu Gln Leu Pro Gly
1 5 10 15

Gln Arg His Met Asp Leu Leu Thr Gly Tyr Ser Lys Leu Ile Gln Ser
20 25 30

Arg Leu Lys Leu Leu Leu His Leu Gly Ser Gln Pro Pro Val Gly Lys
35 40 45

Thr Phe Phe Phe Ser Cys Trp Cys His Pro Leu Phe His Gly Ser Lys
50 55 60

```
Thr Thr Pro Asn Val Trp Tyr Lys Phe Ser Glu Thr Ala Leu Ser Ile
65                  70                  75                  80

Leu Asn Ser Cys Gln Ala Ser Gln Leu Gly Val Arg Lys Met Pro Gly
                85                  90                  95

Asp Met Ser Ser Ser Pro Arg Val Arg Glu Phe Ser Ala Leu Val Ala
            100                 105                 110

Ile Lys Glu Lys Ile His Ile Leu Pro Thr Asn Ala Lys Val Gly Ser
        115                 120                 125

Lys Phe Gly Ser
    130


<210> 1204
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 370; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC243945.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485616"

<400> 1204
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
1               5                   10                  15

His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
            20                  25                  30

Cys Phe Arg Glu His Arg Val Gly Asp Lys Val Thr Asp Gln Gln Asp
        35                  40                  45

Pro Lys Ala Glu Glu Phe Phe Leu Val Gln Asn Lys Met Lys Ser Leu
```

```
    50                  55                  60

Pro Cys Leu Leu Leu Ser Thr Gln Thr Arg Gln Pro Ser Asp Phe Ser
65                  70                  75                  80

Ile Phe Ser Pro Pro Phe Pro Pro Phe Tyr Ser Thr Lys Pro Pro Leu
                85                  90                  95

Ser Ser Trp Pro Ile Pro Asn Glu Pro Leu Gly Thr Pro Pro Arg Arg
            100                 105                 110

Gly Arg Gly Arg Ala Glu Gly Leu Leu Thr Ser Gln
        115                 120


<210> 1205
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 371; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC245015.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489357"

<400> 1205
Ile Pro Ala Gln Ser Leu Thr Ser Leu Leu Ile Arg Leu Gln Gly Arg
1               5                   10                  15

Arg Leu Asp Ile Ile Leu Thr Gln Thr Pro Arg Ser Leu Leu Thr Ser
            20                  25                  30

Phe Gly Lys Arg His Ser Ile Phe Tyr Gln Ala Thr Ala Gln Val His
        35                  40                  45

Gly Glu Ile Ser Trp Phe Gln Met Lys Gly Gln Gly Phe Ala Leu Val
    50                  55                  60
```

```
Ile Ser His Ile Ser Asn Val Pro Lys Asn Val Pro Ala Trp Phe Arg
65                  70                  75                  80


Gly Arg Gly Ser Gly Ser Asn Tyr Ile Ser Ile Ser Gly Leu Gln Pro
                85                  90                  95


<210> 1206
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 371; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC245015.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489377"

<400> 1206
Val Ser Pro Arg Val Pro Glu Asn Val Phe Leu Leu Gly Thr Ile Leu
1               5                   10                  15


Leu Cys Leu Gln Lys Thr Leu Met Asp Ile Ile Leu Thr Gln Thr Pro
            20                  25                  30


Arg Ser Leu Leu Thr Ser Phe Gly Lys Arg His Ser Ile Phe Tyr Gln
        35                  40                  45


Ala Thr Ala Gln Val His Gly Glu Ile Ser Trp Phe Gln Met Lys Gly
    50                  55                  60


Gln Gly Phe Ala Leu Val Ile Ser His Ile Ser Asn Val Pro Lys Asn
65                  70                  75                  80


Val Pro Ala Trp Phe Arg Gly Arg Gly Ser Gly Ser Asn Tyr Ile Ser
                85                  90                  95


Ile Ser Gly Leu Gln Pro
```

100

<210> 1207
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 372; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC245100.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487212"

<400> 1207
Met Arg Arg Ala Pro Asp Trp Val Gln Arg Gln Ala Ala Pro Gly Ser
1 5 10 15

Lys Cys Arg Val Pro Trp Gln Arg Arg Glu Phe Pro Gly Arg Gly Gly
20 25 30

Arg Lys Gln Pro Gln Pro Gly Ser Arg Gln Arg Lys Gln Asn Pro Ile
35 40 45

Ser Leu Pro Gly Glu Gln Asn Gly Arg Thr Ala Thr Pro Gln Ala Gly
50 55 60

Ala Leu Gly Ala Leu Gly Ile Arg Gly Ile Pro Ser Leu Cys Gln Ser
65 70 75 80

Glu Gly Thr Arg Trp Ser Arg Arg Gly Arg Arg Trp Ala Glu Arg Cys
85 90 95

Pro Pro Gly Val Leu Gly Ala Gly Arg Ser Leu Arg Ala Gln Gly Ser
100 105 110

Arg Leu His Ser Arg Pro Pro Pro Leu Ser Pro Leu Arg Lys Pro Gly
115 120 125

```
Gly Ser Asn Gln Pro Arg Ser Ala Ala Ala Ala Gly Thr Gln Glu Ala
    130                 135                 140

Cys Leu Gln Ala Ser Gly Thr Thr Arg Gly Trp Lys Tyr His Ala Leu
145                 150                 155                 160

Pro Leu Arg Leu Asp Pro Arg Ser Gly His Ser Gly Ser Ala Phe Lys
                165                 170                 175

Ala Ser Ser Cys Pro Arg Leu Gly Gly Gly Gly Arg Gly Arg Gly Glu
            180                 185                 190

Ala Gly Ala Pro Ser Arg Phe Trp Leu Pro Arg Ser Leu Gln Gln Leu
        195                 200                 205

Ser Pro Asn Glu Pro Arg Asn Ala Asp Val Gln Thr Leu His Pro Thr
    210                 215                 220

Pro Ser His Thr Arg Arg Gly Arg Arg Thr Glu Lys Gly Ala Leu Gly
225                 230                 235                 240

Pro Arg Phe Trp Lys Ser Lys Asn Ser Pro Ala Asn Arg Gln Ser Ser
                245                 250                 255

Ala Leu Asp Phe Trp Ile Thr Thr Ser Ile Ser Phe
            260                 265


<210> 1208
<211> 236
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 373; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC253572.1; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000485259"

<400> 1208

```
Met Cys Val Thr Tyr His Ser Gly Thr Gly Tyr Cys Lys Cys Pro Glu
1               5                  10                  15

Gly Phe Leu Gly Glu Tyr Cys Gln His Arg Asp Pro Cys Glu Lys Asn
            20                  25                  30

Arg Cys Gln Asn Gly Gly Thr Cys Val Ala Gln Ala Met Leu Gly Lys
        35                  40                  45

Ala Thr Cys Arg Cys Ala Ser Gly Phe Thr Gly Glu Asp Cys Gln Tyr
    50                  55                  60

Ser Thr Pro His Pro Cys Phe Val Ser Arg Pro Cys Leu Asn Gly Gly
65                  70                  75                  80

Thr Cys His Met Leu Ser Arg Asp Thr Tyr Glu Cys Thr Cys Gln Val
                85                  90                  95

Gly Phe Thr Gly Lys Glu Cys Gln Trp Thr Asp Ala Cys Leu Ser His
            100                 105                 110

Leu Cys Ala Asn Gly Ser Thr Cys Thr Thr Val Ala Asn Gln Phe Ser
        115                 120                 125

Cys Lys Cys Leu Thr Gly Phe Thr Gly Gln Lys Cys Glu Thr Asp Val
    130                 135                 140

Asn Glu Cys Asp Ile Pro Gly His Cys Gln His Gly Gly Thr Cys Leu
145                 150                 155                 160

Asn Leu Pro Gly Ser Tyr Gln Cys Gln Cys Leu Gln Gly Phe Thr Gly
                165                 170                 175

Gln Tyr Cys Asp Arg Leu Tyr Val Pro Cys Ala His Ser Pro Cys Val
            180                 185                 190

Asn Gly Gly Thr Cys Arg Gln Thr Gly Asp Phe Thr Phe Glu Cys Asn
        195                 200                 205

Cys Leu Pro Glu Thr Val Arg Arg Gly Thr Glu Leu Trp Glu Arg Asp
    210                 215                 220
```

```
Arg Gln Val Trp Asn Gly Lys Glu His Asp Glu Asn
225                 230                 235


<210> 1209
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 374; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC254560.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486123"

<400> 1209
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1               5                   10                  15


Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
            20                  25                  30


Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
        35                  40                  45


Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
    50                  55                  60


Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65                  70                  75                  80


Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu
                85                  90                  95


Asp Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe
            100                 105                 110
```

```
Gly Pro Arg Ser Gln Gly Val Ile Leu Ser Arg Tyr Gly Pro Ala Trp
        115                 120                 125

Arg Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu
    130                 135                 140

Gly Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu
145                 150                 155                 160

Cys Ala Ala Phe Ala Asp Gln Ala Gly Arg Pro Phe Arg Pro Asn Gly
                165                 170                 175

Leu Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly
            180                 185                 190

Arg Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu
        195                 200                 205

Ala Gln Glu Gly Ser Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu
    210                 215                 220

Asn Ala Val Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val
225                 230                 235                 240

Leu Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr
                245                 250                 255

Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr
            260                 265                 270

Glu Ala Phe Leu Ala Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser
        275                 280                 285

Ser Phe Asn Asp Glu Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu
    290                 295                 300

Ala Gly Met Val Thr Thr Leu Thr Thr Leu Ala Trp Gly Leu Leu Leu
305                 310                 315                 320

Met Ile Leu His Leu Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp
                325                 330                 335

Asp Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His
```

```
            340                 345                 350

Met Pro Tyr Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp
        355                 360                 365

Ile Ile Pro Leu Ser Val Thr His Met Thr Ser His Asp Ile Glu Val
    370                 375                 380

Gln Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser
385                 390                 395                 400

Ser Val Leu Lys Asp Glu Ala Val Trp Lys Lys Pro Phe Arg Phe His
                405                 410                 415

Pro Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala
            420                 425                 430

Phe Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu
        435                 440                 445

Ala Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe
    450                 455                 460

Ser Phe Ser Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val
465                 470                 475                 480

Val Ser Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro
                485                 490                 495

Arg
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<210> 1210
<211> 444
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 374; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>

<221> source
<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000486298"

<400> 1210

```
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1               5                  10                  15

Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
            20                  25                  30

Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu His Val
        35                  40                  45

Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg Phe
    50                  55                  60

Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val Leu
65                  70                  75                  80

Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu Asp
                85                  90                  95

Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe Gly
            100                 105                 110

Pro Arg Ser Gln Gly Arg Pro Phe Arg Pro Asn Gly Leu Leu Asp Lys
        115                 120                 125

Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg Arg Phe Glu
    130                 135                 140

Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala Gln Gly Ser
145                 150                 155                 160

Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn Ala Val Pro Val
                165                 170                 175

Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val Leu Arg Phe Gln Lys
            180                 185                 190
```

```
Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu His Arg Met Thr
        195                 200                 205

Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu Ala Phe Leu Ala
    210                 215                 220

Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser Ser Phe Asn Asp Glu
225                 230                 235                 240

Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu Ala Gly Met Val Thr
                245                 250                 255

Thr Leu Thr Thr Leu Ala Trp Gly Leu Leu Leu Met Ile Leu His Leu
            260                 265                 270

Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp Asp Val Ile Gly Gln
        275                 280                 285

Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met Pro Tyr Thr Thr
    290                 295                 300

Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Ile Pro Leu Ser
305                 310                 315                 320

Val Thr His Met Thr Ser His Asp Ile Glu Val Gln Gly Phe Arg Ile
                325                 330                 335

Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser Val Leu Lys Asp
            340                 345                 350

Glu Ala Val Trp Lys Lys Pro Phe Arg Phe His Pro Glu His Phe Leu
        355                 360                 365

Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe Leu Pro Phe Ser
    370                 375                 380

Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala Arg Met Glu Leu
385                 390                 395                 400

Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser Phe Ser Val Ala
                405                 410                 415

Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val Val Ser Phe Leu Val
```

420 425 430

Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
435 440

<210> 1211
<211> 445
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 375; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC254788.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489211"

<400> 1211
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1 5 10 15

Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
20 25 30

Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu His Val
35 40 45

Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg Phe
50 55 60

Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val Leu
65 70 75 80

Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu Asp
85 90 95

Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe Gly
100 105 110

```
Pro Arg Ser Gln Gly Arg Pro Phe Arg Pro Asn Gly Leu Leu Asp Lys
        115                 120                 125

Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg Arg Phe Glu
    130                 135                 140

Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala Gln Glu Gly
145                 150                 155                 160

Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn Ala Val Pro
                165                 170                 175

Val Leu Pro His Ile Pro Ala Leu Ala Gly Lys Val Leu Arg Phe Gln
            180                 185                 190

Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu His Arg Met
        195                 200                 205

Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu Ala Phe Leu
    210                 215                 220

Ala Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser Ser Phe Asn Asp
225                 230                 235                 240

Glu Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu Ala Gly Met Val
                245                 250                 255

Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu Met Ile Leu His
            260                 265                 270

Leu Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp Asp Val Ile Gly
        275                 280                 285

Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met Pro Cys Thr
    290                 295                 300

Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Ile Pro Leu
305                 310                 315                 320

Ser Val Thr His Met Thr Ser Arg Asp Ile Glu Val Gln Gly Phe Arg
                325                 330                 335
```

```
Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser Val Leu Lys
            340                 345                 350

Asp Glu Ala Val Trp Lys Lys Pro Phe Arg Phe His Pro Glu His Phe
        355                 360                 365

Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe Leu Pro Phe
    370                 375                 380

Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala Arg Met Glu
385                 390                 395                 400

Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser Phe Ser Val
                405                 410                 415

Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val Val Ser Phe Leu
            420                 425                 430

Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
        435                 440                 445


<210> 1212
<211> 497
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 375; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000489366"

<400> 1212
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1               5                   10                  15

Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
            20                  25                  30
```

Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
35 40 45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
50 55 60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65 70 75 80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu
85 90 95

Asp Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe
100 105 110

Gly Pro Arg Ser Gln Gly Val Ile Leu Ser Arg Tyr Gly Pro Ala Trp
115 120 125

Arg Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu
130 135 140

Gly Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu
145 150 155 160

Cys Ala Ala Phe Ala Asp Gln Ala Gly Arg Pro Phe Arg Pro Asn Gly
165 170 175

Leu Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly
180 185 190

Arg Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu
195 200 205

Ala Gln Glu Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu
210 215 220

Asn Ala Val Pro Val Leu Pro His Ile Pro Ala Leu Ala Gly Lys Val
225 230 235 240

Leu Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr
245 250 255

```
Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr
            260                 265                 270

Glu Ala Phe Leu Ala Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser
        275                 280                 285

Ser Phe Asn Asp Glu Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu
    290                 295                 300

Ala Gly Met Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu
305                 310                 315                 320

Met Ile Leu His Leu Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp
                325                 330                 335

Asp Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His
            340                 345                 350

Met Pro Cys Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp
        355                 360                 365

Ile Ile Pro Leu Ser Val Thr His Met Thr Ser Arg Asp Ile Glu Val
    370                 375                 380

Gln Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser
385                 390                 395                 400

Ser Val Leu Lys Asp Glu Ala Val Trp Lys Lys Pro Phe Arg Phe His
                405                 410                 415

Pro Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala
            420                 425                 430

Phe Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu
        435                 440                 445

Ala Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe
    450                 455                 460

Ser Phe Ser Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val
465                 470                 475                 480
```

Val Ser Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro
485 490 495

Arg

<210> 1213
<211> 496
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 375; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
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<223> /note="Gene Name:
AC254788.1; "

<220>
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<223> /note="ENSP ID: ENSP00000489470"

<400> 1213
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1 5 10 15

Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
20 25 30

Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu His Val
35 40 45

Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg Phe
50 55 60

Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val Leu
65 70 75 80

Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu Asp
85 90 95

Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe Gly
100 105 110

```
Pro Arg Ser Gln Gly Val Ile Leu Ser Arg Tyr Gly Pro Ala Trp Arg
        115                 120                 125

Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu Gly
    130                 135                 140

Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu Cys
145                 150                 155                 160

Ala Ala Phe Ala Asp Gln Ala Gly Arg Pro Phe Arg Pro Asn Gly Leu
                165                 170                 175

Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg
            180                 185                 190

Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala
        195                 200                 205

Gln Glu Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn
    210                 215                 220

Ala Val Pro Val Leu Pro His Ile Pro Ala Leu Ala Gly Lys Val Leu
225                 230                 235                 240

Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu
                245                 250                 255

His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu
            260                 265                 270

Ala Phe Leu Ala Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser Ser
        275                 280                 285

Phe Asn Asp Glu Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu Ala
    290                 295                 300

Gly Met Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu Met
305                 310                 315                 320

Ile Leu His Leu Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp Asp
                325                 330                 335
```

```
Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met
            340                 345                 350

Pro Cys Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile
        355                 360                 365

Ile Pro Leu Ser Val Thr His Met Thr Ser Arg Asp Ile Glu Val Gln
    370                 375                 380

Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser
385                 390                 395                 400

Val Leu Lys Asp Glu Ala Val Trp Lys Lys Pro Phe Arg Phe His Pro
                405                 410                 415

Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe
            420                 425                 430

Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala
        435                 440                 445

Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser
    450                 455                 460

Phe Ser Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val Val
465                 470                 475                 480

Ser Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
                485                 490                 495


<210> 1214
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 376; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
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AC254847.1; "

<220>
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<223> /note="ENSP ID: ENSP00000488999"

<400> 1214

```
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Val Ile Val Ala Ile Phe
1               5                  10                  15

Leu Leu Leu Val Asp Leu Met His Arg Arg Gln Arg Trp Ala Ala Arg
            20                  25                  30

Tyr Ser Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
        35                  40                  45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
    50                  55                  60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65                  70                  75                  80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Leu Val Thr His Gly Glu
                85                  90                  95

Asp Thr Ala Asp Arg Pro Pro Val Pro Ile Thr Gln Ile Leu Gly Phe
            100                 105                 110

Gly Pro Arg Ser Gln Gly Val Phe Leu Ala Arg Tyr Gly Pro Ala Trp
        115                 120                 125

Arg Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu
    130                 135                 140

Gly Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu
145                 150                 155                 160

Cys Ala Ala Phe Ala Asn His Ser Gly Arg Pro Phe Arg Pro Asn Gly
                165                 170                 175

Leu Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly
            180                 185                 190

Arg Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu
        195                 200                 205
```

```
Ala Gln Glu Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu
    210                 215                 220

Asn Ala Val Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val
225                 230                 235                 240

Leu Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr
                245                 250                 255

Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr
            260                 265                 270

Glu Ala Phe Leu Ala Glu Met Glu Lys Ala Lys Gly Asn Pro Glu Ser
        275                 280                 285

Ser Phe Asn Asp Glu Asn Leu Arg Ile Val Val Ala Asp Leu Phe Ser
    290                 295                 300

Ala Gly Met Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu
305                 310                 315                 320

Met Ile Leu His Pro Asp Val Gln Arg Arg Val Gln Gln Glu Ile Asp
                325                 330                 335

Asp Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His
            340                 345                 350

Met Pro Tyr Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp
        355                 360                 365

Ile Val Pro Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val
    370                 375                 380

Gln Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser
385                 390                 395                 400

Ser Val Leu Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His
                405                 410                 415

Pro Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala
            420                 425                 430
```

```
Phe Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu
        435                 440                 445

Ala Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe
    450                 455                 460

Ser Phe Ser Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val
465                 470                 475                 480

Val Ser Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro
                485                 490                 495

Arg
```

<210> 1215
<211> 446
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 376; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
AC254847.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489410"

<400> 1215

```
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Val Ile Val Ala Ile Phe
1               5                  10                  15

Leu Leu Leu Val Asp Leu Met His Arg Arg Gln Arg Trp Ala Ala Arg
            20                  25                  30

Tyr Ser Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
        35                  40                  45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
```

```
    50                  55                  60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65                  70                  75                  80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Leu Val Thr His Gly Glu
                85                  90                  95

Asp Thr Ala Asp Arg Pro Pro Val Pro Ile Thr Gln Ile Leu Gly Phe
            100                 105                 110

Gly Pro Arg Ser Gln Gly Arg Pro Phe Arg Pro Asn Gly Leu Leu Asp
        115                 120                 125

Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg Arg Phe
    130                 135                 140

Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala Gln Glu
145                 150                 155                 160

Gly Leu Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn Ala Val
                165                 170                 175

Pro Val Leu Leu His Ile Pro Ala Leu Ala Gly Lys Val Leu Arg Phe
            180                 185                 190

Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu His Arg
        195                 200                 205

Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu Ala Phe
    210                 215                 220

Leu Ala Glu Met Glu Lys Ala Lys Gly Asn Pro Glu Ser Ser Phe Asn
225                 230                 235                 240

Asp Glu Asn Leu Arg Ile Val Val Ala Asp Leu Phe Ser Ala Gly Met
                245                 250                 255

Val Thr Thr Ser Thr Thr Leu Ala Trp Gly Leu Leu Leu Met Ile Leu
            260                 265                 270

His Pro Asp Val Gln Arg Arg Val Gln Gln Glu Ile Asp Asp Val Ile
        275                 280                 285
```

```
Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met Pro Tyr
    290                 295                 300

Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Val Pro
305                 310                 315                 320

Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val Gln Gly Phe
                325                 330                 335

Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser Val Leu
            340                 345                 350

Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His Pro Glu His
        355                 360                 365

Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe Leu Pro
    370                 375                 380

Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala Arg Met
385                 390                 395                 400

Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser Phe Ser
                405                 410                 415

Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val Val Ser Phe
            420                 425                 430

Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
        435                 440                 445


<210> 1216
<211> 267
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 377; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
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<223> /note="Gene Name:
AC254944.3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488249"

<400> 1216

```
Met Trp Asp Gln Arg Leu Val Lys Leu Ala Leu Leu Gln His Leu Arg
1               5                  10                  15

Ala Phe Tyr Gly Ile Lys Val Lys Gly Val Arg Gly Gln Cys Asp Arg
            20                  25                  30

Arg Arg His Glu Thr Ala Ala Thr Glu Ile Gly Gly Lys Ile Phe Gly
        35                  40                  45

Val Pro Phe Asn Ala Leu Pro His Ser Ala Val Pro Glu Tyr Gly His
    50                  55                  60

Ile Pro Ser Phe Leu Val Asp Ala Cys Thr Ser Leu Glu Glu His Ile
65                  70                  75                  80

His Thr Glu Gly Leu Phe Arg Lys Ser Gly Ser Val Ile Arg Leu Lys
                85                  90                  95

Ala Leu Lys Asn Lys Val Asp His Gly Glu Gly Cys Leu Ser Ser Ala
            100                 105                 110

Pro Pro Cys Asp Ile Ala Gly Leu Leu Lys Gln Phe Phe Arg Glu Leu
        115                 120                 125

Pro Glu Pro Ile Leu Pro Ala Asp Leu His Glu Ala Leu Leu Lys Ala
    130                 135                 140

Gln Gln Leu Gly Thr Glu Glu Lys Asn Lys Ala Ile Leu Leu Leu Ser
145                 150                 155                 160

Cys Leu Leu Ala Asp His Thr Val His Val Leu Arg Tyr Phe Phe Asn
                165                 170                 175

Phe Leu Arg Asn Val Ser Leu Arg Ser Ser Glu Asn Lys Met Asp Ser
            180                 185                 190

Ser Asn Leu Ala Val Ile Phe Ala Pro Asn Leu Leu Gln Thr Ser Glu
```

```
        195                 200                 205

Gly His Glu Lys Met Ser Ser Asn Ala Glu Lys Lys Gly Val Tyr Gln
    210                 215                 220

Thr Leu Ser Trp Lys Arg Tyr Gln Pro Cys Trp Val Leu Met Val Ser
225                 230                 235                 240

Val Leu Leu His His Trp Lys Ala Leu Lys Lys Val Asn Met Lys Leu
                245                 250                 255

Leu Val Asn Ile Arg Glu Arg Glu Asp Asn Val
            260                 265


<210> 1217
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 378; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC254995.1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486942"

<400> 1217
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1               5                   10                  15

Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
            20                  25                  30

Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu His Val
        35                  40                  45

Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg Phe
    50                  55                  60
```

```
Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val Leu
65                  70                  75                  80

Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu Asp
                85                  90                  95

Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe Gly
            100                 105                 110

Pro Arg Ser Gln Gly Arg Pro Phe Arg Pro Asn Gly Leu Leu Asp Lys
        115                 120                 125

Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly Arg Arg Phe Glu
    130                 135                 140

Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu Ala Gln Gly Ser
145                 150                 155                 160

Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu Asn Ala Val Pro Val
                165                 170                 175

Leu Pro His Ile Pro Ala Leu Ala Gly Lys Val Leu Arg Phe Gln Lys
            180                 185                 190

Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr Glu His Arg Met Thr
        195                 200                 205

Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr Glu Ala Phe Leu Ala
    210                 215                 220

Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser Ser Phe Asn Asp Glu
225                 230                 235                 240

Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu Ala Gly Met Val Thr
                245                 250                 255

Thr Leu Thr Thr Leu Ala Trp Gly Leu Leu Leu Met Ile Leu His Leu
            260                 265                 270

Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp Asp Val Ile Gly Gln
        275                 280                 285
```

```
Val Arg Arg Pro Glu Met Gly Asp Gln Ala His Met Pro Tyr Thr Thr
    290                 295                 300

Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Val Pro Leu Gly
305                 310                 315                 320

Val Thr His Met Thr Ser Arg Asp Ile Glu Val Gln Gly Phe Arg Ile
                325                 330                 335

Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser Ser Val Leu Lys Asp
            340                 345                 350

Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His Pro Glu His Phe Leu
        355                 360                 365

Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala Phe Leu Pro Phe Ser
    370                 375                 380

Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu Ala Arg Met Glu Leu
385                 390                 395                 400

Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe Ser Phe Ser Val Ala
                405                 410                 415

Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val Val Ser Phe Leu Val
            420                 425                 430

Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro Arg
        435                 440


<210> 1218
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 378; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AC254995.1; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000487070"

<400> 1218
Met Gly Leu Glu Ala Leu Val Pro Leu Ala Met Ile Val Ala Ile Phe
1   5   10   15

Leu Leu Leu Val Asp Leu Met His Arg His Gln Arg Trp Ala Ala Arg
            20   25   30

Tyr Pro Pro Gly Pro Leu Pro Leu Pro Gly Leu Gly Asn Leu Leu His
        35   40   45

Val Asp Phe Gln Asn Thr Pro Tyr Cys Phe Asp Gln Leu Arg Arg Arg
    50   55   60

Phe Gly Asp Val Phe Ser Leu Gln Leu Ala Trp Thr Pro Val Val Val
65   70   75   80

Leu Asn Gly Leu Ala Ala Val Arg Glu Ala Met Val Thr Arg Gly Glu
                85   90   95

Asp Thr Ala Asp Arg Pro Pro Ala Pro Ile Tyr Gln Val Leu Gly Phe
            100   105   110

Gly Pro Arg Ser Gln Gly Val Ile Leu Ser Arg Tyr Gly Pro Ala Trp
        115   120   125

Arg Glu Gln Arg Arg Phe Ser Val Ser Thr Leu Arg Asn Leu Gly Leu
    130   135   140

Gly Lys Lys Ser Leu Glu Gln Trp Val Thr Glu Glu Ala Ala Cys Leu
145   150   155   160

Cys Ala Ala Phe Ala Asp Gln Ala Gly Arg Pro Phe Arg Pro Asn Gly
                165   170   175

Leu Leu Asp Lys Ala Val Ser Asn Val Ile Ala Ser Leu Thr Cys Gly
            180   185   190

Arg Arg Phe Glu Tyr Asp Asp Pro Arg Phe Leu Arg Leu Leu Asp Leu
        195   200   205

```
Ala Gln Glu Gly Ser Lys Glu Glu Ser Gly Phe Leu Arg Glu Val Leu
    210                 215                 220

Asn Ala Val Pro Val Leu Pro His Ile Pro Ala Leu Ala Gly Lys Val
225                 230                 235                 240

Leu Arg Phe Gln Lys Ala Phe Leu Thr Gln Leu Asp Glu Leu Leu Thr
                245                 250                 255

Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg Asp Leu Thr
            260                 265                 270

Glu Ala Phe Leu Ala Lys Lys Glu Lys Ala Lys Gly Ser Pro Glu Ser
        275                 280                 285

Ser Phe Asn Asp Glu Asn Leu Arg Ile Val Val Gly Asn Leu Phe Leu
    290                 295                 300

Ala Gly Met Val Thr Thr Leu Thr Thr Leu Ala Trp Gly Leu Leu Leu
305                 310                 315                 320

Met Ile Leu His Leu Asp Val Gln Leu Arg Val Gln Gln Glu Ile Asp
                325                 330                 335

Asp Val Ile Gly Gln Val Arg Arg Pro Glu Met Gly Asp Gln Ala His
            340                 345                 350

Met Pro Tyr Thr Thr Ala Val Ile His Glu Val Gln Arg Phe Gly Asp
        355                 360                 365

Ile Val Pro Leu Gly Val Thr His Met Thr Ser Arg Asp Ile Glu Val
    370                 375                 380

Gln Gly Phe Arg Ile Pro Lys Gly Thr Thr Leu Ile Thr Asn Leu Ser
385                 390                 395                 400

Ser Val Leu Lys Asp Glu Ala Val Trp Glu Lys Pro Phe Arg Phe His
                405                 410                 415

Pro Glu His Phe Leu Asp Ala Gln Gly His Phe Val Lys Pro Glu Ala
            420                 425                 430
```

```
Phe Leu Pro Phe Ser Ala Gly Arg Arg Ala Cys Leu Gly Glu Pro Leu
        435                 440                 445

Ala Arg Met Glu Leu Phe Leu Phe Phe Thr Ser Leu Leu Gln His Phe
    450                 455                 460

Ser Phe Ser Val Ala Ala Gly Gln Pro Arg Pro Ser His Ser Arg Val
465                 470                 475                 480

Val Ser Phe Leu Val Thr Pro Ser Pro Tyr Glu Leu Cys Ala Val Pro
                485                 490                 495

Arg
```

<210> 1219
<211> 672
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 379; "

<220>
<221> source
<223> /note="Gene Symbol: AACS; "

<220>
<221> source
<223> /note="Gene Name:
acetoacetyl-CoA
synthetase; "

<220>
<221> source
<223> /note="Uniprot ID: Q86V21; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000324842"

<400> 1219

```
Met Ser Lys Glu Glu Arg Pro Gly Arg Glu Glu Ile Leu Glu Cys Gln
1               5                   10                  15

Val Met Trp Glu Pro Asp Ser Lys Lys Asn Thr Gln Met Asp Arg Phe
            20                  25                  30

Arg Ala Ala Val Gly Ala Ala Cys Gly Leu Ala Leu Glu Ser Tyr Asp
```

```
        35                  40                  45

Asp Leu Tyr His Trp Ser Val Glu Ser Tyr Ser Asp Phe Trp Ala Glu
    50                  55                  60

Phe Trp Lys Phe Ser Gly Ile Val Phe Ser Arg Val Tyr Asp Glu Val
65                  70                  75                  80

Val Asp Thr Ser Lys Gly Ile Ala Asp Val Pro Glu Trp Phe Lys Gly
                85                  90                  95

Ser Arg Leu Asn Tyr Ala Glu Asn Leu Leu Arg His Lys Glu Asn Asp
            100                 105                 110

Arg Val Ala Leu Tyr Ile Ala Arg Glu Gly Lys Glu Glu Ile Val Lys
        115                 120                 125

Val Thr Phe Glu Glu Leu Arg Gln Glu Val Ala Leu Phe Ala Ala Ala
    130                 135                 140

Met Arg Lys Met Gly Val Lys Lys Gly Asp Arg Val Val Gly Tyr Leu
145                 150                 155                 160

Pro Asn Ser Glu His Ala Val Glu Ala Met Leu Ala Ala Ala Ser Ile
                165                 170                 175

Gly Ala Ile Trp Ser Ser Thr Ser Pro Asp Phe Gly Val Asn Gly Val
            180                 185                 190

Leu Asp Arg Phe Ser Gln Ile Gln Pro Lys Leu Ile Phe Ser Val Glu
        195                 200                 205

Ala Val Val Tyr Asn Gly Lys Glu His Asn His Met Glu Lys Leu Gln
    210                 215                 220

Gln Val Val Lys Gly Leu Pro Asp Leu Lys Lys Val Val Val Ile Pro
225                 230                 235                 240

Tyr Val Ser Ser Arg Glu Asn Ile Asp Leu Ser Lys Ile Pro Asn Ser
                245                 250                 255

Val Phe Leu Asp Asp Phe Leu Ala Thr Gly Thr Ser Glu Gln Ala Pro
            260                 265                 270
```

```
Gln Leu Glu Phe Glu Gln Leu Pro Phe Ser His Pro Leu Phe Ile Met
        275                 280                 285

Phe Ser Ser Gly Thr Thr Gly Ala Pro Lys Cys Met Val His Ser Ala
    290                 295                 300

Gly Gly Thr Leu Ile Gln His Leu Lys Glu His Leu Leu His Gly Asn
305                 310                 315                 320

Met Thr Ser Ser Asp Ile Leu Leu Cys Tyr Thr Thr Val Gly Trp Met
                325                 330                 335

Met Trp Asn Trp Met Val Ser Leu Leu Ala Thr Gly Ala Ala Met Val
            340                 345                 350

Leu Tyr Asp Gly Ser Pro Leu Val Pro Thr Pro Asn Val Leu Trp Asp
        355                 360                 365

Leu Val Asp Arg Ile Gly Ile Thr Val Leu Val Thr Gly Ala Lys Trp
    370                 375                 380

Leu Ser Val Leu Glu Glu Lys Ala Met Lys Pro Val Glu Thr His Ser
385                 390                 395                 400

Leu Gln Met Leu His Thr Ile Leu Ser Thr Gly Ser Pro Leu Lys Ala
                405                 410                 415

Gln Ser Tyr Glu Tyr Val Tyr Arg Cys Ile Lys Ser Ser Ile Leu Leu
            420                 425                 430

Gly Ser Ile Ser Gly Gly Thr Asp Ile Ile Ser Cys Phe Met Gly His
        435                 440                 445

Asn Phe Ser Leu Pro Val Tyr Lys Gly Glu Ile Gln Ala Arg Asn Leu
    450                 455                 460

Gly Met Ala Val Glu Ala Trp Asn Glu Glu Gly Lys Ala Val Trp Gly
465                 470                 475                 480

Glu Ser Gly Glu Leu Val Cys Thr Lys Pro Ile Pro Cys Gln Pro Thr
                485                 490                 495
```

```
His Phe Trp Asn Asp Glu Asn Gly Asn Lys Tyr Arg Lys Ala Tyr Phe
            500                 505                 510

Ser Lys Phe Pro Gly Ile Trp Ala His Gly Asp Tyr Cys Arg Ile Asn
        515                 520                 525

Pro Lys Thr Gly Gly Ile Val Met Leu Gly Arg Ser Asp Gly Thr Leu
    530                 535                 540

Asn Pro Asn Gly Val Arg Phe Gly Ser Ser Glu Ile Tyr Asn Ile Val
545                 550                 555                 560

Glu Ser Phe Glu Glu Val Glu Asp Ser Leu Cys Val Pro Gln Tyr Asn
                565                 570                 575

Lys Tyr Arg Glu Glu Arg Val Ile Leu Phe Leu Lys Met Ala Ser Gly
            580                 585                 590

His Ala Phe Gln Pro Asp Leu Val Lys Arg Ile Arg Asp Ala Ile Arg
        595                 600                 605

Met Gly Leu Ser Ala Arg His Val Pro Ser Leu Ile Leu Glu Thr Lys
    610                 615                 620

Gly Ile Pro Tyr Thr Leu Asn Gly Lys Lys Val Glu Val Ala Val Lys
625                 630                 635                 640

Gln Ile Ile Ala Gly Lys Ala Val Glu Gln Gly Gly Ala Phe Ser Asn
                645                 650                 655

Pro Glu Thr Leu Asp Leu Tyr Arg Asp Ile Pro Glu Leu Gln Gly Phe
            660                 665                 670
```

<210> 1220
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 379; "

<220>
<221> source
<223> /note="Gene Symbol: AACS; "

<220>
<221> source
<223> /note="Gene Name:
acetoacetyl-CoA
synthetase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416461"

<400> 1220
Met Ser Lys Glu Glu Arg Pro Gly Arg Glu Glu Ile Leu Glu Cys Gln
1 5 10 15

Val Met Trp Glu Pro Asp Ser Lys Lys Asn Thr Gln Met Asp Arg Phe
20 25 30

Arg Ala Ala Val Gly Ala Ala Cys Gly Leu Ala Leu Glu Ser Tyr Asp
35 40 45

Asp Leu Tyr His Trp Ser Val Glu Ser Tyr Ser Asp Phe Trp Ala Glu
50 55 60

Phe Trp Lys Phe Ser Gly Ile Val Phe Ser Arg Val Tyr Asp Glu Val
65 70 75 80

Val Asp Thr Ser Lys Gly Ile Ala Asp Val Pro Glu Trp Phe Lys Gly
85 90 95

Ser Arg Leu Asn Tyr Ala Glu Asn Leu Leu Arg His Lys Glu Asn Asp
100 105 110

Arg Val Ala Leu Tyr Ile Ala Asn Gln His Lys Lys Pro Asn His Trp
115 120 125

Lys Gln Ala Val Ser Gly Pro Ala Gln Ala Thr Glu Gln Gly Leu Pro
130 135 140

Ser Ala Ile Val Gly Arg Thr Ser Ser Pro Cys Ala Val Gly Lys Asp
145 150 155 160

His Gly Ser Pro Val Pro Thr Glu Thr Tyr Trp Asp Thr Ser Ser Gly
165 170 175

Ala Gly Ala Gln Ala Ser Met Tyr Phe Gln Ser Pro Trp Ala Leu Leu

180 185 190

Met His Ile Pro Gly Glu Glu Pro Trp Ser Asn Val Ser Thr Tyr His
195 200 205

Met Gly Leu Gly Lys Ala Lys Arg Lys Leu
210 215

<210> 1221
<211> 614
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
acetylcholinesterase (Yt
blood group); "

<220>
<221> source
<223> /note="Uniprot ID: P22303; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000241069"

<400> 1221
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1 5 10 15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
20 25 30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
35 40 45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
50 55 60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65 70 75 80

```
Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300
```

```
Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Val Ser Asp Leu Ala Ala Glu Ala Val Val Leu His Tyr Thr Asp Trp
                405                 410                 415

Leu His Pro Glu Asp Pro Ala Arg Leu Arg Glu Ala Leu Ser Asp Val
            420                 425                 430

Val Gly Asp His Asn Val Val Cys Pro Val Ala Gln Leu Ala Gly Arg
        435                 440                 445

Leu Ala Ala Gln Gly Ala Arg Val Tyr Ala Tyr Val Phe Glu His Arg
    450                 455                 460

Ala Ser Thr Leu Ser Trp Pro Leu Trp Met Gly Val Pro His Gly Tyr
465                 470                 475                 480

Glu Ile Glu Phe Ile Phe Gly Ile Pro Leu Asp Pro Ser Arg Asn Tyr
                485                 490                 495

Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
            500                 505                 510

Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
        515                 520                 525
```

```
Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
    530                 535                 540

Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
545                 550                 555                 560

Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Asp Thr
                565                 570                 575

Leu Asp Glu Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser
            580                 585                 590

Ser Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln
        595                 600                 605

Asp Arg Cys Ser Asp Leu
    610


<210> 1222
<211> 617
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "

<220>
<221> source
<223> /note="Uniprot ID:  P22303; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000303211"

<400> 1222
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                   10                  15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
```

```
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255
```

```
Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Val Ser Asp Leu Ala Ala Glu Ala Val Val Leu His Tyr Thr Asp Trp
                405                 410                 415

Leu His Pro Glu Asp Pro Ala Arg Leu Arg Glu Ala Leu Ser Asp Val
            420                 425                 430

Val Gly Asp His Asn Val Val Cys Pro Val Ala Gln Leu Ala Gly Arg
        435                 440                 445

Leu Ala Ala Gln Gly Ala Arg Val Tyr Ala Tyr Val Phe Glu His Arg
    450                 455                 460

Ala Ser Thr Leu Ser Trp Pro Leu Trp Met Gly Val Pro His Gly Tyr
465                 470                 475                 480
```

```
Glu Ile Glu Phe Ile Phe Gly Ile Pro Leu Asp Pro Ser Arg Asn Tyr
                485                 490                 495

Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
            500                 505                 510

Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
        515                 520                 525

Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
    530                 535                 540

Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
545                 550                 555                 560

Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Ala Ser
                565                 570                 575

Glu Ala Pro Ser Thr Cys Pro Gly Phe Thr His Gly Glu Ala Ala Pro
            580                 585                 590

Arg Pro Gly Leu Pro Leu Pro Leu Leu Leu Leu His Gln Leu Leu Leu
        595                 600                 605

Leu Phe Leu Ser His Leu Arg Arg Leu
    610                 615


<210> 1223
<211> 403
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000390004"

<400> 1223
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1 5 10 15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
20 25 30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
35 40 45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
50 55 60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65 70 75 80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
85 90 95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
100 105 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
115 120 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
130 135 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145 150 155 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
165 170 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
180 185 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
195 200 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp

```
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Gly Ser Gln
```

<210> 1224
<211> 614
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
acetylcholinesterase (Yt
blood group); "

<220>
<221> source
<223> /note="Uniprot ID: P22303; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394976"

<400> 1224

```
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                  10                  15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140
```

```
Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365
```

```
Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Val Ser Asp Leu Ala Ala Glu Ala Val Val Leu His Tyr Thr Asp Trp
                405                 410                 415

Leu His Pro Glu Asp Pro Ala Arg Leu Arg Glu Ala Leu Ser Asp Val
            420                 425                 430

Val Gly Asp His Asn Val Val Cys Pro Val Ala Gln Leu Ala Gly Arg
        435                 440                 445

Leu Ala Ala Gln Gly Ala Arg Val Tyr Ala Tyr Val Phe Glu His Arg
    450                 455                 460

Ala Ser Thr Leu Ser Trp Pro Leu Trp Met Gly Val Pro His Gly Tyr
465                 470                 475                 480

Glu Ile Glu Phe Ile Phe Gly Ile Pro Leu Asp Pro Ser Arg Asn Tyr
                485                 490                 495

Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
            500                 505                 510

Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
        515                 520                 525

Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
    530                 535                 540

Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
545                 550                 555                 560

Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Asp Thr
                565                 570                 575

Leu Asp Glu Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser
            580                 585                 590

Ser Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln
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595 600 605

Asp Arg Cys Ser Asp Leu
610

<210> 1225
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
acetylcholinesterase (Yt
blood group); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396360"

<400> 1225
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1 5 10 15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
20 25 30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
35 40 45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
50 55 60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65 70 75 80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
85 90 95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
100 105 110

```
Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala
145                 150                 155


<210> 1226
<211> 397
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
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<223> /note="Gene Name:
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      blood group); "

<220>
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<223> /note="ENSP ID: ENSP00000397143"

<400> 1226
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                   10                  15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80
```

```
Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300
```

```
Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Thr Arg Ser Thr Arg Arg Ser Ala Ser Gly Arg Pro
        355                 360                 365

Ser Ser Thr Ala Gly Ala Pro Thr Trp Cys Thr Gly Arg Thr Ser Ser
    370                 375                 380

Thr Thr Thr Ala Ser Arg Ile Ala Ala Gln Thr Cys Asp
385                 390                 395


<210> 1227
<211> 434
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
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<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399725"

<400> 1227
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                   10                  15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
```

```
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270
```

```
Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Thr Arg Ser Thr Arg Arg Ser
385                 390                 395                 400

Ala Ser Gly Arg Pro Ser Ser Thr Ala Gly Ala Pro Thr Trp Cys Thr
                405                 410                 415

Gly Arg Thr Ser Ser Thr Thr Thr Ala Ser Arg Ile Ala Ala Gln Thr
            420                 425                 430

Cys Asp
```

<210> 1228
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source

<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
acetylcholinesterase (Yt
blood group); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000400933"

<400> 1228
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1 5 10 15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly
20 25

<210> 1229
<211> 526
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
acetylcholinesterase (Yt
blood group); "

<220>
<221> source
<223> /note="Uniprot ID: P22303; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403474"

<400> 1229
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1 5 10 15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
20 25 30

```
Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
```

260 265 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
275 280 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
290 295 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305 310 315 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
325 330 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
340 345 350

His Gly Leu Gln Leu Ala Gly Arg Leu Ala Ala Gln Gly Ala Arg Val
355 360 365

Tyr Ala Tyr Val Phe Glu His Arg Ala Ser Thr Leu Ser Trp Pro Leu
370 375 380

Trp Met Gly Val Pro His Gly Tyr Glu Ile Glu Phe Ile Phe Gly Ile
385 390 395 400

Pro Leu Asp Pro Ser Arg Asn Tyr Thr Ala Glu Glu Lys Ile Phe Ala
405 410 415

Gln Arg Leu Met Arg Tyr Trp Ala Asn Phe Ala Arg Thr Gly Asp Pro
420 425 430

Asn Glu Pro Arg Asp Pro Lys Ala Pro Gln Trp Pro Pro Tyr Thr Ala
435 440 445

Gly Ala Gln Gln Tyr Val Ser Leu Asp Leu Arg Pro Leu Glu Val Arg
450 455 460

Arg Gly Leu Arg Ala Gln Ala Cys Ala Phe Trp Asn Arg Phe Leu Pro
465 470 475 480

Lys Leu Leu Ser Ala Thr Asp Thr Leu Asp Glu Ala Glu Arg Gln Trp
485 490 495

```
Lys Ala Glu Phe His Arg Trp Ser Ser Tyr Met Val His Trp Lys Asn
            500                 505                 510

Gln Phe Asp His Tyr Ser Lys Gln Asp Arg Cys Ser Asp Leu
        515                 520                 525


<210> 1230
<211> 617
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "

<220>
<221> source
<223> /note="Uniprot ID:  P22303; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404865"

<400> 1230
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                   10                  15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80
```

```
Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300
```

```
Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Val Ser Asp Leu Ala Ala Glu Ala Val Val Leu His Tyr Thr Asp Trp
                405                 410                 415

Leu His Pro Glu Asp Pro Ala Arg Leu Arg Glu Ala Leu Ser Asp Val
            420                 425                 430

Val Gly Asp His Asn Val Val Cys Pro Val Ala Gln Leu Ala Gly Arg
        435                 440                 445

Leu Ala Ala Gln Gly Ala Arg Val Tyr Ala Tyr Val Phe Glu His Arg
    450                 455                 460

Ala Ser Thr Leu Ser Trp Pro Leu Trp Met Gly Val Pro His Gly Tyr
465                 470                 475                 480

Glu Ile Glu Phe Ile Phe Gly Ile Pro Leu Asp Pro Ser Arg Asn Tyr
                485                 490                 495

Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
            500                 505                 510

Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
        515                 520                 525

Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
```

```
    530                 535                 540

Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
545                 550                 555                 560

Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Ala Ser
                565                 570                 575

Glu Ala Pro Ser Thr Cys Pro Gly Phe Thr His Gly Glu Ala Ala Pro
            580                 585                 590

Arg Pro Gly Leu Pro Leu Pro Leu Leu Leu Leu His Gln Leu Leu Leu
        595                 600                 605

Leu Phe Leu Ser His Leu Arg Arg Leu
    610                 615


<210> 1231
<211> 359
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410380"

<400> 1231
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                   10                  15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45
```

```
Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270
```

```
Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Gly Ser Gln
        355


<210> 1232
<211> 614
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "

<220>
<221> source
<223> /note="Uniprot ID:  P22303; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414858"

<400> 1232
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1               5                   10                  15
```

```
Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20                  25                  30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
    50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
    130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
                165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
    210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
```

```
                245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
            260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
                325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
            340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Val Ser Asp Leu Ala Ala Glu Ala Val Val Leu His Tyr Thr Asp Trp
                405                 410                 415

Leu His Pro Glu Asp Pro Ala Arg Leu Arg Glu Ala Leu Ser Asp Val
            420                 425                 430

Val Gly Asp His Asn Val Val Cys Pro Val Ala Gln Leu Ala Gly Arg
        435                 440                 445

Leu Ala Ala Gln Gly Ala Arg Val Tyr Ala Tyr Val Phe Glu His Arg
    450                 455                 460

Ala Ser Thr Leu Ser Trp Pro Leu Trp Met Gly Val Pro His Gly Tyr
465                 470                 475                 480
```

```
Glu Ile Glu Phe Ile Phe Gly Ile Pro Leu Asp Pro Ser Arg Asn Tyr
                485                 490                 495

Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
            500                 505                 510

Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
        515                 520                 525

Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
    530                 535                 540

Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
545                 550                 555                 560

Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Asp Thr
                565                 570                 575

Leu Asp Glu Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser
            580                 585                 590

Ser Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln
        595                 600                 605

Asp Arg Cys Ser Asp Leu
    610


<210> 1233
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 380; "

<220>
<221> source
<223> /note="Gene Symbol: ACHE; "

<220>
<221> source
<223> /note="Gene Name:
      acetylcholinesterase (Yt
      blood group); "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000415901"

<400> 1233
Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
1   5   10   15

Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
            20   25   30

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Leu Arg Ala Pro Arg
        35   40   45

Cys Gly Thr Pro Thr Val Ser
    50   55

<210> 1234
<211> 427
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 381; "

<220>
<221> source
<223> /note="Gene Symbol: ACAT1; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA acetyltransferase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P24752; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000265838"

<400> 1234
Met Ala Val Leu Ala Ala Leu Leu Arg Ser Gly Ala Arg Ser Arg Ser
1   5   10   15

Pro Leu Leu Arg Arg Leu Val Gln Glu Ile Arg Tyr Val Glu Arg Ser
            20   25   30

Tyr Val Ser Lys Pro Thr Leu Lys Glu Val Val Ile Val Ser Ala Thr

```
        35                  40                  45

Arg Thr Pro Ile Gly Ser Phe Leu Gly Ser Leu Ser Leu Leu Pro Ala
    50                  55                  60

Thr Lys Leu Gly Ser Ile Ala Ile Gln Gly Ala Ile Glu Lys Ala Gly
65                  70                  75                  80

Ile Pro Lys Glu Glu Val Lys Glu Ala Tyr Met Gly Asn Val Leu Gln
                85                  90                  95

Gly Gly Glu Gly Gln Ala Pro Thr Arg Gln Ala Val Leu Gly Ala Gly
            100                 105                 110

Leu Pro Ile Ser Thr Pro Cys Thr Thr Ile Asn Lys Val Cys Ala Ser
        115                 120                 125

Gly Met Lys Ala Ile Met Met Ala Ser Gln Ser Leu Met Cys Gly His
    130                 135                 140

Gln Asp Val Met Val Ala Gly Gly Met Glu Ser Met Ser Asn Val Pro
145                 150                 155                 160

Tyr Val Met Asn Arg Gly Ser Thr Pro Tyr Gly Gly Val Lys Leu Glu
                165                 170                 175

Asp Leu Ile Val Lys Asp Gly Leu Thr Asp Val Tyr Asn Lys Ile His
            180                 185                 190

Met Gly Ser Cys Ala Glu Asn Thr Ala Lys Lys Leu Asn Ile Ala Arg
        195                 200                 205

Asn Glu Gln Asp Ala Tyr Ala Ile Asn Ser Tyr Thr Arg Ser Lys Ala
    210                 215                 220

Ala Trp Glu Ala Gly Lys Phe Gly Asn Glu Val Ile Pro Val Thr Val
225                 230                 235                 240

Thr Val Lys Gly Gln Pro Asp Val Val Val Lys Glu Asp Glu Glu Tyr
                245                 250                 255

Lys Arg Val Asp Phe Ser Lys Val Pro Lys Leu Lys Thr Val Phe Gln
            260                 265                 270
```

```
Lys Glu Asn Gly Thr Val Thr Ala Ala Asn Ala Ser Thr Leu Asn Asp
        275                 280                 285

Gly Ala Ala Ala Leu Val Leu Met Thr Ala Asp Ala Ala Lys Arg Leu
    290                 295                 300

Asn Val Thr Pro Leu Ala Arg Ile Val Ala Phe Ala Asp Ala Ala Val
305                 310                 315                 320

Glu Pro Ile Asp Phe Pro Ile Ala Pro Val Tyr Ala Ala Ser Met Val
                325                 330                 335

Leu Lys Asp Val Gly Leu Lys Lys Glu Asp Ile Ala Met Trp Glu Val
            340                 345                 350

Asn Glu Ala Phe Ser Leu Val Val Leu Ala Asn Ile Lys Met Leu Glu
        355                 360                 365

Ile Asp Pro Gln Lys Val Asn Ile Asn Gly Gly Ala Val Ser Leu Gly
    370                 375                 380

His Pro Ile Gly Met Ser Gly Ala Arg Ile Val Gly His Leu Thr His
385                 390                 395                 400

Ala Leu Lys Gln Gly Glu Tyr Gly Leu Ala Ser Ile Cys Asn Gly Gly
                405                 410                 415

Gly Gly Ala Ser Ala Met Leu Ile Gln Lys Leu
            420                 425


<210> 1235
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 381; "

<220>
<221> source
<223> /note="Gene Symbol: ACAT1; "

<220>
<221> source
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<223> /note="Gene Name:
acetyl-CoA acetyltransferase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P24752; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000299355"

<400> 1235

```
Met Ala Val Leu Ala Ala Leu Leu Arg Ser Gly Ala Arg Ser Arg Ser
1               5                  10                  15

Pro Leu Leu Arg Arg Leu Val Gln Glu Ile Arg Tyr Val Glu Arg Ser
            20                  25                  30

Tyr Val Ser Lys Pro Thr Leu Lys Glu Val Val Ile Val Ser Ala Thr
        35                  40                  45

Arg Thr Pro Ile Gly Ser Phe Leu Gly Ser Leu Ser Leu Leu Pro Ala
    50                  55                  60

Thr Lys Leu Gly Ser Ile Ala Ile Gln Gly Ala Ile Glu Lys Ala Gly
65                  70                  75                  80

Ile Pro Lys Glu Glu Val Lys Glu Ala Tyr Met Gly Asn Val Leu Gln
                85                  90                  95

Gly Gly Glu Gly Gln Ala Pro Thr Arg Gln Ala Val Leu Gly Ala Gly
            100                 105                 110

Leu Pro Ile Ser Thr Pro Cys Thr Thr Ile Asn Lys Val Cys Ala Ser
        115                 120                 125

Gly Met Lys Ala Ile Met Met Ala Ser Gln Ser Leu Met Cys Gly His
    130                 135                 140

Gln Ile Lys Gln Glu Thr Gly Ser Leu Ala Lys Ile Cys Cys His Val
145                 150                 155                 160

Arg Arg
```

<210> 1236

<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 381; "

<220>
<221> source
<223> /note="Gene Symbol: ACAT1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acetyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433568"

<400> 1236
Met Gly Asn Val Leu Gln Gly Gly Glu Gly Gln Ala Pro Thr Arg Gln
1 5 10 15

Ala Val Leu Gly Ala Gly Leu Pro Ile Ser Thr Pro Cys Thr Thr Ile
20 25 30

Asn Lys Val Cys Ala Ser Gly Met Lys Ala Ile Met Met Ala Ser Gln
35 40 45

Ser Leu Met Cys Gly His
50

<210> 1237
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 381; "

<220>
<221> source
<223> /note="Gene Symbol: ACAT1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acetyltransferase 1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000435965"

<400> 1237
Met Ala Val Leu Ala Ala Leu Leu Arg Ser Gly Ala Arg Ser Arg Ser
1   5   10   15

Pro Leu Leu Arg Arg Leu Val Gln Glu Ile Arg Tyr Val Glu Arg Ser
            20   25   30

Tyr Val Ser Lys Pro Thr Leu Lys Glu Val Val Ile Val Ser Ala Thr
        35   40   45

Arg Thr Pro Ile Gly Ser Phe Leu Gly Ser Leu Ser Leu Leu Pro Ala
    50   55   60

Thr Lys Leu Gly Ser Ile Ala Ile Gln Gly Ala Ile Glu Lys Ala Gly
65   70   75   80

Ile Pro Lys Glu Glu Val Lys Glu Ala Tyr Met Gly Asn Val Leu Gln
                85   90   95

Gly Gly Glu Gly Gln Ala Pro Thr Arg Gln Ala Val Leu Gly Ala Gly
            100   105   110

Cys Asp Gly Gly Arg Trp Asp Gly Glu His Val Gln Cys Ser Ile Cys
        115   120   125

Asn Glu Gln Arg Ile Asn Thr Ile Trp Trp Gly Lys Ala
    130   135   140

<210> 1238
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 381; "

<220>
<221> source
<223> /note="Gene Symbol: ACAT1; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA acetyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436096"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1238
Xaa Lys Leu Gly Ser Ile Ala Ile Gln Gly Ala Ile Glu Lys Ala Gly
1 5 10 15

Ile Pro Lys Glu Glu Val Lys Glu Ala Tyr Met Gly Asn Val Leu Gln
20 25 30

Gly Gly Glu Gly Gln Ala Pro Thr Arg Gln Ala Val Leu Gly Ala Gly
35 40 45

Leu Pro Ile Ser Thr Pro Cys Thr Thr Ile Asn Lys Val Cys Ala Ser
50 55 60

Gly Met Lys Ala Ile Met Met Ala Ser Gln Ser Leu Met Cys Gly His
65 70 75 80

Gln Asp Val Met Val Ala Gly Gly Met Glu Ser Met Ser Asn Val Pro
85 90 95

Tyr Val Met Asn Arg Gly Ser Thr Pro Tyr Gly Gly Val Lys Leu Glu
100 105 110

Asp Leu Ile Val Lys Asp Gly Leu Thr Asp Val Tyr Asn Lys Ile His
115 120 125

Met Val Asn Val Ile Phe Ser Gly
130 135

<210> 1239
<211> 397
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 382; "

<220>
<221> source
<223> /note="Gene Symbol: ACAT2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acetyltransferase 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BWD1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356015"

<400> 1239

```
Met Asn Ala Gly Ser Asp Pro Val Val Ile Val Ser Ala Ala Arg Thr
1               5                  10                  15

Ile Ile Gly Ser Phe Asn Gly Ala Leu Ala Ala Val Pro Val Gln Asp
            20                  25                  30

Leu Gly Ser Thr Val Ile Lys Glu Val Leu Lys Arg Ala Thr Val Ala
        35                  40                  45

Pro Glu Asp Val Ser Glu Val Ile Phe Gly His Val Leu Ala Ala Gly
    50                  55                  60

Cys Gly Gln Asn Pro Val Arg Gln Ala Ser Val Gly Ala Gly Ile Pro
65                  70                  75                  80

Tyr Ser Val Pro Ala Trp Ser Cys Gln Met Ile Cys Gly Ser Gly Leu
                85                  90                  95

Lys Ala Val Cys Leu Ala Val Gln Ser Ile Gly Ile Gly Asp Ser Ser
            100                 105                 110

Ile Val Val Ala Gly Gly Met Glu Asn Met Ser Lys Ala Pro His Leu
        115                 120                 125

Ala Tyr Leu Arg Thr Gly Val Lys Ile Gly Glu Met Pro Leu Thr Asp
    130                 135                 140

Ser Ile Leu Cys Asp Gly Leu Thr Asp Ala Phe His Asn Cys His Met
145                 150                 155                 160
```

```
Gly Ile Thr Ala Glu Asn Val Ala Lys Lys Trp Gln Val Ser Arg Glu
                165                 170                 175

Asp Gln Asp Lys Val Ala Val Leu Ser Gln Asn Arg Thr Glu Asn Ala
            180                 185                 190

Gln Lys Ala Gly His Phe Asp Lys Glu Ile Val Pro Val Leu Val Ser
        195                 200                 205

Thr Arg Lys Gly Leu Ile Glu Val Lys Thr Asp Glu Phe Pro Arg His
    210                 215                 220

Gly Ser Asn Ile Glu Ala Met Ser Lys Leu Lys Pro Tyr Phe Leu Thr
225                 230                 235                 240

Asp Gly Thr Gly Thr Val Thr Pro Ala Asn Ala Ser Gly Ile Asn Asp
                245                 250                 255

Gly Ala Ala Ala Val Val Leu Met Lys Lys Ser Glu Ala Asp Lys Arg
            260                 265                 270

Gly Leu Thr Pro Leu Ala Arg Ile Val Ser Trp Ser Gln Val Gly Val
        275                 280                 285

Glu Pro Ser Ile Met Gly Ile Gly Pro Ile Pro Ala Ile Lys Gln Ala
    290                 295                 300

Val Thr Lys Ala Gly Trp Ser Leu Glu Asp Val Asp Ile Phe Glu Ile
305                 310                 315                 320

Asn Glu Ala Phe Ala Ala Val Ser Ala Ala Ile Val Lys Glu Leu Gly
                325                 330                 335

Leu Asn Pro Glu Lys Val Asn Ile Glu Gly Gly Ala Ile Ala Leu Gly
            340                 345                 350

His Pro Leu Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His
        355                 360                 365

Thr Leu Glu Arg Met Gly Arg Ser Arg Gly Val Ala Ala Leu Cys Ile
    370                 375                 380
```

Gly Gly Gly Met Gly Ile Ala Met Cys Val Gln Arg Glu
385 390 395

<210> 1240
<211> 331
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P09110; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000301810"

<400> 1240
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
85 90 95

Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu
100 105 110

```
Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln
        115                 120                 125

Ala Val Ala Ser Ile Ala Gly Gly Ile Arg Asn Gly Ser Tyr Asp Ile
    130                 135                 140

Gly Met Ala Cys Gly Ile Thr Ser Glu Asn Val Ala Glu Arg Phe Gly
145                 150                 155                 160

Ile Ser Arg Glu Lys Gln Asp Thr Phe Ala Leu Ala Ser Gln Gln Lys
                165                 170                 175

Ala Ala Arg Ala Gln Ser Lys Gly Cys Phe Gln Ala Glu Ile Val Pro
            180                 185                 190

Val Thr Thr Thr Val His Asp Asp Lys Gly Thr Lys Arg Ser Ile Thr
        195                 200                 205

Val Thr Gln Asp Glu Gly Ile Arg Pro Ser Thr Thr Met Glu Gly Leu
    210                 215                 220

Ala Lys Leu Lys Pro Ala Phe Lys Lys Asp Gly Ser Thr Thr Ala Gly
225                 230                 235                 240

Leu Thr Val Ser Asp Val Asp Ile Phe Glu Ile Asn Glu Ala Phe Ala
                245                 250                 255

Ser Gln Ala Ala Tyr Cys Val Glu Lys Leu Arg Leu Pro Pro Glu Lys
            260                 265                 270

Val Asn Pro Leu Gly Gly Ala Val Ala Leu Gly His Pro Leu Gly Cys
        275                 280                 285

Thr Gly Ala Arg Gln Val Ile Thr Leu Leu Asn Glu Leu Lys Arg Arg
    290                 295                 300

Gly Lys Arg Ala Tyr Gly Val Val Ser Met Cys Ile Gly Thr Gly Met
305                 310                 315                 320

Gly Ala Ala Ala Val Phe Glu Tyr Pro Gly Asn
                325                 330
```

<210> 1241
<211> 424
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="Uniprot ID: P09110; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000333664"

<400> 1241
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1   5   10   15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
            20   25   30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
        35   40   45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
    50   55   60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65   70   75   80

Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
                85   90   95

Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu
            100   105   110

Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln

```
        115                 120                 125

Ala Val Ala Ser Ile Ala Gly Gly Ile Arg Asn Gly Ser Tyr Asp Ile
    130                 135                 140

Gly Met Ala Cys Gly Val Glu Ser Met Ser Leu Ala Asp Arg Gly Asn
145                 150                 155                 160

Pro Gly Asn Ile Thr Ser Arg Leu Met Glu Lys Glu Lys Ala Arg Asp
                165                 170                 175

Cys Leu Ile Pro Met Gly Ile Thr Ser Glu Asn Val Ala Glu Arg Phe
            180                 185                 190

Gly Ile Ser Arg Glu Lys Gln Asp Thr Phe Ala Leu Ala Ser Gln Gln
        195                 200                 205

Lys Ala Ala Arg Ala Gln Ser Lys Gly Cys Phe Gln Ala Glu Ile Val
    210                 215                 220

Pro Val Thr Thr Thr Val His Asp Asp Lys Gly Thr Lys Arg Ser Ile
225                 230                 235                 240

Thr Val Thr Gln Asp Glu Gly Ile Arg Pro Ser Thr Thr Met Glu Gly
                245                 250                 255

Leu Ala Lys Leu Lys Pro Ala Phe Lys Lys Asp Gly Ser Thr Thr Ala
            260                 265                 270

Gly Asn Ser Ser Gln Val Ser Asp Gly Ala Ala Ala Ile Leu Leu Ala
        275                 280                 285

Arg Arg Ser Lys Ala Glu Glu Leu Gly Leu Pro Ile Leu Gly Val Leu
    290                 295                 300

Arg Ser Tyr Ala Val Val Gly Val Pro Pro Asp Ile Met Gly Ile Gly
305                 310                 315                 320

Pro Ala Tyr Ala Ile Pro Val Ala Leu Gln Lys Ala Gly Leu Thr Val
                325                 330                 335

Ser Asp Val Asp Ile Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Ala
            340                 345                 350
```

```
Ala Tyr Cys Val Glu Lys Leu Arg Leu Pro Pro Glu Lys Val Asn Pro
        355                 360                 365

Leu Gly Gly Ala Val Ala Leu Gly His Pro Leu Gly Cys Thr Gly Ala
    370                 375                 380

Arg Gln Val Ile Thr Leu Leu Asn Glu Leu Lys Arg Arg Gly Lys Arg
385                 390                 395                 400

Ala Tyr Gly Val Val Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala
                405                 410                 415

Ala Val Phe Glu Tyr Pro Gly Asn
            420
```

<210> 1242
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389226"

<400> 1242

```
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1               5                   10                  15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
            20                  25                  30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
        35                  40                  45
```

```
Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
    50                  55                  60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65                  70                  75                  80

Glu Gln Leu Gly Asp Ile Cys Val Asp Gln His Gly Val Ser Tyr Val
                85                  90                  95

Phe Leu Phe Tyr Ile His Thr Glu Met Cys Cys Ser Leu Gly Pro Gly
            100                 105                 110

Gln Ser Trp Pro Glu Ser Pro Ser Phe
        115                 120


<210> 1243
<211> 237
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391078"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1243
Xaa Ala Val Ala Ser Ile Ala Gly Gly Ile Arg Asn Gly Ser Tyr Asp
1               5                   10                  15

Ile Gly Met Ala Cys Gly Val Glu Ser Met Ser Leu Ala Asp Arg Gly
            20                  25                  30
```

```
Asn Pro Gly Asn Ile Thr Ser Arg Leu Met Glu Lys Glu Lys Ala Arg
        35                  40                  45

Asp Cys Leu Ile Pro Met Gly Ile Thr Ser Glu Asn Val Ala Glu Arg
    50                  55                  60

Phe Gly Ile Ser Arg Glu Lys Gln Asp Thr Phe Ala Leu Ala Ser Gln
65                  70                  75                  80

Gln Lys Ala Ala Arg Ala Gln Ser Lys Gly Cys Phe Gln Ala Glu Ile
                85                  90                  95

Val Pro Val Thr Thr Thr Val His Asp Asp Lys Gly Thr Lys Arg Ser
            100                 105                 110

Ile Thr Val Thr Gln Asp Glu Gly Ile Arg Pro Ser Thr Thr Met Glu
        115                 120                 125

Gly Leu Ala Lys Leu Lys Pro Ala Phe Lys Lys Asp Gly Ser Thr Thr
    130                 135                 140

Ala Gly Leu Thr Val Ser Asp Val Asp Ile Phe Glu Ile Asn Glu Ala
145                 150                 155                 160

Phe Ala Ser Gln Ala Ala Tyr Cys Val Glu Lys Leu Arg Leu Pro Pro
                165                 170                 175

Glu Lys Val Asn Pro Leu Gly Gly Ala Val Ala Leu Gly His Pro Leu
            180                 185                 190

Gly Cys Thr Gly Ala Arg Gln Val Ile Thr Leu Leu Asn Glu Leu Lys
        195                 200                 205

Arg Arg Gly Lys Arg Ala Tyr Gly Val Val Ser Met Cys Ile Gly Thr
    210                 215                 220

Gly Met Gly Ala Ala Ala Val Phe Glu Tyr Pro Gly Asn
225                 230                 235
```

<210> 1244
<211> 383
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000395183"

<400> 1244
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
85 90 95

Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Arg Val Glu Ser Met
100 105 110

Ser Leu Ala Asp Arg Gly Asn Pro Gly Asn Ile Thr Ser Arg Leu Met
115 120 125

Glu Lys Glu Lys Ala Arg Asp Cys Leu Ile Pro Met Gly Ile Thr Ser
130 135 140

Glu Asn Val Ala Glu Arg Phe Gly Ile Ser Arg Glu Lys Gln Asp Thr
145 150 155 160

```
Phe Ala Leu Ala Ser Gln Gln Lys Ala Ala Arg Ala Gln Ser Lys Gly
                165                 170                 175

Cys Phe Gln Ala Glu Ile Val Pro Val Thr Thr Thr Val His Asp Asp
            180                 185                 190

Lys Gly Thr Lys Arg Ser Ile Thr Val Thr Gln Asp Glu Gly Ile Arg
        195                 200                 205

Pro Ser Thr Thr Met Glu Gly Leu Ala Lys Leu Lys Pro Ala Phe Lys
    210                 215                 220

Lys Asp Gly Ser Thr Thr Ala Gly Asn Ser Ser Gln Val Ser Asp Gly
225                 230                 235                 240

Ala Ala Ala Ile Leu Leu Ala Arg Arg Ser Lys Ala Glu Glu Leu Gly
                245                 250                 255

Leu Pro Ile Leu Gly Val Leu Arg Ser Tyr Ala Val Val Gly Val Pro
            260                 265                 270

Pro Asp Ile Met Gly Ile Gly Pro Ala Tyr Ala Ile Pro Val Ala Leu
        275                 280                 285

Gln Lys Ala Gly Leu Thr Val Ser Asp Val Asp Ile Phe Glu Ile Asn
    290                 295                 300

Glu Ala Phe Ala Ser Gln Ala Ala Tyr Cys Val Glu Lys Leu Arg Leu
305                 310                 315                 320

Pro Pro Glu Lys Val Asn Pro Leu Gly Gly Ala Val Ala Leu Gly His
                325                 330                 335

Pro Leu Gly Cys Thr Gly Ala Arg Gln Val Ile Thr Leu Leu Asn Glu
            340                 345                 350

Leu Lys Arg Arg Gly Lys Arg Ala Tyr Gly Val Val Ser Met Cys Ile
        355                 360                 365

Gly Thr Gly Met Gly Ala Ala Ala Val Phe Glu Tyr Pro Gly Asn
    370                 375                 380
```

<210> 1245
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396485"

<400> 1245
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Val Thr Ser Arg Arg Leu Cys Leu
85 90 95

Cys Pro Leu Ser Ile Asp Ser Val Arg Arg Gly Tyr Arg Gln Trp Pro
100 105 110

Ala

<210> 1246
<211> 290

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398172"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1246
Xaa Arg Pro Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln
1 5 10 15

Pro Gly Ala Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp
20 25 30

Ile Pro Glu Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser
35 40 45

Gly Leu Gln Ala Val Ala Ser Ile Ala Gly Gly Ile Arg Asn Gly Ser
50 55 60

Tyr Asp Ile Gly Met Ala Cys Gly Ile Thr Ser Glu Asn Val Ala Glu
65 70 75 80

Arg Phe Gly Ile Ser Arg Glu Lys Gln Asp Thr Phe Ala Leu Ala Ser
85 90 95

Gln Gln Lys Ala Ala Arg Ala Gln Ser Lys Gly Cys Phe Gln Ala Glu
100 105 110

Ile Val Pro Val Thr Thr Thr Val His Asp Asp Lys Gly Thr Lys Arg
115 120 125

```
Ser Ile Thr Val Thr Gln Asp Glu Gly Ile Arg Pro Ser Thr Thr Met
    130                 135                 140

Glu Gly Leu Ala Lys Leu Lys Pro Ala Phe Lys Lys Asp Gly Ser Thr
145                 150                 155                 160

Thr Ala Gly Asn Ser Ser Gln Val Ser Asp Gly Ala Ala Ala Ile Leu
                165                 170                 175

Leu Ala Arg Arg Ser Lys Ala Glu Glu Leu Gly Leu Pro Ile Leu Gly
            180                 185                 190

Val Leu Arg Ser Tyr Ala Val Val Gly Val Pro Pro Asp Ile Met Gly
        195                 200                 205

Ile Gly Pro Ala Tyr Ala Ile Pro Val Ala Leu Gln Lys Ala Gly Leu
    210                 215                 220

Thr Val Ser Asp Val Asp Ile Phe Glu Ile Asn Glu Ala Phe Ala Ser
225                 230                 235                 240

Gln Ala Ala Tyr Cys Val Glu Lys Leu Arg Leu Pro Pro Glu Lys Val
                245                 250                 255

Asn Pro Leu Gly Gly Ala Val Ala Leu Gly His Pro Leu Gly Cys Thr
            260                 265                 270

Gly Ala Arg Gln Val Ile Thr Leu Leu Asn Glu Leu Lys Arg Arg Gly
        275                 280                 285

Lys Arg
    290
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<210> 1247
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 383; "

<220>
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<223> /note="Gene Symbol: ACAA1; "

<220>
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<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403124"

<400> 1247
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Val Thr Ser Arg Arg Leu Cys Leu
85 90 95

Cys Pro Leu Ser Ile Asp Ser Val Arg Arg Gly Tyr Arg Gln Trp Pro
100 105 110

Ala

<210> 1248
<211> 121
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACAA1; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
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<400> 1248
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Asp Gln His Gly Val Ser Tyr Val
85 90 95

Phe Leu Phe Tyr Ile His Thr Glu Met Cys Cys Ser Leu Gly Pro Gly
100 105 110

Gln Ser Trp Pro Glu Ser Pro Ser Phe
115 120

<210> 1249
<211> 153
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414021"

<400> 1249
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
85 90 95

Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu
100 105 110

Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln
115 120 125

Ala Val Ala Ser Ile Ala Gly Trp Ser Pro Cys Pro Trp Leu Thr Glu
130 135 140

Gly Thr Leu Glu Ile Leu Leu Arg Ala
145 150

<210> 1250
<211> 113
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486456"

<400> 1250
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Val Thr Ser Arg Arg Leu Cys Leu
85 90 95

Cys Pro Leu Ser Ile Asp Ser Val Arg Arg Gly Tyr Arg Gln Trp Pro
100 105 110

Ala

<210> 1251
<211> 121
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACAA1; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486920"

<400> 1251
Met Gln Arg Leu Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp
1 5 10 15

Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
20 25 30

Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
35 40 45

Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
50 55 60

Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
65 70 75 80

Glu Gln Leu Gly Asp Ile Cys Val Asp Gln His Gly Val Ser Tyr Val
85 90 95

Phe Leu Phe Tyr Ile His Thr Glu Met Cys Cys Ser Leu Gly Pro Gly
100 105 110

Gln Ser Trp Pro Glu Ser Pro Ser Phe
115 120

<210> 1252
<211> 397
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 384; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 2; "

<220>
<221> source
<223> /note="Uniprot ID: P42765; "

<220>
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<223> /note="ENSP ID: ENSP00000285093"

<400> 1252
Met Ala Leu Leu Arg Gly Val Phe Val Val Ala Ala Lys Arg Thr Pro
1 5 10 15

Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu
20 25 30

Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro
35 40 45

Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser
50 55 60

Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro
65 70 75 80

Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe
85 90 95

Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu
100 105 110

Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys
115 120 125

Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu
130 135 140

Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro
145 150 155 160

Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg
165 170 175

```
Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala
            180                 185                 190

Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val
        195                 200                 205

Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg
    210                 215                 220

Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys
225                 230                 235                 240

Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly
                245                 250                 255

Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn
            260                 265                 270

Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val Ser Gly Cys Asp
        275                 280                 285

Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile Ser Gly Ala Leu
    290                 295                 300

Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu Val Glu Val Asn
305                 310                 315                 320

Glu Ala Phe Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu
                325                 330                 335

Asp Ile Ser Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His
            340                 345                 350

Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu
        355                 360                 365

Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly
    370                 375                 380

Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
385                 390                 395
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<210> 1253
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 384; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465045"

<400> 1253
Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg
1 5 10 15

His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr
20 25 30

Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys
35 40 45

Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr
50 55 60

Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly
65 70 75 80

Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser
85 90 95

Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn
100 105 110

Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys
115 120

<210> 1254
<211> 84

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 384; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465095"

<400> 1254
Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg
1 5 10 15

His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr
20 25 30

Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys
35 40 45

Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr
50 55 60

Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly
65 70 75 80

Thr Lys Leu Gly

<210> 1255
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 384; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466015"

<400> 1255
Met Met Gly Val Phe Val Val Ala Ala Lys Arg Thr Pro Phe Gly Ala
1 5 10 15

Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu Ser Glu Phe
20 25 30

Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val
35 40 45

Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile
50 55 60

Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr
65 70 75 80

Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile
85 90 95

Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu
100 105 110

Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn
115 120 125

Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser
130 135 140

Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met
145 150 155 160

Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys
165 170 175

Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp
180 185 190

Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys
195 200 205

Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr
210 215 220

Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly
225 230 235 240

Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala
245 250 255

Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro
260 265 270

Leu Ala Arg Ile Val Gly Tyr Phe Val Ser Gly Cys Asp Pro Ser Ile
275 280 285

Met Gly Ile Gly Pro Val Pro Ala Ile Ser Gly Ala Leu Lys Lys Ala
290 295 300

Gly Leu Ser Leu Lys Asp Met Asp Leu Val Glu Val Asn Glu Ala Phe
305 310 315 320

Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser
325 330 335

Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly
340 345 350

Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg
355 360 365

Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln
370 375 380

Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
385 390

<210> 1256
<211> 342
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 384; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466466"

<400> 1256
Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg
1 5 10 15

His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr
20 25 30

Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys
35 40 45

Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr
50 55 60

Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly
65 70 75 80

Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser
85 90 95

Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn
100 105 110

Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala
115 120 125

Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe
130 135 140

Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln

145 150 155 160

Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln
165 170 175

Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala
180 185 190

Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala
195 200 205

Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile
210 215 220

Val Gly Tyr Phe Val Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly
225 230 235 240

Pro Val Pro Ala Ile Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu
245 250 255

Lys Asp Met Asp Leu Val Glu Val Asn Glu Ala Phe Ala Pro Gln Tyr
260 265 270

Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser Lys Thr Asn Val
275 280 285

Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser
290 295 300

Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys
305 310 315 320

Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val
325 330 335

Ile Ile Gln Ser Thr Ala
340

<210> 1257
<211> 72
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 384; "

<220>
<221> source
<223> /note="Gene Symbol: ACAA2; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA acyltransferase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468157"

<400> 1257
Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg
1 5 10 15

His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr
20 25 30

Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys
35 40 45

Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr
50 55 60

Glu Ser Met Ser Gln Ala Pro Tyr
65 70

<210> 1258
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000477912"

<400> 1258
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1   5   10   15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
            20   25   30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
        35   40   45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
    50   55   60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65   70   75   80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
                85   90   95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
            100   105   110

Gly Gly Asn Lys Val Ile Glu Lys
        115   120

<210> 1259
<211> 2346
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="Uniprot ID: Q13085; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478547"

<400> 1259
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
100 105 110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile
115 120 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met
130 135 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu
145 150 155 160

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val
165 170 175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
180 185 190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
195 200 205

```
Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys
    210                 215                 220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu
225                 230                 235                 240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro
                245                 250                 255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn
            260                 265                 270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys
        275                 280                 285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Gln Ala Ala Glu Glu Val
    290                 295                 300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
305                 310                 315                 320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln
                325                 330                 335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala
            340                 345                 350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly
        355                 360                 365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
    370                 375                 380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val
385                 390                 395                 400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly
                405                 410                 415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser
            420                 425                 430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
```

```
        435                 440                 445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
    450                 455                 460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr
465                 470                 475                 480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala
                485                 490                 495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser
            500                 505                 510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu
        515                 520                 525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala
    530                 535                 540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
545                 550                 555                 560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val
                565                 570                 575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
            580                 585                 590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile
        595                 600                 605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu
    610                 615                 620

Arg Pro Asp Thr Met Leu Gly Val Val Cys Gly Ala Leu His Val Ala
625                 630                 635                 640

Asp Val Ser Leu Arg Asn Ser Val Ser Asn Phe Leu His Ser Leu Glu
                645                 650                 655

Arg Gly Gln Val Leu Pro Ala His Thr Leu Leu Asn Thr Val Asp Val
            660                 665                 670
```

```
Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val Leu Lys Val Thr Arg Gln
        675                 680                 685

Ser Pro Asn Ser Tyr Val Val Ile Met Asn Gly Ser Cys Val Glu Val
    690                 695                 700

Asp Val His Arg Leu Ser Asp Gly Gly Leu Leu Leu Ser Tyr Asp Gly
705                 710                 715                 720

Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Arg Tyr Arg Ile
                725                 730                 735

Thr Ile Gly Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp Pro Ser
            740                 745                 750

Val Met Arg Ser Pro Ser Ala Gly Lys Leu Ile Gln Tyr Ile Val Glu
        755                 760                 765

Asp Gly Gly His Val Phe Ala Gly Gln Cys Tyr Ala Glu Ile Glu Val
    770                 775                 780

Met Lys Met Val Met Thr Leu Thr Ala Val Glu Ser Gly Cys Ile His
785                 790                 795                 800

Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp Pro Gly Cys Val Leu Ala
                805                 810                 815

Lys Met Gln Leu Asp Asn Pro Ser Lys Val Gln Gln Ala Glu Leu His
            820                 825                 830

Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr Ala Leu Arg Gly Glu Lys
        835                 840                 845

Leu His Arg Val Phe His Tyr Val Leu Asp Asn Leu Val Asn Val Met
    850                 855                 860

Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe Ser Ser Lys Val Lys Asp
865                 870                 875                 880

Trp Val Glu Arg Leu Met Lys Thr Leu Arg Asp Pro Ser Leu Pro Leu
                885                 890                 895
```

```
Leu Glu Leu Gln Asp Ile Met Thr Ser Val Ser Gly Arg Ile Pro Pro
            900                 905                 910

Asn Val Glu Lys Ser Ile Lys Lys Glu Met Ala Gln Tyr Ala Ser Asn
        915                 920                 925

Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln Gln Ile Ala Asn Ile
    930                 935                 940

Leu Asp Ser His Ala Ala Thr Leu Asn Arg Lys Ser Glu Arg Glu Val
945                 950                 955                 960

Phe Phe Met Asn Thr Gln Ser Ile Val Gln Leu Val Gln Arg Tyr Arg
                965                 970                 975

Ser Gly Ile Arg Gly His Met Lys Ala Val Val Met Asp Leu Leu Arg
            980                 985                 990

Gln Tyr Leu Arg Val Glu Thr Gln  Phe Gln Asn Gly His  Tyr Asp
Lys
        995                 1000                1005

Cys Val  Phe Ala Leu Arg Glu  Glu Asn Lys Ser Asp  Met Asn Thr
    1010                1015                1020

Val Leu  Asn Tyr Ile Phe Ser  His Ala Gln Val Thr  Lys Lys Asn
    1025                1030                1035

Leu Leu  Val Thr Met Leu Ile  Asp Gln Leu Cys Gly  Arg Asp Pro
    1040                1045                1050

Thr Leu  Thr Asp Glu Leu Leu  Asn Ile Leu Thr Glu  Leu Thr Gln
    1055                1060                1065

Leu Ser  Lys Thr Thr Asn Ala  Lys Val Ala Leu Arg  Ala Arg Gln
    1070                1075                1080

Val Leu  Ile Ala Ser His Leu  Pro Ser Tyr Glu Leu  Arg His Asn
    1085                1090                1095

Gln Val  Glu Ser Ile Phe Leu  Ser Ala Ile Asp Met  Tyr Gly His
    1100                1105                1110
```

```
Gln Phe  Cys Ile Glu Asn Leu  Gln Lys Leu Ile Leu  Ser Glu Thr
    1115                1120                1125

Ser Ile  Phe Asp Val Leu Pro  Asn Phe Phe Tyr His  Ser Asn Gln
    1130                1135                1140

Val Val  Arg Met Ala Ala Leu  Glu Val Tyr Val Arg  Arg Ala Tyr
    1145                1150                1155

Ile Ala  Tyr Glu Leu Asn Ser  Val Gln His Arg Gln  Leu Lys Asp
    1160                1165                1170

Asn Thr  Cys Val Val Glu Phe  Gln Phe Met Leu Pro  Thr Ser His
    1175                1180                1185

Pro Asn  Arg Gly Asn Ile Pro  Thr Leu Asn Arg Met  Ser Phe Ser
    1190                1195                1200

Ser Asn  Leu Asn His Tyr Gly  Met Thr His Val Ala  Ser Val Ser
    1205                1210                1215

Asp Val  Leu Leu Asp Asn Ser  Phe Thr Pro Pro Cys  Gln Arg Met
    1220                1225                1230

Gly Gly  Met Val Ser Phe Arg  Thr Phe Glu Asp Phe  Val Arg Ile
    1235                1240                1245

Phe Asp  Glu Val Met Gly Cys  Phe Ser Asp Ser Pro  Pro Gln Ser
    1250                1255                1260

Pro Thr  Phe Pro Glu Ala Gly  His Thr Ser Leu Tyr  Asp Glu Asp
    1265                1270                1275

Lys Val  Pro Arg Asp Glu Pro  Ile His Ile Leu Asn  Val Ala Ile
    1280                1285                1290

Lys Thr  Asp Cys Asp Ile Glu  Asp Asp Arg Leu Ala  Ala Met Phe
    1295                1300                1305

Arg Glu  Phe Thr Gln Gln Asn  Lys Ala Thr Leu Val  Asp His Gly
    1310                1315                1320
```

Ile Arg Arg Leu Thr Phe Leu Val Ala Gln Lys Asp Phe Arg Lys
1325 1330 1335

Gln Val Asn Tyr Glu Val Asp Arg Arg Phe His Arg Glu Phe Pro
1340 1345 1350

Lys Phe Phe Thr Phe Arg Ala Arg Asp Lys Phe Glu Glu Asp Arg
1355 1360 1365

Ile Tyr Arg His Leu Glu Pro Ala Leu Ala Phe Gln Leu Glu Leu
1370 1375 1380

Asn Arg Met Arg Asn Phe Asp Leu Thr Ala Ile Pro Cys Ala Asn
1385 1390 1395

His Lys Met His Leu Tyr Leu Gly Ala Ala Lys Val Glu Val Gly
1400 1405 1410

Thr Glu Val Thr Asp Tyr Arg Phe Phe Val Arg Ala Ile Ile Arg
1415 1420 1425

His Ser Asp Leu Val Thr Lys Glu Ala Ser Phe Glu Tyr Leu Gln
1430 1435 1440

Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp Glu Leu Glu
1445 1450 1455

Val Ala Phe Asn Asn Thr Asn Val Arg Thr Asp Cys Asn His Ile
1460 1465 1470

Phe Leu Asn Phe Val Pro Thr Val Ile Met Asp Pro Ser Lys Ile
1475 1480 1485

Glu Glu Ser Val Arg Ser Met Val Met Arg Tyr Gly Ser Arg Leu
1490 1495 1500

Trp Lys Leu Arg Val Leu Gln Ala Glu Leu Lys Ile Asn Ile Arg
1505 1510 1515

Leu Thr Pro Thr Gly Lys Ala Ile Pro Ile Arg Leu Phe Leu Thr
1520 1525 1530

Asn Glu Ser Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val

1535 1540 1545

Thr Asp Ser Arg Thr Ala Gln Ile Met Phe Gln Ala Tyr Gly Asp
1550 1555 1560

Lys Gln Gly Pro Leu His Gly Met Leu Ile Asn Thr Pro Tyr Val
1565 1570 1575

Thr Lys Asp Leu Leu Gln Ser Lys Arg Phe Gln Ala Gln Ser Leu
1580 1585 1590

Gly Thr Thr Tyr Ile Tyr Asp Ile Pro Glu Met Phe Arg Gln Ser
1595 1600 1605

Leu Ile Lys Leu Trp Glu Ser Met Ser Thr Gln Ala Phe Leu Pro
1610 1615 1620

Ser Pro Pro Leu Pro Ser Asp Met Leu Thr Tyr Thr Glu Leu Val
1625 1630 1635

Leu Asp Asp Gln Gly Gln Leu Val His Met Asn Arg Leu Pro Gly
1640 1645 1650

Gly Asn Glu Ile Gly Met Val Ala Trp Lys Met Thr Phe Lys Ser
1655 1660 1665

Pro Glu Tyr Pro Glu Gly Arg Asp Ile Ile Val Ile Gly Asn Asp
1670 1675 1680

Ile Thr Tyr Arg Ile Gly Ser Phe Gly Pro Gln Glu Asp Leu Leu
1685 1690 1695

Phe Leu Arg Ala Ser Glu Leu Ala Arg Ala Glu Gly Ile Pro Arg
1700 1705 1710

Ile Tyr Val Ser Ala Asn Ser Gly Ala Arg Ile Gly Leu Ala Glu
1715 1720 1725

Glu Ile Arg His Met Phe His Val Ala Trp Val Asp Pro Glu Asp
1730 1735 1740

Pro Tyr Lys Gly Tyr Arg Tyr Leu Tyr Leu Thr Pro Gln Asp Tyr
1745 1750 1755

```
Lys Arg  Val Ser Ala Leu Asn  Ser Val His Cys Glu  His Val Glu
    1760                1765                1770

Asp Glu  Gly Glu Ser Arg Tyr  Lys Ile Thr Asp Ile  Ile Gly Lys
    1775                1780                1785

Glu Glu  Gly Ile Gly Pro Glu  Asn Leu Arg Gly Ser  Gly Met Ile
    1790                1795                1800

Ala Gly  Glu Ser Ser Leu Ala  Tyr Asn Glu Ile Ile  Thr Ile Ser
    1805                1810                1815

Leu Val  Thr Cys Arg Ala Ile  Gly Ile Gly Ala Tyr  Leu Val Arg
    1820                1825                1830

Leu Gly  Gln Arg Thr Ile Gln  Val Glu Asn Ser His  Leu Ile Leu
    1835                1840                1845

Thr Gly  Ala Gly Ala Leu Asn  Lys Val Leu Gly Arg  Glu Val Tyr
    1850                1855                1860

Thr Ser  Asn Asn Gln Leu Gly  Gly Ile Gln Ile Met  His Asn Asn
    1865                1870                1875

Gly Val  Thr His Cys Thr Val  Cys Asp Asp Phe Glu  Gly Val Phe
    1880                1885                1890

Thr Val  Leu His Trp Leu Ser  Tyr Met Pro Lys Ser  Val His Ser
    1895                1900                1905

Ser Val  Pro Leu Leu Asn Ser  Lys Asp Pro Ile Asp  Arg Ile Ile
    1910                1915                1920

Glu Phe  Val Pro Thr Lys Thr  Pro Tyr Asp Pro Arg  Trp Met Leu
    1925                1930                1935

Ala Gly  Arg Pro His Pro Thr  Gln Lys Gly Gln Trp  Leu Ser Gly
    1940                1945                1950

Phe Phe  Asp Tyr Gly Ser Phe  Ser Glu Ile Met Gln  Pro Trp Ala
    1955                1960                1965
```

```
Gln Thr  Val Val Val Gly Arg  Ala Arg Leu Gly Gly  Ile Pro Val
    1970                 1975                 1980

Gly Val  Val Ala Val Glu Thr  Arg Thr Val Glu Leu  Ser Ile Pro
    1985                 1990                 1995

Ala Asp  Pro Ala Asn Leu Asp  Ser Glu Ala Lys Ile  Ile Gln Gln
    2000                 2005                 2010

Ala Gly  Gln Val Trp Phe Pro  Asp Ser Ala Phe Lys  Thr Tyr Gln
    2015                 2020                 2025

Ala Ile  Lys Asp Phe Asn Arg  Glu Gly Leu Pro Leu  Met Val Phe
    2030                 2035                 2040

Ala Asn  Trp Arg Gly Phe Ser  Gly Gly Met Lys Asp  Met Tyr Asp
    2045                 2050                 2055

Gln Val  Leu Lys Phe Gly Ala  Tyr Ile Val Asp Gly  Leu Arg Glu
    2060                 2065                 2070

Cys Cys  Gln Pro Val Leu Val  Tyr Ile Pro Pro Gln  Ala Glu Leu
    2075                 2080                 2085

Arg Gly  Gly Ser Trp Val Val  Ile Asp Ser Ser Ile  Asn Pro Arg
    2090                 2095                 2100

His Met  Glu Met Tyr Ala Asp  Arg Glu Ser Arg Gly  Ser Val Leu
    2105                 2110                 2115

Glu Pro  Glu Gly Thr Val Glu  Ile Lys Phe Arg Arg  Lys Asp Leu
    2120                 2125                 2130

Val Lys  Thr Met Arg Arg Val  Asp Pro Val Tyr Ile  His Leu Ala
    2135                 2140                 2145

Glu Arg  Leu Gly Thr Pro Glu  Leu Ser Thr Ala Glu  Arg Lys Glu
    2150                 2155                 2160

Leu Glu  Asn Lys Leu Lys Glu  Arg Glu Glu Phe Leu  Ile Pro Ile
    2165                 2170                 2175
```

```
Tyr His  Gln Val Ala Val Gln  Phe Ala Asp Leu His  Asp Thr Pro
    2180                2185                2190

Gly Arg  Met Gln Glu Lys Gly  Val Ile Ser Asp Ile  Leu Asp Trp
    2195                2200                2205

Lys Thr  Ser Arg Thr Phe Phe  Tyr Trp Arg Leu Arg  Arg Leu Leu
    2210                2215                2220

Leu Glu  Asp Leu Val Lys Lys  Lys Ile His Asn Ala  Asn Pro Glu
    2225                2230                2235

Leu Thr  Asp Gly Gln Ile Gln  Ala Met Leu Arg Arg  Trp Phe Val
    2240                2245                2250

Glu Val  Glu Gly Thr Val Lys  Ala Tyr Val Trp Asp  Asn Asn Lys
    2255                2260                2265

Asp Leu  Ala Glu Trp Leu Glu  Lys Gln Leu Thr Glu  Glu Asp Gly
    2270                2275                2280

Val His  Ser Val Ile Glu Glu  Asn Ile Lys Cys Ile  Ser Arg Asp
    2285                2290                2295

Tyr Val  Leu Lys Gln Ile Arg  Ser Leu Val Gln Ala  Asn Pro Glu
    2300                2305                2310

Val Ala  Met Asp Ser Ile Ile  His Met Thr Gln His  Ile Ser Pro
    2315                2320                2325

Thr Gln  Arg Ala Glu Val Ile  Arg Ile Leu Ser Thr  Met Asp Ser
    2330                2335                2340

Pro Ser  Thr
    2345


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His Phe Gly Gly Ile Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu
35 40 45

Glu Leu Asn Gln His Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp
50 55 60

Asn Ser Glu Asp Glu Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu
65 70 75 80

Glu Lys Glu Gly Ser Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu
85 90 95

Ser Asp Leu Gly Ile Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile
100 105 110

Arg Ser Ser Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg
115 120 125

Lys Lys Ile Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu
130 135 140

Phe Val Thr Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile
145 150 155 160

Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg
165 170 175

Trp Ser Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val
180 185 190

Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met
195 200 205

Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr
210 215 220

Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln
225 230 235 240

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro
245 250 255

Glu Leu Leu Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln
260 265 270

Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln
275 280 285

Thr Ala Gly Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val
290 295 300

Asp Trp Gln Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln
305 310 315 320

Glu Leu Tyr Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Gln
325 330 335

Ala Ala Glu Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly
340 345 350

Gly Gly Gly Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro
355 360 365

Asn Leu Phe Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe
370 375 380

```
Val Met Arg Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu
385                 390                 395                 400

Ala Asp Gln Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser
                405                 410                 415

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile
            420                 425                 430

Ala Thr Pro Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys Leu
        435                 440                 445

Ala Lys Met Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr
    450                 455                 460

Ser Gln Asp Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
465                 470                 475                 480

Val Glu His Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala
                485                 490                 495

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp
            500                 505                 510

Ile Arg Met Met Tyr Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp
        515                 520                 525

Phe Glu Asp Ser Ala His Val Pro Cys Pro Arg Gly His Val Ile Ala
    530                 535                 540

Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser
545                 550                 555                 560

Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly
                565                 570                 575

Tyr Phe Ser Val Ala Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser
            580                 585                 590

Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile
        595                 600                 605

Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
```

610 615 620

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe
625 630 635 640

Gln Met Asn Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu
645 650 655

Lys Val Gln Ala Glu Arg Pro Asp Thr Met Leu Gly Val Val Cys Gly
660 665 670

Ala Leu His Val Ala Asp Val Ser Leu Arg Asn Ser Val Ser Asn Phe
675 680 685

Leu His Ser Leu Glu Arg Gly Gln Val Leu Pro Ala His Thr Leu Leu
690 695 700

Asn Thr Val Asp Val Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val Leu
705 710 715 720

Lys Val Thr Arg Gln Ser Pro Asn Ser Tyr Val Val Ile Met Asn Gly
725 730 735

Ser Cys Val Glu Val Asp Val His Arg Leu Ser Asp Gly Gly Leu Leu
740 745 750

Leu Ser Tyr Asp Gly Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val
755 760 765

Asp Arg Tyr Arg Ile Thr Ile Gly Asn Lys Thr Cys Val Phe Glu Lys
770 775 780

Glu Asn Asp Pro Ser Val Met Arg Ser Pro Ser Ala Gly Lys Leu Ile
785 790 795 800

Gln Tyr Ile Val Glu Asp Gly Gly His Val Phe Ala Gly Gln Cys Tyr
805 810 815

Ala Glu Ile Glu Val Met Lys Met Val Met Thr Leu Thr Ala Val Glu
820 825 830

Ser Gly Cys Ile His Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp Pro
835 840 845

```
Gly Cys Val Leu Ala Lys Met Gln Leu Asp Asn Pro Ser Lys Val Gln
    850                 855                 860

Gln Ala Glu Leu His Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr Ala
865                 870                 875                 880

Leu Arg Gly Glu Lys Leu His Arg Val Phe His Tyr Val Leu Asp Asn
                885                 890                 895

Leu Val Asn Val Met Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe Ser
            900                 905                 910

Ser Lys Val Lys Asp Trp Val Glu Arg Leu Met Lys Thr Leu Arg Asp
        915                 920                 925

Pro Ser Leu Pro Leu Leu Glu Leu Gln Asp Ile Met Thr Ser Val Ser
    930                 935                 940

Gly Arg Ile Pro Pro Asn Val Glu Lys Ser Ile Lys Lys Glu Met Ala
945                 950                 955                 960

Gln Tyr Ala Ser Asn Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln
                965                 970                 975

Gln Ile Ala Asn Ile Leu Asp Ser His Ala Ala Thr Leu Asn Arg Lys
            980                 985                 990

Ser Glu Arg Glu Val Phe Phe Met  Asn Thr Gln Ser Ile  Val Gln
Leu
        995                 1000                1005

Val Gln  Arg Tyr Arg Ser Gly  Ile Arg Gly His Met  Lys Ala Val
    1010                1015                1020

Val Met  Asp Leu Leu Arg Gln  Tyr Leu Arg Val Glu  Thr Gln Phe
    1025                1030                1035

Gln Asn  Gly His Tyr Asp Lys  Cys Val Phe Ala Leu  Arg Glu Glu
    1040                1045                1050

Asn Lys  Ser Asp Met Asn Thr  Val Leu Asn Tyr Ile  Phe Ser His
    1055                1060                1065
```

```
Ala Gln  Val Thr Lys Lys Asn  Leu Leu Val Thr Met  Leu Ile Asp
    1070                1075                1080

Gln Leu  Cys Gly Arg Asp Pro  Thr Leu Thr Asp Glu  Leu Leu Asn
    1085                1090                1095

Ile Leu  Thr Glu Leu Thr Gln  Leu Ser Lys Thr Thr  Asn Ala Lys
    1100                1105                1110

Val Ala  Leu Arg Ala Arg Gln  Val Leu Ile Ala Ser  His Leu Pro
    1115                1120                1125

Ser Tyr  Glu Leu Arg His Asn  Gln Val Glu Ser Ile  Phe Leu Ser
    1130                1135                1140

Ala Ile  Asp Met Tyr Gly His  Gln Phe Cys Ile Glu  Asn Leu Gln
    1145                1150                1155

Lys Leu  Ile Leu Ser Glu Thr  Ser Ile Phe Asp Val  Leu Pro Asn
    1160                1165                1170

Phe Phe  Tyr His Ser Asn Gln  Val Val Arg Met Ala  Ala Leu Glu
    1175                1180                1185

Val Tyr  Val Arg Arg Ala Tyr  Ile Ala Tyr Glu Leu  Asn Ser Val
    1190                1195                1200

Gln His  Arg Gln Leu Lys Asp  Asn Thr Cys Val Val  Glu Phe Gln
    1205                1210                1215

Phe Met  Leu Pro Thr Ser His  Pro Asn Arg Gly Asn  Ile Pro Thr
    1220                1225                1230

Leu Asn  Arg Met Ser Phe Ser  Ser Asn Leu Asn His  Tyr Gly Met
    1235                1240                1245

Thr His  Val Ala Ser Val Ser  Asp Val Leu Leu Asp  Asn Ser Phe
    1250                1255                1260

Thr Pro  Pro Cys Gln Arg Met  Gly Gly Met Val Ser  Phe Arg Thr
    1265                1270                1275
```

```
Phe Glu  Asp Phe Val Arg Ile  Phe Asp Glu Val Met  Gly Cys Phe
    1280                1285                1290

Ser Asp  Ser Pro Pro Gln Ser  Pro Thr Phe Pro Glu  Ala Gly His
    1295                1300                1305

Thr Ser  Leu Tyr Asp Glu Asp  Lys Val Pro Arg Asp  Glu Pro Ile
    1310                1315                1320

His Ile  Leu Asn Val Ala Ile  Lys Thr Asp Cys Asp  Ile Glu Asp
    1325                1330                1335

Asp Arg  Leu Ala Ala Met Phe  Arg Glu Phe Thr Gln  Gln Asn Lys
    1340                1345                1350

Ala Thr  Leu Val Asp His Gly  Ile Arg Arg Leu Thr  Phe Leu Val
    1355                1360                1365

Ala Gln  Lys Asp Phe Arg Lys  Gln Val Asn Tyr Glu  Val Asp Arg
    1370                1375                1380

Arg Phe  His Arg Glu Phe Pro  Lys Phe Phe Thr Phe  Arg Ala Arg
    1385                1390                1395

Asp Lys  Phe Glu Glu Asp Arg  Ile Tyr Arg His Leu  Glu Pro Ala
    1400                1405                1410

Leu Ala  Phe Gln Leu Glu Leu  Asn Arg Met Arg Asn  Phe Asp Leu
    1415                1420                1425

Thr Ala  Ile Pro Cys Ala Asn  His Lys Met His Leu  Tyr Leu Gly
    1430                1435                1440

Ala Ala  Lys Val Glu Val Gly  Thr Glu Val Thr Asp  Tyr Arg Phe
    1445                1450                1455

Phe Val  Arg Ala Ile Ile Arg  His Ser Asp Leu Val  Thr Lys Glu
    1460                1465                1470

Ala Ser  Phe Glu Tyr Leu Gln  Asn Glu Gly Glu Arg  Leu Leu Leu
    1475                1480                1485
```

```
Glu Ala  Met Asp Glu Leu Glu  Val Ala Phe Asn Asn  Thr Asn Val
    1490                 1495                 1500

Arg Thr  Asp Cys Asn His Ile  Phe Leu Asn Phe Val  Pro Thr Val
    1505                 1510                 1515

Ile Met  Asp Pro Ser Lys Ile  Glu Glu Ser Val Arg  Ser Met Val
    1520                 1525                 1530

Met Arg  Tyr Gly Ser Arg Leu  Trp Lys Leu Arg Val  Leu Gln Ala
    1535                 1540                 1545

Glu Leu  Lys Ile Asn Ile Arg  Leu Thr Pro Thr Gly  Lys Ala Ile
    1550                 1555                 1560

Pro Ile  Arg Leu Phe Leu Thr  Asn Glu Ser Gly Tyr  Tyr Leu Asp
    1565                 1570                 1575

Ile Ser  Leu Tyr Lys Glu Val  Thr Asp Ser Arg Thr  Ala Gln Ile
    1580                 1585                 1590

Met Phe  Gln Ala Tyr Gly Asp  Lys Gln Gly Pro Leu  His Gly Met
    1595                 1600                 1605

Leu Ile  Asn Thr Pro Tyr Val  Thr Lys Asp Leu Leu  Gln Ser Lys
    1610                 1615                 1620

Arg Phe  Gln Ala Gln Ser Leu  Gly Thr Thr Tyr Ile  Tyr Asp Ile
    1625                 1630                 1635

Pro Glu  Met Phe Arg Gln Ser  Leu Ile Lys Leu Trp  Glu Ser Met
    1640                 1645                 1650

Ser Thr  Gln Ala Phe Leu Pro  Ser Pro Pro Leu Pro  Ser Asp Met
    1655                 1660                 1665

Leu Thr  Tyr Thr Glu Leu Val  Leu Asp Asp Gln Gly  Gln Leu Val
    1670                 1675                 1680

His Met  Asn Arg Leu Pro Gly  Gly Asn Glu Ile Gly  Met Val Ala
    1685                 1690                 1695

Trp Lys  Met Thr Phe Lys Ser  Pro Glu Tyr Pro Glu  Gly Arg Asp
```

1700 1705 1710

Ile Ile Val Ile Gly Asn Asp Ile Thr Tyr Arg Ile Gly Ser Phe
1715 1720 1725

Gly Pro Gln Glu Asp Leu Leu Phe Leu Arg Ala Ser Glu Leu Ala
1730 1735 1740

Arg Ala Glu Gly Ile Pro Arg Ile Tyr Val Ser Ala Asn Ser Gly
1745 1750 1755

Ala Arg Ile Gly Leu Ala Glu Glu Ile Arg His Met Phe His Val
1760 1765 1770

Ala Trp Val Asp Pro Glu Asp Pro Tyr Lys Gly Tyr Arg Tyr Leu
1775 1780 1785

Tyr Leu Thr Pro Gln Asp Tyr Lys Arg Val Ser Ala Leu Asn Ser
1790 1795 1800

Val His Cys Glu His Val Glu Asp Glu Gly Glu Ser Arg Tyr Lys
1805 1810 1815

Ile Thr Asp Ile Ile Gly Lys Glu Glu Gly Ile Gly Pro Glu Asn
1820 1825 1830

Leu Arg Gly Ser Gly Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr
1835 1840 1845

Asn Glu Ile Ile Thr Ile Ser Leu Val Thr Cys Arg Ala Ile Gly
1850 1855 1860

Ile Gly Ala Tyr Leu Val Arg Leu Gly Gln Arg Thr Ile Gln Val
1865 1870 1875

Glu Asn Ser His Leu Ile Leu Thr Gly Ala Gly Ala Leu Asn Lys
1880 1885 1890

Val Leu Gly Arg Glu Val Tyr Thr Ser Asn Asn Gln Leu Gly Gly
1895 1900 1905

Ile Gln Ile Met His Asn Asn Gly Val Thr His Cys Thr Val Cys
1910 1915 1920

```
Asp Asp  Phe Glu Gly Val Phe  Thr Val Leu His Trp  Leu Ser Tyr
    1925                1930                1935

Met Pro  Lys Ser Val His Ser  Ser Val Pro Leu Leu  Asn Ser Lys
    1940                1945                1950

Asp Pro  Ile Asp Arg Ile Ile  Glu Phe Val Pro Thr  Lys Thr Pro
    1955                1960                1965

Tyr Asp  Pro Arg Trp Met Leu  Ala Gly Arg Pro His  Pro Thr Gln
    1970                1975                1980

Lys Gly  Gln Trp Leu Ser Gly  Phe Phe Asp Tyr Gly  Ser Phe Ser
    1985                1990                1995

Glu Ile  Met Gln Pro Trp Ala  Gln Thr Val Val Val  Gly Arg Ala
    2000                2005                2010

Arg Leu  Gly Gly Ile Pro Val  Gly Val Val Ala Val  Glu Thr Arg
    2015                2020                2025

Thr Val  Glu Leu Ser Ile Pro  Ala Asp Pro Ala Asn  Leu Asp Ser
    2030                2035                2040

Glu Ala  Lys Ile Ile Gln Gln  Ala Gly Gln Val Trp  Phe Pro Asp
    2045                2050                2055

Ser Ala  Phe Lys Thr Tyr Gln  Ala Ile Lys Asp Phe  Asn Arg Glu
    2060                2065                2070

Gly Leu  Pro Leu Met Val Phe  Ala Asn Trp Arg Gly  Phe Ser Gly
    2075                2080                2085

Gly Met  Lys Asp Met Tyr Asp  Gln Val Leu Lys Phe  Gly Ala Tyr
    2090                2095                2100

Ile Val  Asp Gly Leu Arg Glu  Cys Cys Gln Pro Val  Leu Val Tyr
    2105                2110                2115

Ile Pro  Pro Gln Ala Glu Leu  Arg Gly Gly Ser Trp  Val Val Ile
    2120                2125                2130
```

```
Asp Ser  Ser Ile Asn Pro Arg  His Met Glu Met Tyr  Ala Asp Arg
    2135                2140                2145

Glu Ser  Arg Gly Ser Val Leu  Glu Pro Glu Gly Thr  Val Glu Ile
    2150                2155                2160

Lys Phe  Arg Arg Lys Asp Leu  Val Lys Thr Met Arg  Arg Val Asp
    2165                2170                2175

Pro Val  Tyr Ile His Leu Ala  Glu Arg Leu Gly Thr  Pro Glu Leu
    2180                2185                2190

Ser Thr  Ala Glu Arg Lys Glu  Leu Glu Asn Lys Leu  Lys Glu Arg
    2195                2200                2205

Glu Glu  Phe Leu Ile Pro Ile  Tyr His Gln Val Ala  Val Gln Phe
    2210                2215                2220

Ala Asp  Leu His Asp Thr Pro  Gly Arg Met Gln Glu  Lys Gly Val
    2225                2230                2235

Ile Ser  Asp Ile Leu Asp Trp  Lys Thr Ser Arg Thr  Phe Phe Tyr
    2240                2245                2250

Trp Arg  Leu Arg Arg Leu Leu  Leu Glu Asp Leu Val  Lys Lys Lys
    2255                2260                2265

Ile His  Asn Ala Asn Pro Glu  Leu Thr Asp Gly Gln  Ile Gln Ala
    2270                2275                2280

Met Leu  Arg Arg Trp Phe Val  Glu Val Glu Gly Thr  Val Lys Ala
    2285                2290                2295

Tyr Val  Trp Asp Asn Asn Lys  Asp Leu Ala Glu Trp  Leu Glu Lys
    2300                2305                2310

Gln Leu  Thr Glu Glu Asp Gly  Val His Ser Val Ile  Glu Glu Asn
    2315                2320                2325

Ile Lys  Cys Ile Ser Arg Asp  Tyr Val Leu Lys Gln  Ile Arg Ser
    2330                2335                2340
```

```
Leu Val  Gln Ala Asn Pro Glu  Val Ala Met Asp Ser  Ile Ile His
    2345                2350                2355


Met Thr  Gln His Ile Ser Pro  Thr Gln Arg Ala Glu  Val Ile Arg
    2360                2365                2370


Ile Leu  Ser Thr Met Asp Ser  Pro Ser Thr
    2375                2380


<210> 1261
<211> 114
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 385; "

<220>
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<223> /note="Gene Symbol: ACACA; "

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<223> /note="Gene Name:
      acetyl-CoA carboxylase alpha; "

<220>
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<400> 1261
Met Trp Trp Ser Thr Leu Met Ser Ile Leu Arg Ala Arg Ser Phe Trp
1               5                  10                  15


Lys Trp Ile Ser Thr Gln Thr Val Arg Ile Ile Arg Ala Val Arg Ala
            20                  25                  30


His Phe Gly Gly Ile Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu
        35                  40                  45


Glu Leu Asn Gln His Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp
    50                  55                  60


Asn Ser Glu Asp Glu Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu
65                  70                  75                  80


Glu Lys Glu Gly Ser Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu
                85                  90                  95
```

Ser Asp Leu Gly Ile Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile
100 105 110

Arg Leu

<210> 1262
<211> 42
<212> PRT
<213> Homo sapiens

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<220>
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<400> 1262
Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile
1 5 10 15

Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr
20 25 30

Arg Phe Gly Gly Asn Lys Val Ile Glu Lys
35 40

<210> 1263
<211> 2288
<212> PRT
<213> Homo sapiens

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<400> 1263

```
Met Glu Gly Ser Pro Glu Glu Asn Lys Glu Met Arg Tyr Tyr Met Leu
1               5                  10                  15

Gln Arg Ser Ser Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp
            20                  25                  30

Arg Lys Lys Ile Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala
        35                  40                  45

Glu Phe Val Thr Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu
    50                  55                  60

Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg
65                  70                  75                  80

Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val
                85                  90                  95

Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys
            100                 105                 110

Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn
        115                 120                 125

Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val
    130                 135                 140

Gln Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu
145                 150                 155                 160

Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser
                165                 170                 175
```

```
Gln Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala
            180                 185                 190

Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg
        195                 200                 205

Val Asp Trp Gln Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro
    210                 215                 220

Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu
225                 230                 235                 240

Gln Ala Ala Glu Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu
                245                 250                 255

Gly Gly Gly Gly Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe
            260                 265                 270

Pro Asn Leu Phe Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile
        275                 280                 285

Phe Val Met Arg Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile
    290                 295                 300

Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys
305                 310                 315                 320

Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr
                325                 330                 335

Ile Ala Thr Pro Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys
            340                 345                 350

Leu Ala Lys Met Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu
        355                 360                 365

Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu
    370                 375                 380

Gln Val Glu His Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro
385                 390                 395                 400
```

Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys
405 410 415

Asp Ile Arg Met Met Tyr Gly Val Ser Pro Trp Gly Asp Ser Pro Ile
420 425 430

Asp Phe Glu Asp Ser Ala His Val Pro Cys Pro Arg Gly His Val Ile
435 440 445

Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser
450 455 460

Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Asn Lys Asn Val Trp
465 470 475 480

Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly Leu His Glu Phe Ala Asp
485 490 495

Ser Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala
500 505 510

Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp
515 520 525

Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser
530 535 540

Phe Gln Met Asn Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala
545 550 555 560

Glu Lys Val Gln Ala Glu Arg Pro Asp Thr Met Leu Gly Val Val Cys
565 570 575

Gly Ala Leu His Val Ala Asp Val Ser Leu Arg Asn Ser Val Ser Asn
580 585 590

Phe Leu His Ser Leu Glu Arg Gly Gln Val Leu Pro Ala His Thr Leu
595 600 605

Leu Asn Thr Val Asp Val Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val
610 615 620

```
Leu Lys Val Thr Arg Gln Ser Pro Asn Ser Tyr Val Val Ile Met Asn
625                 630                 635                 640

Gly Ser Cys Val Glu Val Asp Val His Arg Leu Ser Asp Gly Gly Leu
                645                 650                 655

Leu Leu Ser Tyr Asp Gly Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu
            660                 665                 670

Val Asp Arg Tyr Arg Ile Thr Ile Gly Asn Lys Thr Cys Val Phe Glu
        675                 680                 685

Lys Glu Asn Asp Pro Ser Val Met Arg Ser Pro Ser Ala Gly Lys Leu
    690                 695                 700

Ile Gln Tyr Ile Val Glu Asp Gly Gly His Val Phe Ala Gly Gln Cys
705                 710                 715                 720

Tyr Ala Glu Ile Glu Val Met Lys Met Val Met Thr Leu Thr Ala Val
                725                 730                 735

Glu Ser Gly Cys Ile His Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp
            740                 745                 750

Pro Gly Cys Val Leu Ala Lys Met Gln Leu Asp Asn Pro Ser Lys Val
        755                 760                 765

Gln Gln Ala Glu Leu His Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr
    770                 775                 780

Ala Leu Arg Gly Glu Lys Leu His Arg Val Phe His Tyr Val Leu Asp
785                 790                 795                 800

Asn Leu Val Asn Val Met Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe
                805                 810                 815

Ser Ser Lys Val Lys Asp Trp Val Glu Arg Leu Met Lys Thr Leu Arg
            820                 825                 830

Asp Pro Ser Leu Pro Leu Leu Glu Leu Gln Asp Ile Met Thr Ser Val
        835                 840                 845

Ser Gly Arg Ile Pro Pro Asn Val Glu Lys Ser Ile Lys Lys Glu Met
```

```
    850                 855                 860

Ala Gln Tyr Ala Ser Asn Ile Thr Ser Val Leu Cys Gln Phe Pro Ser
865                 870                 875                 880

Gln Gln Ile Ala Asn Ile Leu Asp Ser His Ala Ala Thr Leu Asn Arg
                885                 890                 895

Lys Ser Glu Arg Glu Val Phe Phe Met Asn Thr Gln Ser Ile Val Gln
            900                 905                 910

Leu Val Gln Arg Tyr Arg Ser Gly Ile Arg Gly His Met Lys Ala Val
        915                 920                 925

Val Met Asp Leu Leu Arg Gln Tyr Leu Arg Val Glu Thr Gln Phe Gln
    930                 935                 940

Asn Gly His Tyr Asp Lys Cys Val Phe Ala Leu Arg Glu Glu Asn Lys
945                 950                 955                 960

Ser Asp Met Asn Thr Val Leu Asn Tyr Ile Phe Ser His Ala Gln Val
                965                 970                 975

Thr Lys Lys Asn Leu Leu Val Thr Met Leu Ile Asp Gln Leu Cys Gly
            980                 985                 990

Arg Asp Pro Thr Leu Thr Asp Glu  Leu Leu Asn Ile Leu  Thr Glu
Leu
        995                 1000                1005

Thr Gln  Leu Ser Lys Thr Thr  Asn Ala Lys Val Ala  Leu Arg Ala
    1010                1015                1020

Arg Gln  Val Leu Ile Ala Ser  His Leu Pro Ser Tyr  Glu Leu Arg
    1025                1030                1035

His Asn  Gln Val Glu Ser Ile  Phe Leu Ser Ala Ile  Asp Met Tyr
    1040                1045                1050

Gly His  Gln Phe Cys Ile Glu  Asn Leu Gln Lys Leu  Ile Leu Ser
    1055                1060                1065

Glu Thr  Ser Ile Phe Asp Val  Leu Pro Asn Phe Phe  Tyr His Ser
```

1070 1075 1080

Asn Gln Val Val Arg Met Ala Ala Leu Glu Val Tyr Val Arg Arg
1085 1090 1095

Ala Tyr Ile Ala Tyr Glu Leu Asn Ser Val Gln His Arg Gln Leu
1100 1105 1110

Lys Asp Asn Thr Cys Val Val Glu Phe Gln Phe Met Leu Pro Thr
1115 1120 1125

Ser His Pro Asn Arg Gly Asn Ile Pro Thr Leu Asn Arg Met Ser
1130 1135 1140

Phe Ser Ser Asn Leu Asn His Tyr Gly Met Thr His Val Ala Ser
1145 1150 1155

Val Ser Asp Val Leu Leu Asp Asn Ser Phe Thr Pro Pro Cys Gln
1160 1165 1170

Arg Met Gly Gly Met Val Ser Phe Arg Thr Phe Glu Asp Phe Val
1175 1180 1185

Arg Ile Phe Asp Glu Val Met Gly Cys Phe Ser Asp Ser Pro Pro
1190 1195 1200

Gln Ser Pro Thr Phe Pro Glu Ala Gly His Thr Ser Leu Tyr Asp
1205 1210 1215

Glu Asp Lys Val Pro Arg Asp Glu Pro Ile His Ile Leu Asn Val
1220 1225 1230

Ala Ile Lys Thr Asp Cys Asp Ile Glu Asp Asp Arg Leu Ala Ala
1235 1240 1245

Met Phe Arg Glu Phe Thr Gln Gln Asn Lys Ala Thr Leu Val Asp
1250 1255 1260

His Gly Ile Arg Arg Leu Thr Phe Leu Val Ala Gln Lys Asp Phe
1265 1270 1275

Arg Lys Gln Val Asn Tyr Glu Val Asp Arg Arg Phe His Arg Glu
1280 1285 1290

```
Phe Pro  Lys Phe Phe Thr Phe  Arg Ala Arg Asp Lys  Phe Glu Glu
    1295                1300                1305

Asp Arg  Ile Tyr Arg His Leu  Glu Pro Ala Leu Ala  Phe Gln Leu
    1310                1315                1320

Glu Leu  Asn Arg Met Arg Asn  Phe Asp Leu Thr Ala  Ile Pro Cys
    1325                1330                1335

Ala Asn  His Lys Met His Leu  Tyr Leu Gly Ala Ala  Lys Val Glu
    1340                1345                1350

Val Gly  Thr Glu Val Thr Asp  Tyr Arg Phe Phe Val  Arg Ala Ile
    1355                1360                1365

Ile Arg  His Ser Asp Leu Val  Thr Lys Glu Ala Ser  Phe Glu Tyr
    1370                1375                1380

Leu Gln  Asn Glu Gly Glu Arg  Leu Leu Leu Glu Ala  Met Asp Glu
    1385                1390                1395

Leu Glu  Val Ala Phe Asn Asn  Thr Asn Val Arg Thr  Asp Cys Asn
    1400                1405                1410

His Ile  Phe Leu Asn Phe Val  Pro Thr Val Ile Met  Asp Pro Ser
    1415                1420                1425

Lys Ile  Glu Glu Ser Val Arg  Ser Met Val Met Arg  Tyr Gly Ser
    1430                1435                1440

Arg Leu  Trp Lys Leu Arg Val  Leu Gln Ala Glu Leu  Lys Ile Asn
    1445                1450                1455

Ile Arg  Leu Thr Pro Thr Gly  Lys Ala Ile Pro Ile  Arg Leu Phe
    1460                1465                1470

Leu Thr  Asn Glu Ser Gly Tyr  Tyr Leu Asp Ile Ser  Leu Tyr Lys
    1475                1480                1485

Glu Val  Thr Asp Ser Arg Thr  Ala Gln Ile Met Phe  Gln Ala Tyr
    1490                1495                1500
```

Gly Asp Lys Gln Gly Pro Leu His Gly Met Leu Ile Asn Thr Pro
1505 1510 1515

Tyr Val Thr Lys Asp Leu Leu Gln Ser Lys Arg Phe Gln Ala Gln
1520 1525 1530

Ser Leu Gly Thr Thr Tyr Ile Tyr Asp Ile Pro Glu Met Phe Arg
1535 1540 1545

Gln Ser Leu Ile Lys Leu Trp Glu Ser Met Ser Thr Gln Ala Phe
1550 1555 1560

Leu Pro Ser Pro Pro Leu Pro Ser Asp Met Leu Thr Tyr Thr Glu
1565 1570 1575

Leu Val Leu Asp Asp Gln Gly Gln Leu Val His Met Asn Arg Leu
1580 1585 1590

Pro Gly Gly Asn Glu Ile Gly Met Val Ala Trp Lys Met Thr Phe
1595 1600 1605

Lys Ser Pro Glu Tyr Pro Glu Gly Arg Asp Ile Ile Val Ile Gly
1610 1615 1620

Asn Asp Ile Thr Tyr Arg Ile Gly Ser Phe Gly Pro Gln Glu Asp
1625 1630 1635

Leu Leu Phe Leu Arg Ala Ser Glu Leu Ala Arg Ala Glu Gly Ile
1640 1645 1650

Pro Arg Ile Tyr Val Ser Ala Asn Ser Gly Ala Arg Ile Gly Leu
1655 1660 1665

Ala Glu Glu Ile Arg His Met Phe His Val Ala Trp Val Asp Pro
1670 1675 1680

Glu Asp Pro Tyr Lys Gly Tyr Arg Tyr Leu Tyr Leu Thr Pro Gln
1685 1690 1695

Asp Tyr Lys Arg Val Ser Ala Leu Asn Ser Val His Cys Glu His
1700 1705 1710

Val Glu Asp Glu Gly Glu Ser Arg Tyr Lys Ile Thr Asp Ile Ile
1715 1720 1725

Gly Lys Glu Glu Gly Ile Gly Pro Glu Asn Leu Arg Gly Ser Gly
1730 1735 1740

Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr Asn Glu Ile Ile Thr
1745 1750 1755

Ile Ser Leu Val Thr Cys Arg Ala Ile Gly Ile Gly Ala Tyr Leu
1760 1765 1770

Val Arg Leu Gly Gln Arg Thr Ile Gln Val Glu Asn Ser His Leu
1775 1780 1785

Ile Leu Thr Gly Ala Gly Ala Leu Asn Lys Val Leu Gly Arg Glu
1790 1795 1800

Val Tyr Thr Ser Asn Asn Gln Leu Gly Gly Ile Gln Ile Met His
1805 1810 1815

Asn Asn Gly Val Thr His Cys Thr Val Cys Asp Asp Phe Glu Gly
1820 1825 1830

Val Phe Thr Val Leu His Trp Leu Ser Tyr Met Pro Lys Ser Val
1835 1840 1845

His Ser Ser Val Pro Leu Leu Asn Ser Lys Asp Pro Ile Asp Arg
1850 1855 1860

Ile Ile Glu Phe Val Pro Thr Lys Thr Pro Tyr Asp Pro Arg Trp
1865 1870 1875

Met Leu Ala Gly Arg Pro His Pro Thr Gln Lys Gly Gln Trp Leu
1880 1885 1890

Ser Gly Phe Phe Asp Tyr Gly Ser Phe Ser Glu Ile Met Gln Pro
1895 1900 1905

Trp Ala Gln Thr Val Val Val Gly Arg Ala Arg Leu Gly Gly Ile
1910 1915 1920

Pro Val Gly Val Val Ala Val Glu Thr Arg Thr Val Glu Leu Ser

1925 1930 1935

Ile Pro Ala Asp Pro Ala Asn Leu Asp Ser Glu Ala Lys Ile Ile
1940 1945 1950

Gln Gln Ala Gly Gln Val Trp Phe Pro Asp Ser Ala Phe Lys Thr
1955 1960 1965

Tyr Gln Ala Ile Lys Asp Phe Asn Arg Glu Gly Leu Pro Leu Met
1970 1975 1980

Val Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly Met Lys Asp Met
1985 1990 1995

Tyr Asp Gln Val Leu Lys Phe Gly Ala Tyr Ile Val Asp Gly Leu
2000 2005 2010

Arg Glu Cys Cys Gln Pro Val Leu Val Tyr Ile Pro Pro Gln Ala
2015 2020 2025

Glu Leu Arg Gly Gly Ser Trp Val Val Ile Asp Ser Ser Ile Asn
2030 2035 2040

Pro Arg His Met Glu Met Tyr Ala Asp Arg Glu Ser Arg Gly Ser
2045 2050 2055

Val Leu Glu Pro Glu Gly Thr Val Glu Ile Lys Phe Arg Arg Lys
2060 2065 2070

Asp Leu Val Lys Thr Met Arg Arg Val Asp Pro Val Tyr Ile His
2075 2080 2085

Leu Ala Glu Arg Leu Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg
2090 2095 2100

Lys Glu Leu Glu Asn Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile
2105 2110 2115

Pro Ile Tyr His Gln Val Ala Val Gln Phe Ala Asp Leu His Asp
2120 2125 2130

Thr Pro Gly Arg Met Gln Glu Lys Gly Val Ile Ser Asp Ile Leu
2135 2140 2145

```
Asp Trp  Lys Thr Ser Arg Thr  Phe Phe Tyr Trp Arg  Leu Arg Arg
    2150                 2155                 2160

Leu Leu  Leu Glu Asp Leu Val  Lys Lys Lys Ile His  Asn Ala Asn
    2165                 2170                 2175

Pro Glu  Leu Thr Asp Gly Gln  Ile Gln Ala Met Leu  Arg Arg Trp
    2180                 2185                 2190

Phe Val  Glu Val Glu Gly Thr  Val Lys Ala Tyr Val  Trp Asp Asn
    2195                 2200                 2205

Asn Lys  Asp Leu Ala Glu Trp  Leu Glu Lys Gln Leu  Thr Glu Glu
    2210                 2215                 2220

Asp Gly  Val His Ser Val Ile  Glu Glu Asn Ile Lys  Cys Ile Ser
    2225                 2230                 2235

Arg Asp  Tyr Val Leu Lys Gln  Ile Arg Ser Leu Val  Gln Ala Asn
    2240                 2245                 2250

Pro Glu  Val Ala Met Asp Ser  Ile Ile His Met Thr  Gln His Ile
    2255                 2260                 2265

Ser Pro  Thr Gln Arg Ala Glu  Val Ile Arg Ile Leu  Ser Thr Met
    2270                 2275                 2280

Asp Ser  Pro Ser Thr
    2285


<210> 1264
<211> 2268
<212> PRT
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<220>
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<223> /note="Gene Name:
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<400> 1264

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Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile
1               5                  10                  15

Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr
            20                  25                  30

Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn
        35                  40                  45

Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr
    50                  55                  60

Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr
65                  70                  75                  80

Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His
                85                  90                  95

Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val
            100                 105                 110

Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp
        115                 120                 125

Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu
    130                 135                 140

Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp
145                 150                 155                 160

Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly
                165                 170                 175

Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln
```

```
            180                 185                 190

Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr
        195                 200                 205

Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Gln Ala Ala Glu
    210                 215                 220

Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly
225                 230                 235                 240

Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe
                245                 250                 255

Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg
            260                 265                 270

Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln
        275                 280                 285

Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg
    290                 295                 300

Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro
305                 310                 315                 320

Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met
                325                 330                 335

Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp
            340                 345                 350

Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His
        355                 360                 365

Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu
    370                 375                 380

Gln Ile Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met
385                 390                 395                 400

Met Tyr Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp
                405                 410                 415
```

```
Ser Ala His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile
            420                 425                 430

Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val
        435                 440                 445

Gln Glu Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser
    450                 455                 460

Val Ala Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly
465                 470                 475                 480

His Cys Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met
                485                 490                 495

Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr
            500                 505                 510

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn
        515                 520                 525

Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln
    530                 535                 540

Ala Glu Arg Pro Asp Thr Met Leu Gly Val Val Cys Gly Ala Leu His
545                 550                 555                 560

Val Ala Asp Val Ser Leu Arg Asn Ser Val Ser Asn Phe Leu His Ser
                565                 570                 575

Leu Glu Arg Gly Gln Val Leu Pro Ala His Thr Leu Leu Asn Thr Val
            580                 585                 590

Asp Val Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val Leu Lys Val Thr
        595                 600                 605

Arg Gln Ser Pro Asn Ser Tyr Val Val Ile Met Asn Gly Ser Cys Val
    610                 615                 620

Glu Val Asp Val His Arg Leu Ser Asp Gly Gly Leu Leu Leu Ser Tyr
625                 630                 635                 640
```

```
Asp Gly Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Arg Tyr
                645                 650                 655

Arg Ile Thr Ile Gly Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp
            660                 665                 670

Pro Ser Val Met Arg Ser Pro Ser Ala Gly Lys Leu Ile Gln Tyr Ile
        675                 680                 685

Val Glu Asp Gly Gly His Val Phe Ala Gly Gln Cys Tyr Ala Glu Ile
    690                 695                 700

Glu Val Met Lys Met Val Met Thr Leu Thr Ala Val Glu Ser Gly Cys
705                 710                 715                 720

Ile His Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp Pro Gly Cys Val
                725                 730                 735

Leu Ala Lys Met Gln Leu Asp Asn Pro Ser Lys Val Gln Gln Ala Glu
            740                 745                 750

Leu His Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr Ala Leu Arg Gly
        755                 760                 765

Glu Lys Leu His Arg Val Phe His Tyr Val Leu Asp Asn Leu Val Asn
    770                 775                 780

Val Met Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe Ser Ser Lys Val
785                 790                 795                 800

Lys Asp Trp Val Glu Arg Leu Met Lys Thr Leu Arg Asp Pro Ser Leu
                805                 810                 815

Pro Leu Leu Glu Leu Gln Asp Ile Met Thr Ser Val Ser Gly Arg Ile
            820                 825                 830

Pro Pro Asn Val Glu Lys Ser Ile Lys Lys Glu Met Ala Gln Tyr Ala
        835                 840                 845

Ser Asn Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln Gln Ile Ala
    850                 855                 860
```

```
Asn Ile Leu Asp Ser His Ala Ala Thr Leu Asn Arg Lys Ser Glu Arg
865                 870                 875                 880

Glu Val Phe Phe Met Asn Thr Gln Ser Ile Val Gln Leu Val Gln Arg
                885                 890                 895

Tyr Arg Ser Gly Ile Arg Gly His Met Lys Ala Val Val Met Asp Leu
            900                 905                 910

Leu Arg Gln Tyr Leu Arg Val Glu Thr Gln Phe Gln Asn Gly His Tyr
        915                 920                 925

Asp Lys Cys Val Phe Ala Leu Arg Glu Glu Asn Lys Ser Asp Met Asn
    930                 935                 940

Thr Val Leu Asn Tyr Ile Phe Ser His Ala Gln Val Thr Lys Lys Asn
945                 950                 955                 960

Leu Leu Val Thr Met Leu Ile Asp Gln Leu Cys Gly Arg Asp Pro Thr
                965                 970                 975

Leu Thr Asp Glu Leu Leu Asn Ile Leu Thr Glu Leu Thr Gln Leu Ser
            980                 985                 990

Lys Thr Thr Asn Ala Lys Val Ala  Leu Arg Ala Arg Gln  Val Leu
Ile
        995                 1000                1005

Ala Ser  His Leu Pro Ser Tyr  Glu Leu Arg His Asn  Gln Val Glu
    1010                1015                1020

Ser Ile  Phe Leu Ser Ala Ile  Asp Met Tyr Gly His  Gln Phe Cys
    1025                1030                1035

Ile Glu  Asn Leu Gln Lys Leu  Ile Leu Ser Glu Thr  Ser Ile Phe
    1040                1045                1050

Asp Val  Leu Pro Asn Phe Phe  Tyr His Ser Asn Gln  Val Val Arg
    1055                1060                1065

Met Ala  Ala Leu Glu Val Tyr  Val Arg Arg Ala Tyr  Ile Ala Tyr
    1070                1075                1080
```

```
Glu Leu  Asn Ser Val Gln His  Arg Gln Leu Lys Asp  Asn Thr Cys
    1085                 1090                 1095

Val Val  Glu Phe Gln Phe Met  Leu Pro Thr Ser His  Pro Asn Arg
    1100                 1105                 1110

Gly Asn  Ile Pro Thr Leu Asn  Arg Met Ser Phe Ser  Ser Asn Leu
    1115                 1120                 1125

Asn His  Tyr Gly Met Thr His  Val Ala Ser Val Ser  Asp Val Leu
    1130                 1135                 1140

Leu Asp  Asn Ser Phe Thr Pro  Pro Cys Gln Arg Met  Gly Gly Met
    1145                 1150                 1155

Val Ser  Phe Arg Thr Phe Glu  Asp Phe Val Arg Ile  Phe Asp Glu
    1160                 1165                 1170

Val Met  Gly Cys Phe Ser Asp  Ser Pro Pro Gln Ser  Pro Thr Phe
    1175                 1180                 1185

Pro Glu  Ala Gly His Thr Ser  Leu Tyr Asp Glu Asp  Lys Val Pro
    1190                 1195                 1200

Arg Asp  Glu Pro Ile His Ile  Leu Asn Val Ala Ile  Lys Thr Asp
    1205                 1210                 1215

Cys Asp  Ile Glu Asp Asp Arg  Leu Ala Ala Met Phe  Arg Glu Phe
    1220                 1225                 1230

Thr Gln  Gln Asn Lys Ala Thr  Leu Val Asp His Gly  Ile Arg Arg
    1235                 1240                 1245

Leu Thr  Phe Leu Val Ala Gln  Lys Asp Phe Arg Lys  Gln Val Asn
    1250                 1255                 1260

Tyr Glu  Val Asp Arg Arg Phe  His Arg Glu Phe Pro  Lys Phe Phe
    1265                 1270                 1275

Thr Phe  Arg Ala Arg Asp Lys  Phe Glu Glu Asp Arg  Ile Tyr Arg
    1280                 1285                 1290

His Leu  Glu Pro Ala Leu Ala  Phe Gln Leu Glu Leu  Asn Arg Met
```

```
    1295                1300                1305

Arg Asn  Phe Asp Leu Thr Ala  Ile Pro Cys Ala Asn  His Lys Met
    1310                1315                1320

His Leu  Tyr Leu Gly Ala Ala  Lys Val Glu Val Gly  Thr Glu Val
    1325                1330                1335

Thr Asp  Tyr Arg Phe Phe Val  Arg Ala Ile Ile Arg  His Ser Asp
    1340                1345                1350

Leu Val  Thr Lys Glu Ala Ser  Phe Glu Tyr Leu Gln  Asn Glu Gly
    1355                1360                1365

Glu Arg  Leu Leu Leu Glu Ala  Met Asp Glu Leu Glu  Val Ala Phe
    1370                1375                1380

Asn Asn  Thr Asn Val Arg Thr  Asp Cys Asn His Ile  Phe Leu Asn
    1385                1390                1395

Phe Val  Pro Thr Val Ile Met  Asp Pro Ser Lys Ile  Glu Glu Ser
    1400                1405                1410

Val Arg  Ser Met Val Met Arg  Tyr Gly Ser Arg Leu  Trp Lys Leu
    1415                1420                1425

Arg Val  Leu Gln Ala Glu Leu  Lys Ile Asn Ile Arg  Leu Thr Pro
    1430                1435                1440

Thr Gly  Lys Ala Ile Pro Ile  Arg Leu Phe Leu Thr  Asn Glu Ser
    1445                1450                1455

Gly Tyr  Tyr Leu Asp Ile Ser  Leu Tyr Lys Glu Val  Thr Asp Ser
    1460                1465                1470

Arg Thr  Ala Gln Ile Met Phe  Gln Ala Tyr Gly Asp  Lys Gln Gly
    1475                1480                1485

Pro Leu  His Gly Met Leu Ile  Asn Thr Pro Tyr Val  Thr Lys Asp
    1490                1495                1500

Leu Leu  Gln Ser Lys Arg Phe  Gln Ala Gln Ser Leu  Gly Thr Thr
    1505                1510                1515
```

```
Tyr Ile  Tyr Asp Ile Pro Glu  Met Phe Arg Gln Ser  Leu Ile Lys
    1520                1525                1530

Leu Trp  Glu Ser Met Ser Thr  Gln Ala Phe Leu Pro  Ser Pro Pro
    1535                1540                1545

Leu Pro  Ser Asp Met Leu Thr  Tyr Thr Glu Leu Val  Leu Asp Asp
    1550                1555                1560

Gln Gly  Gln Leu Val His Met  Asn Arg Leu Pro Gly  Gly Asn Glu
    1565                1570                1575

Ile Gly  Met Val Ala Trp Lys  Met Thr Phe Lys Ser  Pro Glu Tyr
    1580                1585                1590

Pro Glu  Gly Arg Asp Ile Ile  Val Ile Gly Asn Asp  Ile Thr Tyr
    1595                1600                1605

Arg Ile  Gly Ser Phe Gly Pro  Gln Glu Asp Leu Leu  Phe Leu Arg
    1610                1615                1620

Ala Ser  Glu Leu Ala Arg Ala  Glu Gly Ile Pro Arg  Ile Tyr Val
    1625                1630                1635

Ser Ala  Asn Ser Gly Ala Arg  Ile Gly Leu Ala Glu  Glu Ile Arg
    1640                1645                1650

His Met  Phe His Val Ala Trp  Val Asp Pro Glu Asp  Pro Tyr Lys
    1655                1660                1665

Gly Tyr  Arg Tyr Leu Tyr Leu  Thr Pro Gln Asp Tyr  Lys Arg Val
    1670                1675                1680

Ser Ala  Leu Asn Ser Val His  Cys Glu His Val Glu  Asp Glu Gly
    1685                1690                1695

Glu Ser  Arg Tyr Lys Ile Thr  Asp Ile Ile Gly Lys  Glu Glu Gly
    1700                1705                1710

Ile Gly  Pro Glu Asn Leu Arg  Gly Ser Gly Met Ile  Ala Gly Glu
    1715                1720                1725
```

```
Ser Ser  Leu Ala Tyr Asn Glu  Ile Ile Thr Ile Ser  Leu Val Thr
    1730                1735                1740

Cys Arg  Ala Ile Gly Ile Gly  Ala Tyr Leu Val Arg  Leu Gly Gln
    1745                1750                1755

Arg Thr  Ile Gln Val Glu Asn  Ser His Leu Ile Leu  Thr Gly Ala
    1760                1765                1770

Gly Ala  Leu Asn Lys Val Leu  Gly Arg Glu Val Tyr  Thr Ser Asn
    1775                1780                1785

Asn Gln  Leu Gly Gly Ile Gln  Ile Met His Asn Asn  Gly Val Thr
    1790                1795                1800

His Cys  Thr Val Cys Asp Asp  Phe Glu Gly Val Phe  Thr Val Leu
    1805                1810                1815

His Trp  Leu Ser Tyr Met Pro  Lys Ser Val His Ser  Ser Val Pro
    1820                1825                1830

Leu Leu  Asn Ser Lys Asp Pro  Ile Asp Arg Ile Ile  Glu Phe Val
    1835                1840                1845

Pro Thr  Lys Thr Pro Tyr Asp  Pro Arg Trp Met Leu  Ala Gly Arg
    1850                1855                1860

Pro His  Pro Thr Gln Lys Gly  Gln Trp Leu Ser Gly  Phe Phe Asp
    1865                1870                1875

Tyr Gly  Ser Phe Ser Glu Ile  Met Gln Pro Trp Ala  Gln Thr Val
    1880                1885                1890

Val Val  Gly Arg Ala Arg Leu  Gly Gly Ile Pro Val  Gly Val Val
    1895                1900                1905

Ala Val  Glu Thr Arg Thr Val  Glu Leu Ser Ile Pro  Ala Asp Pro
    1910                1915                1920

Ala Asn  Leu Asp Ser Glu Ala  Lys Ile Ile Gln Gln  Ala Gly Gln
    1925                1930                1935
```

Val Trp Phe Pro Asp Ser Ala Phe Lys Thr Tyr Gln Ala Ile Lys
1940 1945 1950

Asp Phe Asn Arg Glu Gly Leu Pro Leu Met Val Phe Ala Asn Trp
1955 1960 1965

Arg Gly Phe Ser Gly Gly Met Lys Asp Met Tyr Asp Gln Val Leu
1970 1975 1980

Lys Phe Gly Ala Tyr Ile Val Asp Gly Leu Arg Glu Cys Cys Gln
1985 1990 1995

Pro Val Leu Val Tyr Ile Pro Pro Gln Ala Glu Leu Arg Gly Gly
2000 2005 2010

Ser Trp Val Val Ile Asp Ser Ser Ile Asn Pro Arg His Met Glu
2015 2020 2025

Met Tyr Ala Asp Arg Glu Ser Arg Gly Ser Val Leu Glu Pro Glu
2030 2035 2040

Gly Thr Val Glu Ile Lys Phe Arg Arg Lys Asp Leu Val Lys Thr
2045 2050 2055

Met Arg Arg Val Asp Pro Val Tyr Ile His Leu Ala Glu Arg Leu
2060 2065 2070

Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg Lys Glu Leu Glu Asn
2075 2080 2085

Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile Pro Ile Tyr His Gln
2090 2095 2100

Val Ala Val Gln Phe Ala Asp Leu His Asp Thr Pro Gly Arg Met
2105 2110 2115

Gln Glu Lys Gly Val Ile Ser Asp Ile Leu Asp Trp Lys Thr Ser
2120 2125 2130

Arg Thr Phe Phe Tyr Trp Arg Leu Arg Arg Leu Leu Leu Glu Asp
2135 2140 2145

Leu Val Lys Lys Lys Ile His Asn Ala Asn Pro Glu Leu Thr Asp

```
    2150                2155                2160

Gly Gln  Ile Gln Ala Met Leu  Arg Arg Trp Phe Val  Glu Val Glu
    2165                2170                2175

Gly Thr  Val Lys Ala Tyr Val  Trp Asp Asn Asn Lys  Asp Leu Ala
    2180                2185                2190

Glu Trp  Leu Glu Lys Gln Leu  Thr Glu Glu Asp Gly  Val His Ser
    2195                2200                2205

Val Ile  Glu Glu Asn Ile Lys  Cys Ile Ser Arg Asp  Tyr Val Leu
    2210                2215                2220

Lys Gln  Ile Arg Ser Leu Val  Gln Ala Asn Pro Glu  Val Ala Met
    2225                2230                2235

Asp Ser  Ile Ile His Met Thr  Gln His Ile Ser Pro  Thr Gln Arg
    2240                2245                2250

Ala Glu  Val Ile Arg Ile Leu  Ser Thr Met Asp Ser  Pro Ser Thr
    2255                2260                2265


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Xaa Glu Ile Arg His Met Phe His Val Ala Trp Val Asp Pro Glu Asp
1 5 10 15

Pro Tyr Lys Gly Tyr Arg Tyr Leu Tyr Leu Thr Pro Gln Asp Tyr Lys
20 25 30

Arg Val Ser Ala Leu Asn Ser Val His Cys Glu His Val Glu Asp Glu
35 40 45

Gly Glu Ser Arg
50

<210> 1266
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Met Trp Trp Ser Thr Leu Met Ser Ile Leu Arg Ala Arg Ser Phe Trp
1 5 10 15

Lys Trp Ile Ser Thr Gln Thr Val Arg Ile Ile Arg Ala Val Arg Ala
20 25 30

His Phe Gly Gly Ile Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu
35 40 45

Glu Leu Asn Gln His Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp
50 55 60

```
Asn Ser Glu Asp Glu Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu
65                  70                  75                  80

Glu Lys Glu Gly Ser Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu
                85                  90                  95

Ser Asp Leu Gly Ile Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile
            100                 105                 110

Arg Leu
```

<210> 1267
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<223> Any amino acid

<400> 1267

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Xaa Ile Lys Cys Ile Ser Arg Asp Tyr Val Leu Lys Gln Ile Arg Ser
1               5                   10                  15

Leu Val Gln Ala Asn Pro Glu Val Ala Met Asp Ser Ile Ile His Met
            20                  25                  30

Thr Gln His Ile Ser Pro Thr Gln Arg Ala Glu Val Ile Arg Ile Leu
        35                  40                  45
```

```
Ser Thr Met Asp Ser Pro Ser Thr Leu Cys Met Thr Ser Trp Asp Val
    50                  55                  60

Arg Ser Gln Asn Pro Pro Pro Ala His Gln Ser His Leu Pro His Ser
65                  70                  75                  80

Val Phe Ile Thr Leu Ala Arg Pro Ser Pro Pro Leu Pro Ala Gln Asp
                85                  90                  95


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Met Glu Gly Ser Pro Glu Glu Asn Lys Glu Met Arg Tyr Tyr Met Leu
1               5                   10                  15

Gln Arg Ser Ser Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp
            20                  25                  30

Arg Lys Lys Ile Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala
        35                  40                  45

Glu Phe Val Thr Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu
    50                  55                  60

Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg
```

65 70 75 80

Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val
85 90 95

Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys
100 105 110

Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn
115 120 125

Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val
130 135 140

Gln Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu
145 150 155 160

Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser
165 170 175

Gln Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala
180 185 190

Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg
195 200 205

Val Asp Trp Gln Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro
210 215 220

Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu
225 230 235 240

Gln Ala Ala Glu Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu
245 250 255

Gly Gly Gly Gly Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe
260 265 270

Pro Asn Leu Phe Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile
275 280 285

Phe Val Met Arg Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile
290 295 300

```
Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys
305                 310                 315                 320

Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr
                325                 330                 335

Ile Ala Thr Pro Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys
            340                 345                 350

Leu Ala Lys Met Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu
        355                 360                 365

Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu
    370                 375                 380

Gln Val Glu His Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro
385                 390                 395                 400

Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys
                405                 410                 415

Asp Ile Arg Met Met Tyr Gly Val Ser Pro Trp Gly Asp Ser Pro Ile
            420                 425                 430

Asp Phe Glu Asp Ser Ala His Val Pro Cys Pro Arg Gly His Val Ile
        435                 440                 445

Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser
    450                 455                 460

Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Asn Lys Asn Val Trp
465                 470                 475                 480

Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly Leu His Glu Phe Ala Asp
                485                 490                 495

Ser Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala
            500                 505                 510

Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp
        515                 520                 525
```

```
Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser
    530                 535                 540

Phe Gln Met Asn Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala
545                 550                 555                 560

Glu Lys Val Gln Ala Glu Arg Pro Asp Thr Met Leu Gly Val Val Cys
                565                 570                 575

Gly Ala Leu His Val Ala Asp Val Ser Leu Arg Asn Ser Val Ser Asn
            580                 585                 590

Phe Leu His Ser Leu Glu Arg Gly Gln Val Leu Pro Ala His Thr Leu
        595                 600                 605

Leu Asn Thr Val Asp Val Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val
    610                 615                 620

Leu Lys Val Thr Arg Gln Ser Pro Asn Ser Tyr Val Val Ile Met Asn
625                 630                 635                 640

Gly Ser Cys Val Glu Val Asp Val His Arg Leu Ser Asp Gly Gly Leu
                645                 650                 655

Leu Leu Ser Tyr Asp Gly Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu
            660                 665                 670

Val Asp Arg Tyr Arg Ile Thr Ile Gly Asn Lys Thr Cys Val Phe Glu
        675                 680                 685

Lys Glu Asn Asp Pro Ser Val Met Arg Ser Pro Ser Ala Gly Lys Leu
    690                 695                 700

Ile Gln Tyr Ile Val Glu Asp Gly Gly His Val Phe Ala Gly Gln Cys
705                 710                 715                 720

Tyr Ala Glu Ile Glu Val Met Lys Met Val Met Thr Leu Thr Ala Val
                725                 730                 735

Glu Ser Gly Cys Ile His Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp
            740                 745                 750
```

```
Pro Gly Cys Val Leu Ala Lys Met Gln Leu Asp Asn Pro Ser Lys Val
        755                 760                 765

Gln Gln Ala Glu Leu His Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr
    770                 775                 780

Ala Leu Arg Gly Glu Lys Leu His Arg Val Phe His Tyr Val Leu Asp
785                 790                 795                 800

Asn Leu Val Asn Val Met Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe
                805                 810                 815

Ser Ser Lys Val Lys Asp Trp Val Glu Arg Leu Met Lys Thr Leu Arg
            820                 825                 830

Asp Pro Ser Leu Pro Leu Leu Glu Leu Gln Asp Ile Met Thr Ser Val
        835                 840                 845

Ser Gly Arg Ile Pro Pro Asn Val Glu Lys Ser Ile Lys Lys Glu Met
    850                 855                 860

Ala Gln Tyr Ala Ser Asn Ile Thr Ser Val Leu Cys Gln Phe Pro Ser
865                 870                 875                 880

Gln Gln Ile Ala Asn Ile Leu Asp Ser His Ala Ala Thr Leu Asn Arg
                885                 890                 895

Lys Ser Glu Arg Glu Val Phe Phe Met Asn Thr Gln Ser Ile Val Gln
            900                 905                 910

Leu Val Gln Arg Tyr Arg Ser Gly Ile Arg Gly His Met Lys Ala Val
        915                 920                 925

Val Met Asp Leu Leu Arg Gln Tyr Leu Arg Val Glu Thr Gln Phe Gln
    930                 935                 940

Asn Gly His Tyr Asp Lys Cys Val Phe Ala Leu Arg Glu Glu Asn Lys
945                 950                 955                 960

Ser Asp Met Asn Thr Val Leu Asn Tyr Ile Phe Ser His Ala Gln Val
                965                 970                 975

Thr Lys Lys Asn Leu Leu Val Thr Met Leu Ile Asp Gln Leu Cys Gly
```

980 985 990

Arg Asp Pro Thr Leu Thr Asp Glu Leu Leu Asn Ile Leu Thr Glu Leu
995 1000 1005

Thr Gln Leu Ser Lys Thr Thr Asn Ala Lys Val Ala Leu Arg Ala
1010 1015 1020

Arg Gln Val Leu Ile Ala Ser His Leu Pro Ser Tyr Glu Leu Arg
1025 1030 1035

His Asn Gln Val Glu Ser Ile Phe Leu Ser Ala Ile Asp Met Tyr
1040 1045 1050

Gly His Gln Phe Cys Ile Glu Asn Leu Gln Lys Leu Ile Leu Ser
1055 1060 1065

Glu Thr Ser Ile Phe Asp Val Leu Pro Asn Phe Phe Tyr His Ser
1070 1075 1080

Asn Gln Val Val Arg Met Ala Ala Leu Glu Val Tyr Val Arg Arg
1085 1090 1095

Ala Tyr Ile Ala Tyr Glu Leu Asn Ser Val Gln His Arg Gln Leu
1100 1105 1110

Lys Asp Asn Thr Cys Val Val Glu Phe Gln Phe Met Leu Pro Thr
1115 1120 1125

Ser His Pro Asn Arg Gly Asn Ile Pro Thr Leu Asn Arg Met Ser
1130 1135 1140

Phe Ser Ser Asn Leu Asn His Tyr Gly Met Thr His Val Ala Ser
1145 1150 1155

Val Ser Asp Val Leu Leu Asp Asn Ser Phe Thr Pro Pro Cys Gln
1160 1165 1170

Arg Met Gly Gly Met Val Ser Phe Arg Thr Phe Glu Asp Phe Val
1175 1180 1185

Arg Ile Phe Asp Glu Val Met Gly Cys Phe Ser Asp Ser Pro Pro

1190 1195 1200

Gln Ser Pro Thr Phe Pro Glu Ala Gly His Thr Ser Leu Tyr Asp
1205 1210 1215

Glu Asp Lys Val Pro Arg Asp Glu Pro Ile His Ile Leu Asn Val
1220 1225 1230

Ala Ile Lys Thr Asp Cys Asp Ile Glu Asp Asp Arg Leu Ala Ala
1235 1240 1245

Met Phe Arg Glu Phe Thr Gln Gln Asn Lys Ala Thr Leu Val Asp
1250 1255 1260

His Gly Ile Arg Arg Leu Thr Phe Leu Val Ala Gln Lys Asp Phe
1265 1270 1275

Arg Lys Gln Val Asn Tyr Glu Val Asp Arg Arg Phe His Arg Glu
1280 1285 1290

Phe Pro Lys Phe Phe Thr Phe Arg Ala Arg Asp Lys Phe Glu Glu
1295 1300 1305

Asp Arg Ile Tyr Arg His Leu Glu Pro Ala Leu Ala Phe Gln Leu
1310 1315 1320

Glu Leu Asn Arg Met Arg Asn Phe Asp Leu Thr Ala Ile Pro Cys
1325 1330 1335

Ala Asn His Lys Met His Leu Tyr Leu Gly Ala Ala Lys Val Glu
1340 1345 1350

Val Gly Thr Glu Val Thr Asp Tyr Arg Phe Phe Val Arg Ala Ile
1355 1360 1365

Ile Arg His Ser Asp Leu Val Thr Lys Glu Ala Ser Phe Glu Tyr
1370 1375 1380

Leu Gln Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp Glu
1385 1390 1395

Leu Glu Val Ala Phe Asn Asn Thr Asn Val Arg Thr Asp Cys Asn
1400 1405 1410

```
His Ile  Phe Leu Asn Phe Val  Pro Thr Val Ile Met  Asp Pro Ser
    1415                1420                1425

Lys Ile  Glu Glu Ser Val Arg  Ser Met Val Met Arg  Tyr Gly Ser
    1430                1435                1440

Arg Leu  Trp Lys Leu Arg Val  Leu Gln Ala Glu Leu  Lys Ile Asn
    1445                1450                1455

Ile Arg  Leu Thr Pro Thr Gly  Lys Ala Ile Pro Ile  Arg Leu Phe
    1460                1465                1470

Leu Thr  Asn Glu Ser Gly Tyr  Tyr Leu Asp Ile Ser  Leu Tyr Lys
    1475                1480                1485

Glu Val  Thr Asp Ser Arg Thr  Ala Gln Ile Met Phe  Gln Ala Tyr
    1490                1495                1500

Gly Asp  Lys Gln Gly Pro Leu  His Gly Met Leu Ile  Asn Thr Pro
    1505                1510                1515

Tyr Val  Thr Lys Asp Leu Leu  Gln Ser Lys Arg Phe  Gln Ala Gln
    1520                1525                1530

Ser Leu  Gly Thr Thr Tyr Ile  Tyr Asp Ile Pro Glu  Met Phe Arg
    1535                1540                1545

Gln Ser  Leu Ile Lys Leu Trp  Glu Ser Met Ser Thr  Gln Ala Phe
    1550                1555                1560

Leu Pro  Ser Pro Pro Leu Pro  Ser Asp Met Leu Thr  Tyr Thr Glu
    1565                1570                1575

Leu Val  Leu Asp Asp Gln Gly  Gln Leu Val His Met  Asn Arg Leu
    1580                1585                1590

Pro Gly  Gly Asn Glu Ile Gly  Met Val Ala Trp Lys  Met Thr Phe
    1595                1600                1605

Lys Ser  Pro Glu Tyr Pro Glu  Gly Arg Asp Ile Ile  Val Ile Gly
    1610                1615                1620
```

```
Asn Asp  Ile Thr Tyr Arg Ile  Gly Ser Phe Gly Pro  Gln Glu Asp
    1625                1630                1635

Leu Leu  Phe Leu Arg Ala Ser  Glu Leu Ala Arg Ala  Glu Gly Ile
    1640                1645                1650

Pro Arg  Ile Tyr Val Ser Ala  Asn Ser Gly Ala Arg  Ile Gly Leu
    1655                1660                1665

Ala Glu  Glu Ile Arg His Met  Phe His Val Ala Trp  Val Asp Pro
    1670                1675                1680

Glu Asp  Pro Tyr Lys Gly Tyr  Arg Tyr Leu Tyr Leu  Thr Pro Gln
    1685                1690                1695

Asp Tyr  Lys Arg Val Ser Ala  Leu Asn Ser Val His  Cys Glu His
    1700                1705                1710

Val Glu  Asp Glu Gly Glu Ser  Arg Tyr Lys Ile Thr  Asp Ile Ile
    1715                1720                1725

Gly Lys  Glu Glu Gly Ile Gly  Pro Glu Asn Leu Arg  Gly Ser Gly
    1730                1735                1740

Met Ile  Ala Gly Glu Ser Ser  Leu Ala Tyr Asn Glu  Ile Ile Thr
    1745                1750                1755

Ile Ser  Leu Val Thr Cys Arg  Ala Ile Gly Ile Gly  Ala Tyr Leu
    1760                1765                1770

Val Arg  Leu Gly Gln Arg Thr  Ile Gln Val Glu Asn  Ser His Leu
    1775                1780                1785

Ile Leu  Thr Gly Ala Gly Ala  Leu Asn Lys Val Leu  Gly Arg Glu
    1790                1795                1800

Val Tyr  Thr Ser Asn Asn Gln  Leu Gly Gly Ile Gln  Ile Met His
    1805                1810                1815

Asn Asn  Gly Val Thr His Cys  Thr Val Cys Asp Asp  Phe Glu Gly
    1820                1825                1830
```

```
Val Phe  Thr Val Leu His Trp  Leu Ser Tyr Met Pro  Lys Ser Val
    1835                1840                1845

His Ser  Ser Val Pro Leu Leu  Asn Ser Lys Asp Pro  Ile Asp Arg
    1850                1855                1860

Ile Ile  Glu Phe Val Pro Thr  Lys Thr Pro Tyr Asp  Pro Arg Trp
    1865                1870                1875

Met Leu  Ala Gly Arg Pro His  Pro Thr Gln Lys Gly  Gln Trp Leu
    1880                1885                1890

Ser Gly  Phe Phe Asp Tyr Gly  Ser Phe Ser Glu Ile  Met Gln Pro
    1895                1900                1905

Trp Ala  Gln Thr Val Val Val  Gly Arg Ala Arg Leu  Gly Gly Ile
    1910                1915                1920

Pro Val  Gly Val Val Ala Val  Glu Thr Arg Thr Val  Glu Leu Ser
    1925                1930                1935

Ile Pro  Ala Asp Pro Ala Asn  Leu Asp Ser Glu Ala  Lys Ile Ile
    1940                1945                1950

Gln Gln  Ala Gly Gln Val Trp  Phe Pro Asp Ser Ala  Phe Lys Thr
    1955                1960                1965

Tyr Gln  Ala Ile Lys Asp Phe  Asn Arg Glu Gly Leu  Pro Leu Met
    1970                1975                1980

Val Phe  Ala Asn Trp Arg Gly  Phe Ser Gly Gly Met  Lys Asp Met
    1985                1990                1995

Tyr Asp  Gln Val Leu Lys Phe  Gly Ala Tyr Ile Val  Asp Gly Leu
    2000                2005                2010

Arg Glu  Cys Cys Gln Pro Val  Leu Val Tyr Ile Pro  Pro Gln Ala
    2015                2020                2025

Glu Leu  Arg Gly Gly Ser Trp  Val Val Ile Asp Ser  Ser Ile Asn
    2030                2035                2040

Pro Arg  His Met Glu Met Tyr  Ala Asp Arg Glu Ser  Arg Gly Ser
```

2045 2050 2055

Val Leu Glu Pro Glu Gly Thr Val Glu Ile Lys Phe Arg Arg Lys
2060 2065 2070

Asp Leu Val Lys Thr Met Arg Arg Val Asp Pro Val Tyr Ile His
2075 2080 2085

Leu Ala Glu Arg Leu Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg
2090 2095 2100

Lys Glu Leu Glu Asn Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile
2105 2110 2115

Pro Ile Tyr His Gln Val Ala Val Gln Phe Ala Asp Leu His Asp
2120 2125 2130

Thr Pro Gly Arg Met Gln Glu Lys Gly Val Ile Ser Asp Ile Leu
2135 2140 2145

Asp Trp Lys Thr Ser Arg Thr Phe Phe Tyr Trp Arg Leu Arg Arg
2150 2155 2160

Leu Leu Leu Glu Asp Leu Val Lys Lys Lys Ile His Asn Ala Asn
2165 2170 2175

Pro Glu Leu Thr Asp Gly Gln Ile Gln Ala Met Leu Arg Arg Trp
2180 2185 2190

Phe Val Glu Val Glu Gly Thr Val Lys Ala Tyr Val Trp Asp Asn
2195 2200 2205

Asn Lys Asp Leu Ala Glu Trp Leu Glu Lys Gln Leu Thr Glu Glu
2210 2215 2220

Asp Gly Val His Ser Val Ile Glu Glu Asn Ile Lys Cys Ile Ser
2225 2230 2235

Arg Asp Tyr Val Leu Lys Gln Ile Arg Ser Leu Val Gln Ala Asn
2240 2245 2250

Pro Glu Val Ala Met Asp Ser Ile Ile His Met Thr Gln His Ile
2255 2260 2265

Ser Pro Thr Gln Arg Ala Glu Val Ile Arg Ile Leu Ser Thr Met
2270 2275 2280

Asp Ser Pro Ser Thr
2285

<210> 1269
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<213> Homo sapiens

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Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr
20 25 30

Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn
35 40 45

Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr
50 55 60

Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr
65 70 75 80

```
Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His
                85                  90                  95

Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val
            100                 105                 110

Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp
        115                 120                 125

Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu
    130                 135                 140

Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp
145                 150                 155                 160

Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly
                165                 170                 175

Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln
            180                 185                 190

Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr
        195                 200                 205

Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Gln Ala Ala Glu
    210                 215                 220

Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly
225                 230                 235                 240

Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe
                245                 250                 255

Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg
            260                 265                 270

Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln
        275                 280                 285

Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg
    290                 295                 300

Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro
```

305 310 315 320

Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met
325 330 335

Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp
340 345 350

Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His
355 360 365

Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu
370 375 380

Gln Ile Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met
385 390 395 400

Met Tyr Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp
405 410 415

Ser Ala His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile
420 425 430

Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val
435 440 445

Gln Glu Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser
450 455 460

Val Ala Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly
465 470 475 480

His Cys Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met
485 490 495

Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr
500 505 510

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn
515 520 525

Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln
530 535 540

```
Ala Glu Arg Pro Asp Thr Met Leu Gly Val Val Cys Gly Ala Leu His
545                 550                 555                 560

Val Ala Asp Val Ser Leu Arg Asn Ser Val Ser Asn Phe Leu His Ser
                565                 570                 575

Leu Glu Arg Gly Gln Val Leu Pro Ala His Thr Leu Leu Asn Thr Val
            580                 585                 590

Asp Val Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val Leu Lys Val Thr
        595                 600                 605

Arg Gln Ser Pro Asn Ser Tyr Val Val Ile Met Asn Gly Ser Cys Val
    610                 615                 620

Glu Val Asp Val His Arg Leu Ser Asp Gly Gly Leu Leu Leu Ser Tyr
625                 630                 635                 640

Asp Gly Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Arg Tyr
                645                 650                 655

Arg Ile Thr Ile Gly Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp
            660                 665                 670

Pro Ser Val Met Arg Ser Pro Ser Ala Gly Lys Leu Ile Gln Tyr Ile
        675                 680                 685

Val Glu Asp Gly Gly His Val Phe Ala Gly Gln Cys Tyr Ala Glu Ile
    690                 695                 700

Glu Val Met Lys Met Val Met Thr Leu Thr Ala Val Glu Ser Gly Cys
705                 710                 715                 720

Ile His Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp Pro Gly Cys Val
                725                 730                 735

Leu Ala Lys Met Gln Leu Asp Asn Pro Ser Lys Val Gln Gln Ala Glu
            740                 745                 750

Leu His Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr Ala Leu Arg Gly
        755                 760                 765
```

```
Glu Lys Leu His Arg Val Phe His Tyr Val Leu Asp Asn Leu Val Asn
    770                 775                 780

Val Met Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe Ser Ser Lys Val
785                 790                 795                 800

Lys Asp Trp Val Glu Arg Leu Met Lys Thr Leu Arg Asp Pro Ser Leu
                805                 810                 815

Pro Leu Leu Glu Leu Gln Asp Ile Met Thr Ser Val Ser Gly Arg Ile
            820                 825                 830

Pro Pro Asn Val Glu Lys Ser Ile Lys Lys Glu Met Ala Gln Tyr Ala
        835                 840                 845

Ser Asn Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln Gln Ile Ala
    850                 855                 860

Asn Ile Leu Asp Ser His Ala Ala Thr Leu Asn Arg Lys Ser Glu Arg
865                 870                 875                 880

Glu Val Phe Phe Met Asn Thr Gln Ser Ile Val Gln Leu Val Gln Arg
                885                 890                 895

Tyr Arg Ser Gly Ile Arg Gly His Met Lys Ala Val Val Met Asp Leu
            900                 905                 910

Leu Arg Gln Tyr Leu Arg Val Glu Thr Gln Phe Gln Asn Gly His Tyr
        915                 920                 925

Asp Lys Cys Val Phe Ala Leu Arg Glu Glu Asn Lys Ser Asp Met Asn
    930                 935                 940

Thr Val Leu Asn Tyr Ile Phe Ser His Ala Gln Val Thr Lys Lys Asn
945                 950                 955                 960

Leu Leu Val Thr Met Leu Ile Asp Gln Leu Cys Gly Arg Asp Pro Thr
                965                 970                 975

Leu Thr Asp Glu Leu Leu Asn Ile Leu Thr Glu Leu Thr Gln Leu Ser
            980                 985                 990
```

Lys Thr Thr Asn Ala Lys Val Ala Leu Arg Ala Arg Gln Val Leu
Ile
995 1000 1005

Ala Ser His Leu Pro Ser Tyr Glu Leu Arg His Asn Gln Val Glu
1010 1015 1020

Ser Ile Phe Leu Ser Ala Ile Asp Met Tyr Gly His Gln Phe Cys
1025 1030 1035

Ile Glu Asn Leu Gln Lys Leu Ile Leu Ser Glu Thr Ser Ile Phe
1040 1045 1050

Asp Val Leu Pro Asn Phe Phe Tyr His Ser Asn Gln Val Val Arg
1055 1060 1065

Met Ala Ala Leu Glu Val Tyr Val Arg Arg Ala Tyr Ile Ala Tyr
1070 1075 1080

Glu Leu Asn Ser Val Gln His Arg Gln Leu Lys Asp Asn Thr Cys
1085 1090 1095

Val Val Glu Phe Gln Phe Met Leu Pro Thr Ser His Pro Asn Arg
1100 1105 1110

Gly Asn Ile Pro Thr Leu Asn Arg Met Ser Phe Ser Ser Asn Leu
1115 1120 1125

Asn His Tyr Gly Met Thr His Val Ala Ser Val Ser Asp Val Leu
1130 1135 1140

Leu Asp Asn Ser Phe Thr Pro Pro Cys Gln Arg Met Gly Gly Met
1145 1150 1155

Val Ser Phe Arg Thr Phe Glu Asp Phe Val Arg Ile Phe Asp Glu
1160 1165 1170

Val Met Gly Cys Phe Ser Asp Ser Pro Pro Gln Ser Pro Thr Phe
1175 1180 1185

Pro Glu Ala Gly His Thr Ser Leu Tyr Asp Glu Asp Lys Val Pro
1190 1195 1200

```
Arg Asp  Glu Pro Ile His Ile  Leu Asn Val Ala Ile  Lys Thr Asp
    1205                 1210                 1215

Cys Asp  Ile Glu Asp Asp Arg  Leu Ala Ala Met Phe  Arg Glu Phe
    1220                 1225                 1230

Thr Gln  Gln Asn Lys Ala Thr  Leu Val Asp His Gly  Ile Arg Arg
    1235                 1240                 1245

Leu Thr  Phe Leu Val Ala Gln  Lys Asp Phe Arg Lys  Gln Val Asn
    1250                 1255                 1260

Tyr Glu  Val Asp Arg Arg Phe  His Arg Glu Phe Pro  Lys Phe Phe
    1265                 1270                 1275

Thr Phe  Arg Ala Arg Asp Lys  Phe Glu Glu Asp Arg  Ile Tyr Arg
    1280                 1285                 1290

His Leu  Glu Pro Ala Leu Ala  Phe Gln Leu Glu Leu  Asn Arg Met
    1295                 1300                 1305

Arg Asn  Phe Asp Leu Thr Ala  Ile Pro Cys Ala Asn  His Lys Met
    1310                 1315                 1320

His Leu  Tyr Leu Gly Ala Ala  Lys Val Glu Val Gly  Thr Glu Val
    1325                 1330                 1335

Thr Asp  Tyr Arg Phe Phe Val  Arg Ala Ile Ile Arg  His Ser Asp
    1340                 1345                 1350

Leu Val  Thr Lys Glu Ala Ser  Phe Glu Tyr Leu Gln  Asn Glu Gly
    1355                 1360                 1365

Glu Arg  Leu Leu Leu Glu Ala  Met Asp Glu Leu Glu  Val Ala Phe
    1370                 1375                 1380

Asn Asn  Thr Asn Val Arg Thr  Asp Cys Asn His Ile  Phe Leu Asn
    1385                 1390                 1395

Phe Val  Pro Thr Val Ile Met  Asp Pro Ser Lys Ile  Glu Glu Ser
    1400                 1405                 1410

Val Arg  Ser Met Val Met Arg  Tyr Gly Ser Arg Leu  Trp Lys Leu
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1415 1420 1425

Arg Val Leu Gln Ala Glu Leu Lys Ile Asn Ile Arg Leu Thr Pro
1430 1435 1440

Thr Gly Lys Ala Ile Pro Ile Arg Leu Phe Leu Thr Asn Glu Ser
1445 1450 1455

Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr Asp Ser
1460 1465 1470

Arg Thr Ala Gln Ile Met Phe Gln Ala Tyr Gly Asp Lys Gln Gly
1475 1480 1485

Pro Leu His Gly Met Leu Ile Asn Thr Pro Tyr Val Thr Lys Asp
1490 1495 1500

Leu Leu Gln Ser Lys Arg Phe Gln Ala Gln Ser Leu Gly Thr Thr
1505 1510 1515

Tyr Ile Tyr Asp Ile Pro Glu Met Phe Arg Gln Ser Leu Ile Lys
1520 1525 1530

Leu Trp Glu Ser Met Ser Thr Gln Ala Phe Leu Pro Ser Pro Pro
1535 1540 1545

Leu Pro Ser Asp Met Leu Thr Tyr Thr Glu Leu Val Leu Asp Asp
1550 1555 1560

Gln Gly Gln Leu Val His Met Asn Arg Leu Pro Gly Gly Asn Glu
1565 1570 1575

Ile Gly Met Val Ala Trp Lys Met Thr Phe Lys Ser Pro Glu Tyr
1580 1585 1590

Pro Glu Gly Arg Asp Ile Ile Val Ile Gly Asn Asp Ile Thr Tyr
1595 1600 1605

Arg Ile Gly Ser Phe Gly Pro Gln Glu Asp Leu Leu Phe Leu Arg
1610 1615 1620

Ala Ser Glu Leu Ala Arg Ala Glu Gly Ile Pro Arg Ile Tyr Val
1625 1630 1635

```
Ser Ala  Asn Ser Gly Ala Arg  Ile Gly Leu Ala Glu  Glu Ile Arg
    1640                 1645                 1650

His Met  Phe His Val Ala Trp  Val Asp Pro Glu Asp  Pro Tyr Lys
    1655                 1660                 1665

Gly Tyr  Arg Tyr Leu Tyr Leu  Thr Pro Gln Asp Tyr  Lys Arg Val
    1670                 1675                 1680

Ser Ala  Leu Asn Ser Val His  Cys Glu His Val Glu  Asp Glu Gly
    1685                 1690                 1695

Glu Ser  Arg Tyr Lys Ile Thr  Asp Ile Ile Gly Lys  Glu Glu Gly
    1700                 1705                 1710

Ile Gly  Pro Glu Asn Leu Arg  Gly Ser Gly Met Ile  Ala Gly Glu
    1715                 1720                 1725

Ser Ser  Leu Ala Tyr Asn Glu  Ile Ile Thr Ile Ser  Leu Val Thr
    1730                 1735                 1740

Cys Arg  Ala Ile Gly Ile Gly  Ala Tyr Leu Val Arg  Leu Gly Gln
    1745                 1750                 1755

Arg Thr  Ile Gln Val Glu Asn  Ser His Leu Ile Leu  Thr Gly Ala
    1760                 1765                 1770

Gly Ala  Leu Asn Lys Val Leu  Gly Arg Glu Val Tyr  Thr Ser Asn
    1775                 1780                 1785

Asn Gln  Leu Gly Gly Ile Gln  Ile Met His Asn Asn  Gly Val Thr
    1790                 1795                 1800

His Cys  Thr Val Cys Asp Asp  Phe Glu Gly Val Phe  Thr Val Leu
    1805                 1810                 1815

His Trp  Leu Ser Tyr Met Pro  Lys Ser Val His Ser  Ser Val Pro
    1820                 1825                 1830

Leu Leu  Asn Ser Lys Asp Pro  Ile Asp Arg Ile Ile  Glu Phe Val
    1835                 1840                 1845
```

Pro Thr Lys Thr Pro Tyr Asp Pro Arg Trp Met Leu Ala Gly Arg
1850 1855 1860

Pro His Pro Thr Gln Lys Gly Gln Trp Leu Ser Gly Phe Phe Asp
1865 1870 1875

Tyr Gly Ser Phe Ser Glu Ile Met Gln Pro Trp Ala Gln Thr Val
1880 1885 1890

Val Val Gly Arg Ala Arg Leu Gly Gly Ile Pro Val Gly Val Val
1895 1900 1905

Ala Val Glu Thr Arg Thr Val Glu Leu Ser Ile Pro Ala Asp Pro
1910 1915 1920

Ala Asn Leu Asp Ser Glu Ala Lys Ile Ile Gln Gln Ala Gly Gln
1925 1930 1935

Val Trp Phe Pro Asp Ser Ala Phe Lys Thr Tyr Gln Ala Ile Lys
1940 1945 1950

Asp Phe Asn Arg Glu Gly Leu Pro Leu Met Val Phe Ala Asn Trp
1955 1960 1965

Arg Gly Phe Ser Gly Gly Met Lys Asp Met Tyr Asp Gln Val Leu
1970 1975 1980

Lys Phe Gly Ala Tyr Ile Val Asp Gly Leu Arg Glu Cys Cys Gln
1985 1990 1995

Pro Val Leu Val Tyr Ile Pro Pro Gln Ala Glu Leu Arg Gly Gly
2000 2005 2010

Ser Trp Val Val Ile Asp Ser Ser Ile Asn Pro Arg His Met Glu
2015 2020 2025

Met Tyr Ala Asp Arg Glu Ser Arg Gly Ser Val Leu Glu Pro Glu
2030 2035 2040

Gly Thr Val Glu Ile Lys Phe Arg Arg Lys Asp Leu Val Lys Thr
2045 2050 2055

Met Arg Arg Val Asp Pro Val Tyr Ile His Leu Ala Glu Arg Leu
2060 2065 2070

Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg Lys Glu Leu Glu Asn
2075 2080 2085

Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile Pro Ile Tyr His Gln
2090 2095 2100

Val Ala Val Gln Phe Ala Asp Leu His Asp Thr Pro Gly Arg Met
2105 2110 2115

Gln Glu Lys Gly Val Ile Ser Asp Ile Leu Asp Trp Lys Thr Ser
2120 2125 2130

Arg Thr Phe Phe Tyr Trp Arg Leu Arg Arg Leu Leu Leu Glu Asp
2135 2140 2145

Leu Val Lys Lys Lys Ile His Asn Ala Asn Pro Glu Leu Thr Asp
2150 2155 2160

Gly Gln Ile Gln Ala Met Leu Arg Arg Trp Phe Val Glu Val Glu
2165 2170 2175

Gly Thr Val Lys Ala Tyr Val Trp Asp Asn Asn Lys Asp Leu Ala
2180 2185 2190

Glu Trp Leu Glu Lys Gln Leu Thr Glu Glu Asp Gly Val His Ser
2195 2200 2205

Val Ile Glu Glu Asn Ile Lys Cys Ile Ser Arg Asp Tyr Val Leu
2210 2215 2220

Lys Gln Ile Arg Ser Leu Val Gln Ala Asn Pro Glu Val Ala Met
2225 2230 2235

Asp Ser Ile Ile His Met Thr Gln His Ile Ser Pro Thr Gln Arg
2240 2245 2250

Ala Glu Val Ile Arg Ile Leu Ser Thr Met Asp Ser Pro Ser Thr
2255 2260 2265

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<223> /note="Gene Name:
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<400> 1270

Met	Trp	Trp	Ser	Thr	Leu	Met	Ser	Ile	Leu	Arg	Ala	Arg	Ser	Phe	Trp
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Lys	Trp	Ile	Ser	Thr	Gln	Thr	Val	Arg	Ile	Ile	Arg	Ala	Val	Arg	Ala
		20					25					30			

His	Phe	Gly	Gly	Ile	Met	Asp	Glu	Pro	Ser	Pro	Leu	Ala	Gln	Pro	Leu
		35					40					45			

Glu	Leu	Asn	Gln	His	Ser	Arg	Phe	Ile	Ile	Gly	Ser	Val	Ser	Glu	Asp
	50					55					60				

Asn	Ser	Glu	Asp	Glu	Ile	Ser	Asn	Leu	Val	Lys	Leu	Asp	Leu	Leu	Glu
65					70					75					80

Glu	Lys	Glu	Gly	Ser	Leu	Ser	Pro	Ala	Ser	Val	Gly	Ser	Asp	Thr	Leu
				85					90					95	

Ser	Asp	Leu	Gly	Ile	Ser	Ser	Leu	Gln	Asp	Gly	Leu	Ala	Leu	His	Ile
			100					105					110		

Arg	Leu

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Met	Trp	Trp	Ser	Thr	Leu	Met	Ser	Ile	Leu	Arg	Ala	Arg	Ser	Phe	Trp
1				5				10						15	

Lys	Trp	Ile	Ser	Thr	Gln	Thr	Val	Arg	Ile	Ile	Arg	Ala	Val	Arg	Ala
		20					25					30			

His	Phe	Gly	Gly	Ile	Met	Asp	Glu	Pro	Ser	Pro	Leu	Ala	Gln	Pro	Leu
		35					40					45			

Glu	Leu	Asn	Gln	His	Ser	Arg	Phe	Ile	Ile	Gly	Ser	Val	Ser	Glu	Asp
	50					55					60				

Asn	Ser	Glu	Asp	Glu	Ile	Ser	Asn	Leu	Val	Lys	Leu	Asp	Leu	Leu	Glu
65				70					75					80	

Glu	Lys	Glu	Gly	Ser	Leu	Ser	Pro	Ala	Ser	Val	Gly	Ser	Asp	Thr	Leu
				85					90					95	

Ser	Asp	Leu	Gly	Ile	Ser	Ser	Leu	Gln	Asp	Gly	Leu	Ala	Leu	His	Ile
			100					105					110		

Arg	Ser	Ser	Met	Ser	Gly	Leu	His	Leu	Val	Lys	Gln	Gly	Arg	Asp	Arg
		115					120					125			

Lys	Lys	Ile	Asp	Ser	Gln	Arg	Asp	Phe	Thr	Val	Ala	Ser	Pro	Ala	Glu

```
    130                 135                 140

Phe Val Thr Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile
145                 150                 155                 160

Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg
                165                 170                 175

Trp Ser Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val
            180                 185                 190

Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met
        195                 200                 205

Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr
    210                 215                 220

Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln
225                 230                 235                 240

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro
                245                 250                 255

Glu Leu Leu Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln
            260                 265                 270

Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln
        275                 280                 285

Thr Ala Gly Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val
    290                 295                 300

Asp Trp Gln Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln
305                 310                 315                 320

Glu Leu Tyr Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Gln
                325                 330                 335

Ala Ala Glu Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly
            340                 345                 350

Gly Gly Gly Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro
        355                 360                 365
```

```
Asn Leu Phe Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe
    370                 375                 380

Val Met Arg Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu
385                 390                 395                 400

Ala Asp Gln Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser
                405                 410                 415

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile
            420                 425                 430

Ala Thr Pro Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys Leu
        435                 440                 445

Ala Lys Met Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr
    450                 455                 460

Ser Gln Asp Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
465                 470                 475                 480

Val Glu His Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala
                485                 490                 495

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp
            500                 505                 510

Ile Arg Met Met Tyr Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp
        515                 520                 525

Phe Glu Asp Ser Ala His Val Pro Cys Pro Arg Gly His Val Ile Ala
    530                 535                 540

Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser
545                 550                 555                 560

Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly
                565                 570                 575

Tyr Phe Ser Val Ala Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser
            580                 585                 590
```

```
Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile
        595                 600                 605

Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
    610                 615                 620

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe
625                 630                 635                 640

Gln Met Asn Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu
                645                 650                 655

Lys Val Gln Ala Glu Arg Pro Asp Thr Met Leu Gly Val Val Cys Gly
            660                 665                 670

Ala Leu His Val Ala Asp Val Ser Leu Arg Asn Ser Val Ser Asn Phe
        675                 680                 685

Leu His Ser Leu Glu Arg Gly Gln Val Leu Pro Ala His Thr Leu Leu
    690                 695                 700

Asn Thr Val Asp Val Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val Leu
705                 710                 715                 720

Lys Val Thr Arg Gln Ser Pro Asn Ser Tyr Val Val Ile Met Asn Gly
                725                 730                 735

Ser Cys Val Glu Val Asp Val His Arg Leu Ser Asp Gly Gly Leu Leu
            740                 745                 750

Leu Ser Tyr Asp Gly Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val
        755                 760                 765

Asp Arg Tyr Arg Ile Thr Ile Gly Asn Lys Thr Cys Val Phe Glu Lys
    770                 775                 780

Glu Asn Asp Pro Ser Val Met Arg Ser Pro Ser Ala Gly Lys Leu Ile
785                 790                 795                 800

Gln Tyr Ile Val Glu Asp Gly Gly His Val Phe Ala Gly Gln Cys Tyr
                805                 810                 815
```

```
Ala Glu Ile Glu Val Met Lys Met Val Met Thr Leu Thr Ala Val Glu
            820                 825                 830

Ser Gly Cys Ile His Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp Pro
        835                 840                 845

Gly Cys Val Leu Ala Lys Met Gln Leu Asp Asn Pro Ser Lys Val Gln
    850                 855                 860

Gln Ala Glu Leu His Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr Ala
865                 870                 875                 880

Leu Arg Gly Glu Lys Leu His Arg Val Phe His Tyr Val Leu Asp Asn
                885                 890                 895

Leu Val Asn Val Met Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe Ser
            900                 905                 910

Ser Lys Val Lys Asp Trp Val Glu Arg Leu Met Lys Thr Leu Arg Asp
        915                 920                 925

Pro Ser Leu Pro Leu Leu Glu Leu Gln Asp Ile Met Thr Ser Val Ser
    930                 935                 940

Gly Arg Ile Pro Pro Asn Val Glu Lys Ser Ile Lys Lys Glu Met Ala
945                 950                 955                 960

Gln Tyr Ala Ser Asn Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln
                965                 970                 975

Gln Ile Ala Asn Ile Leu Asp Ser His Ala Ala Thr Leu Asn Arg Lys
            980                 985                 990

Ser Glu Arg Glu Val Phe Phe Met  Asn Thr Gln Ser Ile  Val Gln
Leu
        995                 1000                1005

Val Gln  Arg Tyr Arg Ser Gly  Ile Arg Gly His Met  Lys Ala Val
    1010                1015                1020

Val Met  Asp Leu Leu Arg Gln  Tyr Leu Arg Val Glu  Thr Gln Phe
    1025                1030                1035
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Gln Asn Gly His Tyr Asp Lys Cys Val Phe Ala Leu Arg Glu Glu
1040 1045 1050

Asn Lys Ser Asp Met Asn Thr Val Leu Asn Tyr Ile Phe Ser His
1055 1060 1065

Ala Gln Val Thr Lys Lys Asn Leu Leu Val Thr Met Leu Ile Asp
1070 1075 1080

Gln Leu Cys Gly Arg Asp Pro Thr Leu Thr Asp Glu Leu Leu Asn
1085 1090 1095

Ile Leu Thr Glu Leu Thr Gln Leu Ser Lys Thr Thr Asn Ala Lys
1100 1105 1110

Val Ala Leu Arg Ala Arg Gln Val Leu Ile Ala Ser His Leu Pro
1115 1120 1125

Ser Tyr Glu Leu Arg His Asn Gln Val Glu Ser Ile Phe Leu Ser
1130 1135 1140

Ala Ile Asp Met Tyr Gly His Gln Phe Cys Ile Glu Asn Leu Gln
1145 1150 1155

Lys Leu Ile Leu Ser Glu Thr Ser Ile Phe Asp Val Leu Pro Asn
1160 1165 1170

Phe Phe Tyr His Ser Asn Gln Val Val Arg Met Ala Ala Leu Glu
1175 1180 1185

Val Tyr Val Arg Arg Ala Tyr Ile Ala Tyr Glu Leu Asn Ser Val
1190 1195 1200

Gln His Arg Gln Leu Lys Asp Asn Thr Cys Val Val Glu Phe Gln
1205 1210 1215

Phe Met Leu Pro Thr Ser His Pro Asn Arg Gly Asn Ile Pro Thr
1220 1225 1230

Leu Asn Arg Met Ser Phe Ser Ser Asn Leu Asn His Tyr Gly Met
1235 1240 1245

Thr His Val Ala Ser Val Ser Asp Val Leu Leu Asp Asn Ser Phe

1250 1255 1260

Thr Pro Pro Cys Gln Arg Met Gly Gly Met Val Ser Phe Arg Thr
1265 1270 1275

Phe Glu Asp Phe Val Arg Ile Phe Asp Glu Val Met Gly Cys Phe
1280 1285 1290

Ser Asp Ser Pro Pro Gln Ser Pro Thr Phe Pro Glu Ala Gly His
1295 1300 1305

Thr Ser Leu Tyr Asp Glu Asp Lys Val Pro Arg Asp Glu Pro Ile
1310 1315 1320

His Ile Leu Asn Val Ala Ile Lys Thr Asp Cys Asp Ile Glu Asp
1325 1330 1335

Asp Arg Leu Ala Ala Met Phe Arg Glu Phe Thr Gln Gln Asn Lys
1340 1345 1350

Ala Thr Leu Val Asp His Gly Ile Arg Arg Leu Thr Phe Leu Val
1355 1360 1365

Ala Gln Lys Asp Phe Arg Lys Gln Val Asn Tyr Glu Val Asp Arg
1370 1375 1380

Arg Phe His Arg Glu Phe Pro Lys Phe Phe Thr Phe Arg Ala Arg
1385 1390 1395

Asp Lys Phe Glu Glu Asp Arg Ile Tyr Arg His Leu Glu Pro Ala
1400 1405 1410

Leu Ala Phe Gln Leu Glu Leu Asn Arg Met Arg Asn Phe Asp Leu
1415 1420 1425

Thr Ala Ile Pro Cys Ala Asn His Lys Met His Leu Tyr Leu Gly
1430 1435 1440

Ala Ala Lys Val Glu Val Gly Thr Glu Val Thr Asp Tyr Arg Phe
1445 1450 1455

Phe Val Arg Ala Ile Ile Arg His Ser Asp Leu Val Thr Lys Glu
1460 1465 1470

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Ala Ser  Phe Glu Tyr Leu Gln  Asn Glu Gly Glu Arg  Leu Leu Leu
    1475                1480                1485

Glu Ala  Met Asp Glu Leu Glu  Val Ala Phe Asn Asn  Thr Asn Val
    1490                1495                1500

Arg Thr  Asp Cys Asn His Ile  Phe Leu Asn Phe Val  Pro Thr Val
    1505                1510                1515

Ile Met  Asp Pro Ser Lys Ile  Glu Glu Ser Val Arg  Ser Met Val
    1520                1525                1530

Met Arg  Tyr Gly Ser Arg Leu  Trp Lys Leu Arg Val  Leu Gln Ala
    1535                1540                1545

Glu Leu  Lys Ile Asn Ile Arg  Leu Thr Pro Thr Gly  Lys Ala Ile
    1550                1555                1560

Pro Ile  Arg Leu Phe Leu Thr  Asn Glu Ser Gly Tyr  Tyr Leu Asp
    1565                1570                1575

Ile Ser  Leu Tyr Lys Glu Val  Thr Asp Ser Arg Thr  Ala Gln Ile
    1580                1585                1590

Met Phe  Gln Ala Tyr Gly Asp  Lys Gln Gly Pro Leu  His Gly Met
    1595                1600                1605

Leu Ile  Asn Thr Pro Tyr Val  Thr Lys Asp Leu Leu  Gln Ser Lys
    1610                1615                1620

Arg Phe  Gln Ala Gln Ser Leu  Gly Thr Thr Tyr Ile  Tyr Asp Ile
    1625                1630                1635

Pro Glu  Met Phe Arg Gln Ser  Leu Ile Lys Leu Trp  Glu Ser Met
    1640                1645                1650

Ser Thr  Gln Ala Phe Leu Pro  Ser Pro Pro Leu Pro  Ser Asp Met
    1655                1660                1665

Leu Thr  Tyr Thr Glu Leu Val  Leu Asp Asp Gln Gly  Gln Leu Val
    1670                1675                1680
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His Met  Asn Arg Leu Pro Gly  Gly Asn Glu Ile Gly  Met Val Ala
    1685                1690                1695

Trp Lys  Met Thr Phe Lys Ser  Pro Glu Tyr Pro Glu  Gly Arg Asp
    1700                1705                1710

Ile Ile  Val Ile Gly Asn Asp  Ile Thr Tyr Arg Ile  Gly Ser Phe
    1715                1720                1725

Gly Pro  Gln Glu Asp Leu Leu  Phe Leu Arg Ala Ser  Glu Leu Ala
    1730                1735                1740

Arg Ala  Glu Gly Ile Pro Arg  Ile Tyr Val Ser Ala  Asn Ser Gly
    1745                1750                1755

Ala Arg  Ile Gly Leu Ala Glu  Glu Ile Arg His Met  Phe His Val
    1760                1765                1770

Ala Trp  Val Asp Pro Glu Asp  Pro Tyr Lys Gly Tyr  Arg Tyr Leu
    1775                1780                1785

Tyr Leu  Thr Pro Gln Asp Tyr  Lys Arg Val Ser Ala  Leu Asn Ser
    1790                1795                1800

Val His  Cys Glu His Val Glu  Asp Glu Gly Glu Ser  Arg Tyr Lys
    1805                1810                1815

Ile Thr  Asp Ile Ile Gly Lys  Glu Glu Gly Ile Gly  Pro Glu Asn
    1820                1825                1830

Leu Arg  Gly Ser Gly Met Ile  Ala Gly Glu Ser Ser  Leu Ala Tyr
    1835                1840                1845

Asn Glu  Ile Ile Thr Ile Ser  Leu Val Thr Cys Arg  Ala Ile Gly
    1850                1855                1860

Ile Gly  Ala Tyr Leu Val Arg  Leu Gly Gln Arg Thr  Ile Gln Val
    1865                1870                1875

Glu Asn  Ser His Leu Ile Leu  Thr Gly Ala Gly Ala  Leu Asn Lys
    1880                1885                1890
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Val Leu Gly Arg Glu Val Tyr Thr Ser Asn Asn Gln Leu Gly Gly
1895 1900 1905

Ile Gln Ile Met His Asn Asn Gly Val Thr His Cys Thr Val Cys
1910 1915 1920

Asp Asp Phe Glu Gly Val Phe Thr Val Leu His Trp Leu Ser Tyr
1925 1930 1935

Met Pro Lys Ser Val His Ser Ser Val Pro Leu Leu Asn Ser Lys
1940 1945 1950

Asp Pro Ile Asp Arg Ile Ile Glu Phe Val Pro Thr Lys Thr Pro
1955 1960 1965

Tyr Asp Pro Arg Trp Met Leu Ala Gly Arg Pro His Pro Thr Gln
1970 1975 1980

Lys Gly Gln Trp Leu Ser Gly Phe Phe Asp Tyr Gly Ser Phe Ser
1985 1990 1995

Glu Ile Met Gln Pro Trp Ala Gln Thr Val Val Val Gly Arg Ala
2000 2005 2010

Arg Leu Gly Gly Ile Pro Val Gly Val Val Ala Val Glu Thr Arg
2015 2020 2025

Thr Val Glu Leu Ser Ile Pro Ala Asp Pro Ala Asn Leu Asp Ser
2030 2035 2040

Glu Ala Lys Ile Ile Gln Gln Ala Gly Gln Val Trp Phe Pro Asp
2045 2050 2055

Ser Ala Phe Lys Thr Tyr Gln Ala Ile Lys Asp Phe Asn Arg Glu
2060 2065 2070

Gly Leu Pro Leu Met Val Phe Ala Asn Trp Arg Gly Phe Ser Gly
2075 2080 2085

Gly Met Lys Asp Met Tyr Asp Gln Val Leu Lys Phe Gly Ala Tyr
2090 2095 2100

Ile Val Asp Gly Leu Arg Glu Cys Cys Gln Pro Val Leu Val Tyr

2105 2110 2115

Ile Pro Pro Gln Ala Glu Leu Arg Gly Gly Ser Trp Val Val Ile
2120 2125 2130

Asp Ser Ser Ile Asn Pro Arg His Met Glu Met Tyr Ala Asp Arg
2135 2140 2145

Glu Ser Arg Gly Ser Val Leu Glu Pro Glu Gly Thr Val Glu Ile
2150 2155 2160

Lys Phe Arg Arg Lys Asp Leu Val Lys Thr Met Arg Arg Val Asp
2165 2170 2175

Pro Val Tyr Ile His Leu Ala Glu Arg Leu Gly Thr Pro Glu Leu
2180 2185 2190

Ser Thr Ala Glu Arg Lys Glu Leu Glu Asn Lys Leu Lys Glu Arg
2195 2200 2205

Glu Glu Phe Leu Ile Pro Ile Tyr His Gln Val Ala Val Gln Phe
2210 2215 2220

Ala Asp Leu His Asp Thr Pro Gly Arg Met Gln Glu Lys Gly Val
2225 2230 2235

Ile Ser Asp Ile Leu Asp Trp Lys Thr Ser Arg Thr Phe Phe Tyr
2240 2245 2250

Trp Arg Leu Arg Arg Leu Leu Leu Glu Asp Leu Val Lys Lys Lys
2255 2260 2265

Ile His Asn Ala Asn Pro Glu Leu Thr Asp Gly Gln Ile Gln Ala
2270 2275 2280

Met Leu Arg Arg Trp Phe Val Glu Val Glu Gly Thr Val Lys Ala
2285 2290 2295

Tyr Val Trp Asp Asn Asn Lys Asp Leu Ala Glu Trp Leu Glu Lys
2300 2305 2310

Gln Leu Thr Glu Glu Asp Gly Val His Ser Val Ile Glu Glu Asn
2315 2320 2325

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Ile Lys  Cys Ile Ser Arg Asp  Tyr Val Leu Lys Gln  Ile Arg Ser
    2330                2335                2340


Leu Val  Gln Ala Asn Pro Glu  Val Ala Met Asp Ser  Ile Ile His
    2345                2350                2355


Met Thr  Gln His Ile Ser Pro  Thr Gln Arg Ala Glu  Val Ile Arg
    2360                2365                2370


Ile Leu  Ser Thr Met Asp Ser  Pro Ser Thr
    2375                2380


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Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
            20                  25                  30


Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
        35                  40                  45
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Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
    50                  55                  60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65                  70                  75                  80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
                85                  90                  95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
            100                 105                 110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile
        115                 120                 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met
    130                 135                 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu
145                 150                 155                 160

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val
                165                 170                 175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
            180                 185                 190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
        195                 200                 205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys
    210                 215                 220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu
225                 230                 235                 240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro
                245                 250                 255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn
            260                 265                 270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys
```

275 280 285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Gln Ala Ala Glu Glu Val
290 295 300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
305 310 315 320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln
325 330 335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala
340 345 350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly
355 360 365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
370 375 380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val
385 390 395 400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly
405 410 415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser
420 425 430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
435 440 445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
450 455 460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr
465 470 475 480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala
485 490 495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser
500 505 510

```
Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu
        515                 520                 525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala
    530                 535                 540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
545                 550                 555                 560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val
                565                 570                 575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
            580                 585                 590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile
        595                 600                 605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu
    610                 615                 620

Arg Pro Asp Thr Met Leu Gly Val Val Cys Gly Ala Leu His Val Ala
625                 630                 635                 640

Asp Val Ser Leu Arg Asn Ser Val Ser Asn Phe Leu His Ser Leu Glu
                645                 650                 655

Arg Gly Gln Val Leu Pro Ala His Thr Leu Leu Asn Thr Val Asp Val
            660                 665                 670

Glu Leu Ile Tyr Glu Gly Val Lys Tyr Val Leu Lys Val Thr Arg Gln
        675                 680                 685

Ser Pro Asn Ser Tyr Val Val Ile Met Asn Gly Ser Cys Val Glu Val
    690                 695                 700

Asp Val His Arg Leu Ser Asp Gly Gly Leu Leu Leu Ser Tyr Asp Gly
705                 710                 715                 720

Ser Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Arg Tyr Arg Ile
                725                 730                 735
```

```
Thr Ile Gly Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp Pro Ser
            740                 745                 750

Val Met Arg Ser Pro Ser Ala Gly Lys Leu Ile Gln Tyr Ile Val Glu
        755                 760                 765

Asp Gly Gly His Val Phe Ala Gly Gln Cys Tyr Ala Glu Ile Glu Val
    770                 775                 780

Met Lys Met Val Met Thr Leu Thr Ala Val Glu Ser Gly Cys Ile His
785                 790                 795                 800

Tyr Val Lys Arg Pro Gly Ala Ala Leu Asp Pro Gly Cys Val Leu Ala
                805                 810                 815

Lys Met Gln Leu Asp Asn Pro Ser Lys Val Gln Gln Ala Glu Leu His
            820                 825                 830

Thr Gly Ser Leu Pro Arg Ile Gln Ser Thr Ala Leu Arg Gly Glu Lys
        835                 840                 845

Leu His Arg Val Phe His Tyr Val Leu Asp Asn Leu Val Asn Val Met
    850                 855                 860

Asn Gly Tyr Cys Leu Pro Asp Pro Phe Phe Ser Ser Lys Val Lys Asp
865                 870                 875                 880

Trp Val Glu Arg Leu Met Lys Thr Leu Arg Asp Pro Ser Leu Pro Leu
                885                 890                 895

Leu Glu Leu Gln Asp Ile Met Thr Ser Val Ser Gly Arg Ile Pro Pro
            900                 905                 910

Asn Val Glu Lys Ser Ile Lys Lys Glu Met Ala Gln Tyr Ala Ser Asn
        915                 920                 925

Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln Gln Ile Ala Asn Ile
    930                 935                 940

Leu Asp Ser His Ala Ala Thr Leu Asn Arg Lys Ser Glu Arg Glu Val
945                 950                 955                 960
```

```
Phe Phe Met Asn Thr Gln Ser Ile Val Gln Leu Val Gln Arg Tyr Arg
                965                 970                 975

Ser Gly Ile Arg Gly His Met Lys Ala Val Val Met Asp Leu Leu Arg
            980                 985                 990

Gln Tyr Leu Arg Val Glu Thr Gln  Phe Gln Asn Gly His  Tyr Asp
Lys
        995                 1000                1005

Cys Val  Phe Ala Leu Arg Glu  Glu Asn Lys Ser Asp  Met Asn Thr
    1010                1015                1020

Val Leu  Asn Tyr Ile Phe Ser  His Ala Gln Val Thr  Lys Lys Asn
    1025                1030                1035

Leu Leu  Val Thr Met Leu Ile  Asp Gln Leu Cys Gly  Arg Asp Pro
    1040                1045                1050

Thr Leu  Thr Asp Glu Leu Leu  Asn Ile Leu Thr Glu  Leu Thr Gln
    1055                1060                1065

Leu Ser  Lys Thr Thr Asn Ala  Lys Val Ala Leu Arg  Ala Arg Gln
    1070                1075                1080

Val Leu  Ile Ala Ser His Leu  Pro Ser Tyr Glu Leu  Arg His Asn
    1085                1090                1095

Gln Val  Glu Ser Ile Phe Leu  Ser Ala Ile Asp Met  Tyr Gly His
    1100                1105                1110

Gln Phe  Cys Ile Glu Asn Leu  Gln Lys Leu Ile Leu  Ser Glu Thr
    1115                1120                1125

Ser Ile  Phe Asp Val Leu Pro  Asn Phe Phe Tyr His  Ser Asn Gln
    1130                1135                1140

Val Val  Arg Met Ala Ala Leu  Glu Val Tyr Val Arg  Arg Ala Tyr
    1145                1150                1155

Ile Ala  Tyr Glu Leu Asn Ser  Val Gln His Arg Gln  Leu Lys Asp
    1160                1165                1170
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```
Asn Thr  Cys Val Val Glu Phe  Gln Phe Met Leu Pro  Thr Ser His
    1175                1180                1185

Pro Asn  Arg Gly Asn Ile Pro  Thr Leu Asn Arg Met  Ser Phe Ser
    1190                1195                1200

Ser Asn  Leu Asn His Tyr Gly  Met Thr His Val Ala  Ser Val Ser
    1205                1210                1215

Asp Val  Leu Leu Asp Asn Ser  Phe Thr Pro Pro Cys  Gln Arg Met
    1220                1225                1230

Gly Gly  Met Val Ser Phe Arg  Thr Phe Glu Asp Phe  Val Arg Ile
    1235                1240                1245

Phe Asp  Glu Val Met Gly Cys  Phe Ser Asp Ser Pro  Pro Gln Ser
    1250                1255                1260

Pro Thr  Phe Pro Glu Ala Gly  His Thr Ser Leu Tyr  Asp Glu Asp
    1265                1270                1275

Lys Val  Pro Arg Asp Glu Pro  Ile His Ile Leu Asn  Val Ala Ile
    1280                1285                1290

Lys Thr  Asp Cys Asp Ile Glu  Asp Asp Arg Leu Ala  Ala Met Phe
    1295                1300                1305

Arg Glu  Phe Thr Gln Gln Asn  Lys Ala Thr Leu Val  Asp His Gly
    1310                1315                1320

Ile Arg  Arg Leu Thr Phe Leu  Val Ala Gln Lys Asp  Phe Arg Lys
    1325                1330                1335

Gln Val  Asn Tyr Glu Val Asp  Arg Arg Phe His Arg  Glu Phe Pro
    1340                1345                1350

Lys Phe  Phe Thr Phe Arg Ala  Arg Asp Lys Phe Glu  Glu Asp Arg
    1355                1360                1365

Ile Tyr  Arg His Leu Glu Pro  Ala Leu Ala Phe Gln  Leu Glu Leu
    1370                1375                1380

Asn Arg  Met Arg Asn Phe Asp  Leu Thr Ala Ile Pro  Cys Ala Asn
```

1385 1390 1395

His Lys Met His Leu Tyr Leu Gly Ala Ala Lys Val Glu Val Gly
1400 1405 1410

Thr Glu Val Thr Asp Tyr Arg Phe Phe Val Arg Ala Ile Ile Arg
1415 1420 1425

His Ser Asp Leu Val Thr Lys Glu Ala Ser Phe Glu Tyr Leu Gln
1430 1435 1440

Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp Glu Leu Glu
1445 1450 1455

Val Ala Phe Asn Asn Thr Asn Val Arg Thr Asp Cys Asn His Ile
1460 1465 1470

Phe Leu Asn Phe Val Pro Thr Val Ile Met Asp Pro Ser Lys Ile
1475 1480 1485

Glu Glu Ser Val Arg Ser Met Val Met Arg Tyr Gly Ser Arg Leu
1490 1495 1500

Trp Lys Leu Arg Val Leu Gln Ala Glu Leu Lys Ile Asn Ile Arg
1505 1510 1515

Leu Thr Pro Thr Gly Lys Ala Ile Pro Ile Arg Leu Phe Leu Thr
1520 1525 1530

Asn Glu Ser Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val
1535 1540 1545

Thr Asp Ser Arg Thr Ala Gln Ile Met Phe Gln Ala Tyr Gly Asp
1550 1555 1560

Lys Gln Gly Pro Leu His Gly Met Leu Ile Asn Thr Pro Tyr Val
1565 1570 1575

Thr Lys Asp Leu Leu Gln Ser Lys Arg Phe Gln Ala Gln Ser Leu
1580 1585 1590

Gly Thr Thr Tyr Ile Tyr Asp Ile Pro Glu Met Phe Arg Gln Ser
1595 1600 1605

```
Leu Ile  Lys Leu Trp Glu Ser  Met Ser Thr Gln Ala  Phe Leu Pro
    1610                1615                1620

Ser Pro  Pro Leu Pro Ser Asp  Met Leu Thr Tyr Thr  Glu Leu Val
    1625                1630                1635

Leu Asp  Asp Gln Gly Gln Leu  Val His Met Asn Arg  Leu Pro Gly
    1640                1645                1650

Gly Asn  Glu Ile Gly Met Val  Ala Trp Lys Met Thr  Phe Lys Ser
    1655                1660                1665

Pro Glu  Tyr Pro Glu Gly Arg  Asp Ile Ile Val Ile  Gly Asn Asp
    1670                1675                1680

Ile Thr  Tyr Arg Ile Gly Ser  Phe Gly Pro Gln Glu  Asp Leu Leu
    1685                1690                1695

Phe Leu  Arg Ala Ser Glu Leu  Ala Arg Ala Glu Gly  Ile Pro Arg
    1700                1705                1710

Ile Tyr  Val Ser Ala Asn Ser  Gly Ala Arg Ile Gly  Leu Ala Glu
    1715                1720                1725

Glu Ile  Arg His Met Phe His  Val Ala Trp Val Asp  Pro Glu Asp
    1730                1735                1740

Pro Tyr  Lys Gly Tyr Arg Tyr  Leu Tyr Leu Thr Pro  Gln Asp Tyr
    1745                1750                1755

Lys Arg  Val Ser Ala Leu Asn  Ser Val His Cys Glu  His Val Glu
    1760                1765                1770

Asp Glu  Gly Glu Ser Arg Tyr  Lys Ile Thr Asp Ile  Ile Gly Lys
    1775                1780                1785

Glu Glu  Gly Ile Gly Pro Glu  Asn Leu Arg Gly Ser  Gly Met Ile
    1790                1795                1800

Ala Gly  Glu Ser Ser Leu Ala  Tyr Asn Glu Ile Ile  Thr Ile Ser
    1805                1810                1815
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```
Leu Val  Thr Cys Arg Ala Ile  Gly Ile Gly Ala Tyr  Leu Val Arg
    1820                1825                1830

Leu Gly  Gln Arg Thr Ile Gln  Val Glu Asn Ser His  Leu Ile Leu
    1835                1840                1845

Thr Gly  Ala Gly Ala Leu Asn  Lys Val Leu Gly Arg  Glu Val Tyr
    1850                1855                1860

Thr Ser  Asn Asn Gln Leu Gly  Gly Ile Gln Ile Met  His Asn Asn
    1865                1870                1875

Gly Val  Thr His Cys Thr Val  Cys Asp Asp Phe Glu  Gly Val Phe
    1880                1885                1890

Thr Val  Leu His Trp Leu Ser  Tyr Met Pro Lys Ser  Val His Ser
    1895                1900                1905

Ser Val  Pro Leu Leu Asn Ser  Lys Asp Pro Ile Asp  Arg Ile Ile
    1910                1915                1920

Glu Phe  Val Pro Thr Lys Thr  Pro Tyr Asp Pro Arg  Trp Met Leu
    1925                1930                1935

Ala Gly  Arg Pro His Pro Thr  Gln Lys Gly Gln Trp  Leu Ser Gly
    1940                1945                1950

Phe Phe  Asp Tyr Gly Ser Phe  Ser Glu Ile Met Gln  Pro Trp Ala
    1955                1960                1965

Gln Thr  Val Val Val Gly Arg  Ala Arg Leu Gly Gly  Ile Pro Val
    1970                1975                1980

Gly Val  Val Ala Val Glu Thr  Arg Thr Val Glu Leu  Ser Ile Pro
    1985                1990                1995

Ala Asp  Pro Ala Asn Leu Asp  Ser Glu Ala Lys Ile  Ile Gln Gln
    2000                2005                2010

Ala Gly  Gln Val Trp Phe Pro  Asp Ser Ala Phe Lys  Thr Tyr Gln
    2015                2020                2025
```

Ala Ile Lys Asp Phe Asn Arg Glu Gly Leu Pro Leu Met Val Phe
2030 2035 2040

Ala Asn Trp Arg Gly Phe Ser Gly Gly Met Lys Asp Met Tyr Asp
2045 2050 2055

Gln Val Leu Lys Phe Gly Ala Tyr Ile Val Asp Gly Leu Arg Glu
2060 2065 2070

Cys Cys Gln Pro Val Leu Val Tyr Ile Pro Pro Gln Ala Glu Leu
2075 2080 2085

Arg Gly Gly Ser Trp Val Val Ile Asp Ser Ser Ile Asn Pro Arg
2090 2095 2100

His Met Glu Met Tyr Ala Asp Arg Glu Ser Arg Gly Ser Val Leu
2105 2110 2115

Glu Pro Glu Gly Thr Val Glu Ile Lys Phe Arg Arg Lys Asp Leu
2120 2125 2130

Val Lys Thr Met Arg Arg Val Asp Pro Val Tyr Ile His Leu Ala
2135 2140 2145

Glu Arg Leu Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg Lys Glu
2150 2155 2160

Leu Glu Asn Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile Pro Ile
2165 2170 2175

Tyr His Gln Val Ala Val Gln Phe Ala Asp Leu His Asp Thr Pro
2180 2185 2190

Gly Arg Met Gln Glu Lys Gly Val Ile Ser Asp Ile Leu Asp Trp
2195 2200 2205

Lys Thr Ser Arg Thr Phe Phe Tyr Trp Arg Leu Arg Arg Leu Leu
2210 2215 2220

Leu Glu Asp Leu Val Lys Lys Lys Ile His Asn Ala Asn Pro Glu
2225 2230 2235

Leu Thr Asp Gly Gln Ile Gln Ala Met Leu Arg Arg Trp Phe Val

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    2240                2245                2250

Glu Val  Glu Gly Thr Val Lys  Ala Tyr Val Trp Asp  Asn Asn Lys
    2255                2260                2265

Asp Leu  Ala Glu Trp Leu Glu  Lys Gln Leu Thr Glu  Glu Asp Gly
    2270                2275                2280

Val His  Ser Val Ile Glu Glu  Asn Ile Lys Cys Ile  Ser Arg Asp
    2285                2290                2295

Tyr Val  Leu Lys Gln Ile Arg  Ser Leu Val Gln Ala  Asn Pro Glu
    2300                2305                2310

Val Ala  Met Asp Ser Ile Ile  His Met Thr Gln His  Ile Ser Pro
    2315                2320                2325

Thr Gln  Arg Ala Glu Val Ile  Arg Ile Leu Ser Thr  Met Asp Ser
    2330                2335                2340

Pro Ser  Thr
    2345


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Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr
            20                  25                  30

Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn
        35                  40                  45

Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr
    50                  55                  60

Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr
65                  70                  75                  80

Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala
                85                  90


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<211> 112
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<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483852"

<400> 1274
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1               5                   10                  15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
            20                  25                  30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
        35                  40                  45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
```

```
    50                  55                  60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Ser Ser Trp Ile Lys
65                  70                  75                  80

Arg Ser Gly Ser Val Val Leu Gly Ser His Cys Ser Ser Glu Ser Pro
                85                  90                  95

Arg Gly Ala Leu Gly Asp Lys Pro His Pro Gln Arg Phe Arg Phe Ile
            100                 105                 110


<210> 1275
<211> 998
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483969"

<400> 1275
Glu Asp Asp Arg Leu Ala Ala Met Phe Arg Glu Phe Thr Gln Gln Asn
1               5                   10                  15

Lys Ala Thr Leu Val Asp His Gly Ile Arg Arg Leu Thr Phe Leu Val
            20                  25                  30

Ala Gln Lys Asp Phe Arg Lys Gln Val Asn Tyr Glu Val Asp Arg Arg
        35                  40                  45

Phe His Arg Glu Phe Pro Lys Phe Phe Thr Phe Arg Ala Arg Asp Lys
    50                  55                  60

Phe Glu Glu Asp Arg Ile Tyr Arg His Leu Glu Pro Ala Leu Ala Phe
65                  70                  75                  80
```

```
Gln Leu Glu Leu Asn Arg Met Arg Asn Phe Asp Leu Thr Ala Ile Pro
                85                  90                  95

Cys Ala Asn His Lys Met His Leu Tyr Leu Gly Ala Ala Lys Val Glu
            100                 105                 110

Val Gly Thr Glu Val Thr Asp Tyr Arg Phe Phe Val Arg Ala Ile Ile
        115                 120                 125

Arg His Ser Asp Leu Val Thr Lys Glu Ala Ser Phe Glu Tyr Leu Gln
    130                 135                 140

Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp Glu Leu Glu Val
145                 150                 155                 160

Ala Phe Asn Asn Thr Asn Val Arg Thr Asp Cys Asn His Ile Phe Leu
                165                 170                 175

Asn Phe Val Pro Thr Val Ile Met Asp Pro Ser Lys Ile Glu Glu Ser
            180                 185                 190

Val Arg Ser Met Val Met Arg Tyr Gly Ser Arg Leu Trp Lys Leu Arg
        195                 200                 205

Val Leu Gln Ala Glu Leu Lys Ile Asn Ile Arg Leu Thr Pro Thr Gly
    210                 215                 220

Lys Ala Ile Pro Ile Arg Leu Phe Leu Thr Asn Glu Ser Gly Tyr Tyr
225                 230                 235                 240

Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr Asp Ser Arg Thr Ala Gln
                245                 250                 255

Ile Met Phe Gln Ala Tyr Gly Asp Lys Gln Gly Pro Leu His Gly Met
            260                 265                 270

Leu Ile Asn Thr Pro Tyr Val Thr Lys Asp Leu Leu Gln Ser Lys Arg
        275                 280                 285

Phe Gln Ala Gln Ser Leu Gly Thr Thr Tyr Ile Tyr Asp Ile Pro Glu
    290                 295                 300
```

Met Phe Arg Gln Ile Gly Met Val Ala Trp Lys Met Thr Phe Lys Ser
305 310 315 320

Pro Glu Tyr Pro Glu Gly Arg Asp Ile Ile Val Ile Gly Asn Asp Ile
325 330 335

Thr Tyr Arg Ile Gly Ser Phe Gly Pro Gln Glu Asp Leu Leu Phe Leu
340 345 350

Arg Ala Ser Glu Leu Ala Arg Ala Glu Gly Ile Pro Arg Ile Tyr Val
355 360 365

Ser Ala Asn Ser Gly Ala Arg Ile Gly Leu Ala Glu Glu Ile Arg His
370 375 380

Met Phe His Val Ala Trp Val Asp Pro Glu Asp Pro Tyr Lys Gly Tyr
385 390 395 400

Arg Tyr Leu Tyr Leu Thr Pro Gln Asp Tyr Lys Arg Val Ser Ala Leu
405 410 415

Asn Ser Val His Cys Glu His Val Glu Asp Glu Gly Glu Ser Arg Tyr
420 425 430

Lys Ile Thr Asp Ile Ile Gly Lys Glu Glu Gly Ile Gly Pro Glu Asn
435 440 445

Leu Arg Gly Ser Gly Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr Asn
450 455 460

Glu Ile Ile Thr Ile Ser Leu Val Thr Cys Arg Ala Ile Gly Ile Gly
465 470 475 480

Ala Tyr Leu Val Arg Leu Gly Gln Arg Thr Ile Gln Val Glu Asn Ser
485 490 495

His Leu Ile Leu Thr Gly Ala Gly Ala Leu Asn Lys Val Leu Gly Arg
500 505 510

Glu Val Tyr Thr Ser Asn Asn Gln Leu Gly Gly Ile Gln Ile Met His
515 520 525

Asn Asn Gly Val Thr His Cys Thr Val Cys Asp Asp Phe Glu Gly Val

530 535 540

Phe Thr Val Leu His Trp Leu Ser Tyr Met Pro Lys Ser Val His Ser
545 550 555 560

Ser Val Pro Leu Leu Asn Ser Lys Asp Pro Ile Asp Arg Ile Ile Glu
565 570 575

Phe Val Pro Thr Lys Thr Pro Tyr Asp Pro Arg Trp Met Leu Ala Gly
580 585 590

Arg Pro His Pro Thr Gln Lys Gly Gln Trp Leu Ser Gly Phe Phe Asp
595 600 605

Tyr Gly Ser Phe Ser Glu Ile Met Gln Pro Trp Ala Gln Thr Val Val
610 615 620

Val Gly Arg Ala Arg Leu Gly Gly Ile Pro Val Gly Val Val Ala Val
625 630 635 640

Glu Thr Arg Thr Val Glu Leu Ser Ile Pro Ala Asp Pro Ala Asn Leu
645 650 655

Asp Ser Glu Ala Lys Ile Ile Gln Gln Ala Gly Gln Val Trp Phe Pro
660 665 670

Asp Ser Ala Phe Lys Thr Tyr Gln Ala Ile Lys Asp Phe Asn Arg Glu
675 680 685

Gly Leu Pro Leu Met Val Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly
690 695 700

Met Lys Asp Met Tyr Asp Gln Val Leu Lys Phe Gly Ala Tyr Ile Val
705 710 715 720

Asp Gly Leu Arg Glu Cys Cys Gln Pro Val Leu Val Tyr Ile Pro Pro
725 730 735

Gln Ala Glu Leu Arg Gly Gly Ser Trp Val Val Ile Asp Ser Ser Ile
740 745 750

Asn Pro Arg His Met Glu Met Tyr Ala Asp Arg Glu Ser Arg Gly Ser
755 760 765

```
Val Leu Glu Pro Glu Gly Thr Val Glu Ile Lys Phe Arg Arg Lys Asp
    770                 775                 780

Leu Val Lys Thr Met Arg Arg Val Asp Pro Val Tyr Ile His Leu Ala
785                 790                 795                 800

Glu Arg Leu Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg Lys Glu Leu
                805                 810                 815

Glu Asn Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile Pro Ile Tyr His
            820                 825                 830

Gln Val Ala Val Gln Phe Ala Asp Leu His Asp Thr Pro Gly Arg Met
        835                 840                 845

Gln Glu Lys Gly Val Ile Ser Asp Ile Leu Asp Trp Lys Thr Ser Arg
    850                 855                 860

Thr Phe Phe Tyr Trp Arg Leu Arg Arg Leu Leu Leu Glu Asp Leu Val
865                 870                 875                 880

Lys Lys Lys Ile His Asn Ala Asn Pro Glu Leu Thr Asp Gly Gln Ile
                885                 890                 895

Gln Ala Met Leu Arg Arg Trp Phe Val Glu Val Glu Gly Thr Val Lys
            900                 905                 910

Ala Tyr Val Trp Asp Asn Asn Lys Asp Leu Ala Glu Trp Leu Glu Lys
        915                 920                 925

Gln Leu Thr Glu Glu Asp Gly Val His Ser Val Ile Glu Glu Asn Ile
    930                 935                 940

Lys Cys Ile Ser Arg Asp Tyr Val Leu Lys Gln Ile Arg Ser Leu Val
945                 950                 955                 960

Gln Ala Asn Pro Glu Val Ala Met Asp Ser Ile Ile His Met Thr Gln
                965                 970                 975

His Ile Ser Pro Thr Gln Arg Ala Glu Val Ile Arg Ile Leu Ser Thr
            980                 985                 990
```

Met Asp Ser Pro Ser Thr
995

<210> 1276
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484948"

<400> 1276
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Ser Ser Trp Ile Lys
65 70 75 80

Arg Ser Gly Ser

<210> 1277
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487874"

<400> 1277
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
100 105 110

Gly Gly Asn Lys Val Ile Glu Lys
115 120

<210> 1278
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487997"

<400> 1278
Met Trp Trp Ser Thr Leu Met Ser Ile Leu Arg Ala Arg Ser Phe Trp
1 5 10 15

Lys Trp Ile Ser Thr Gln Thr Val Arg Ile Ile Arg Ala Val Arg Ala
20 25 30

His Phe Gly Gly Ile Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu
35 40 45

Glu Leu Asn Gln His Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp
50 55 60

Asn Ser Glu Asp Glu Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu
65 70 75 80

Glu Lys Glu Gly Ser Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu
85 90 95

Ser Asp Leu Gly Ile Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile
100 105 110

Arg Leu

<210> 1279
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488112"

<400> 1279
Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile
1 5 10 15

Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr
20 25 30

Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn
35 40 45

Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr
50 55 60

Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr
65 70 75 80

Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala
85 90

<210> 1280
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000488139"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1280
Xaa Ile Lys Cys Ile Ser Arg Asp Tyr Val Leu Lys Gln Ile Arg Ser
1 5 10 15

Leu Val Gln Ala Asn Pro Glu Val Ala Met Asp Ser Ile Ile His Met
20 25 30

Thr Gln His Ile Ser Pro Thr Gln Arg Ala Glu Val Ile Arg Ile Leu
35 40 45

Ser Thr Met Asp Ser Pro Ser Thr Leu Cys Met Thr Ser Trp Asp Val
50 55 60

Arg Ser Gln Asn Pro Pro Pro Ala His Gln Ser His Leu Pro His Ser
65 70 75 80

Val Phe Ile Thr Leu Ala Arg Pro Ser Pro Pro Leu Pro Ala Gln Asp
85 90 95

<210> 1281
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488145"

<400> 1281

```
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1               5                  10                  15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
            20                  25                  30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
        35                  40                  45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
    50                  55                  60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Ser Ser Trp Ile Lys
65                  70                  75                  80

Arg Ser Gly Ser
```

<210> 1282
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488223"

<400> 1282

```
Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile
1               5                  10                  15

Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr
            20                  25                  30

Arg Phe Gly Gly Asn Lys Val Ile Glu Lys
        35                  40
```

<210> 1283
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488724"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1283
Xaa Glu Ile Arg His Met Phe His Val Ala Trp Val Asp Pro Glu Asp
1 5 10 15

Pro Tyr Lys Gly Tyr Arg Tyr Leu Tyr Leu Thr Pro Gln Asp Tyr Lys
20 25 30

Arg Val Ser Ala Leu Asn Ser Val His Cys Glu His Val Glu Asp Glu
35 40 45

Gly Glu Ser Arg
50

<210> 1284
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>

<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:
acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488774"

<400> 1284
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Ser Ser Trp Ile Lys
65 70 75 80

Arg Ser Gly Ser Val Val Leu Gly Ser His Cys Ser Ser Glu Ser Pro
85 90 95

Arg Gly Ala Leu Gly Asp Lys Pro His Pro Gln Arg Phe Arg Phe Ile
100 105 110

<210> 1285
<211> 998
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 385; "

<220>
<221> source
<223> /note="Gene Symbol: ACACA; "

<220>
<221> source
<223> /note="Gene Name:

acetyl-CoA carboxylase alpha; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488846"

<400> 1285

```
Glu Asp Asp Arg Leu Ala Ala Met Phe Arg Glu Phe Thr Gln Gln Asn
1               5                  10                  15

Lys Ala Thr Leu Val Asp His Gly Ile Arg Arg Leu Thr Phe Leu Val
            20                  25                  30

Ala Gln Lys Asp Phe Arg Lys Gln Val Asn Tyr Glu Val Asp Arg Arg
        35                  40                  45

Phe His Arg Glu Phe Pro Lys Phe Phe Thr Phe Arg Ala Arg Asp Lys
    50                  55                  60

Phe Glu Glu Asp Arg Ile Tyr Arg His Leu Glu Pro Ala Leu Ala Phe
65                  70                  75                  80

Gln Leu Glu Leu Asn Arg Met Arg Asn Phe Asp Leu Thr Ala Ile Pro
                85                  90                  95

Cys Ala Asn His Lys Met His Leu Tyr Leu Gly Ala Ala Lys Val Glu
            100                 105                 110

Val Gly Thr Glu Val Thr Asp Tyr Arg Phe Phe Val Arg Ala Ile Ile
        115                 120                 125

Arg His Ser Asp Leu Val Thr Lys Glu Ala Ser Phe Glu Tyr Leu Gln
    130                 135                 140

Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp Glu Leu Glu Val
145                 150                 155                 160

Ala Phe Asn Asn Thr Asn Val Arg Thr Asp Cys Asn His Ile Phe Leu
                165                 170                 175

Asn Phe Val Pro Thr Val Ile Met Asp Pro Ser Lys Ile Glu Glu Ser
            180                 185                 190

Val Arg Ser Met Val Met Arg Tyr Gly Ser Arg Leu Trp Lys Leu Arg
        195                 200                 205
```

```
Val Leu Gln Ala Glu Leu Lys Ile Asn Ile Arg Leu Thr Pro Thr Gly
    210                 215                 220

Lys Ala Ile Pro Ile Arg Leu Phe Leu Thr Asn Glu Ser Gly Tyr Tyr
225                 230                 235                 240

Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr Asp Ser Arg Thr Ala Gln
                245                 250                 255

Ile Met Phe Gln Ala Tyr Gly Asp Lys Gln Gly Pro Leu His Gly Met
            260                 265                 270

Leu Ile Asn Thr Pro Tyr Val Thr Lys Asp Leu Leu Gln Ser Lys Arg
        275                 280                 285

Phe Gln Ala Gln Ser Leu Gly Thr Thr Tyr Ile Tyr Asp Ile Pro Glu
    290                 295                 300

Met Phe Arg Gln Ile Gly Met Val Ala Trp Lys Met Thr Phe Lys Ser
305                 310                 315                 320

Pro Glu Tyr Pro Glu Gly Arg Asp Ile Ile Val Ile Gly Asn Asp Ile
                325                 330                 335

Thr Tyr Arg Ile Gly Ser Phe Gly Pro Gln Glu Asp Leu Leu Phe Leu
            340                 345                 350

Arg Ala Ser Glu Leu Ala Arg Ala Glu Gly Ile Pro Arg Ile Tyr Val
        355                 360                 365

Ser Ala Asn Ser Gly Ala Arg Ile Gly Leu Ala Glu Glu Ile Arg His
    370                 375                 380

Met Phe His Val Ala Trp Val Asp Pro Glu Asp Pro Tyr Lys Gly Tyr
385                 390                 395                 400

Arg Tyr Leu Tyr Leu Thr Pro Gln Asp Tyr Lys Arg Val Ser Ala Leu
                405                 410                 415

Asn Ser Val His Cys Glu His Val Glu Asp Glu Gly Glu Ser Arg Tyr
            420                 425                 430
```

```
Lys Ile Thr Asp Ile Ile Gly Lys Glu Glu Gly Ile Gly Pro Glu Asn
        435                 440                 445

Leu Arg Gly Ser Gly Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr Asn
    450                 455                 460

Glu Ile Ile Thr Ile Ser Leu Val Thr Cys Arg Ala Ile Gly Ile Gly
465                 470                 475                 480

Ala Tyr Leu Val Arg Leu Gly Gln Arg Thr Ile Gln Val Glu Asn Ser
                485                 490                 495

His Leu Ile Leu Thr Gly Ala Gly Ala Leu Asn Lys Val Leu Gly Arg
            500                 505                 510

Glu Val Tyr Thr Ser Asn Asn Gln Leu Gly Gly Ile Gln Ile Met His
        515                 520                 525

Asn Asn Gly Val Thr His Cys Thr Val Cys Asp Asp Phe Glu Gly Val
    530                 535                 540

Phe Thr Val Leu His Trp Leu Ser Tyr Met Pro Lys Ser Val His Ser
545                 550                 555                 560

Ser Val Pro Leu Leu Asn Ser Lys Asp Pro Ile Asp Arg Ile Ile Glu
                565                 570                 575

Phe Val Pro Thr Lys Thr Pro Tyr Asp Pro Arg Trp Met Leu Ala Gly
            580                 585                 590

Arg Pro His Pro Thr Gln Lys Gly Gln Trp Leu Ser Gly Phe Phe Asp
        595                 600                 605

Tyr Gly Ser Phe Ser Glu Ile Met Gln Pro Trp Ala Gln Thr Val Val
    610                 615                 620

Val Gly Arg Ala Arg Leu Gly Gly Ile Pro Val Gly Val Val Ala Val
625                 630                 635                 640

Glu Thr Arg Thr Val Glu Leu Ser Ile Pro Ala Asp Pro Ala Asn Leu
                645                 650                 655
```

```
Asp Ser Glu Ala Lys Ile Ile Gln Gln Ala Gly Gln Val Trp Phe Pro
            660                 665                 670

Asp Ser Ala Phe Lys Thr Tyr Gln Ala Ile Lys Asp Phe Asn Arg Glu
        675                 680                 685

Gly Leu Pro Leu Met Val Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly
    690                 695                 700

Met Lys Asp Met Tyr Asp Gln Val Leu Lys Phe Gly Ala Tyr Ile Val
705                 710                 715                 720

Asp Gly Leu Arg Glu Cys Cys Gln Pro Val Leu Val Tyr Ile Pro Pro
                725                 730                 735

Gln Ala Glu Leu Arg Gly Gly Ser Trp Val Val Ile Asp Ser Ser Ile
            740                 745                 750

Asn Pro Arg His Met Glu Met Tyr Ala Asp Arg Glu Ser Arg Gly Ser
        755                 760                 765

Val Leu Glu Pro Glu Gly Thr Val Glu Ile Lys Phe Arg Arg Lys Asp
    770                 775                 780

Leu Val Lys Thr Met Arg Arg Val Asp Pro Val Tyr Ile His Leu Ala
785                 790                 795                 800

Glu Arg Leu Gly Thr Pro Glu Leu Ser Thr Ala Glu Arg Lys Glu Leu
                805                 810                 815

Glu Asn Lys Leu Lys Glu Arg Glu Glu Phe Leu Ile Pro Ile Tyr His
            820                 825                 830

Gln Val Ala Val Gln Phe Ala Asp Leu His Asp Thr Pro Gly Arg Met
        835                 840                 845

Gln Glu Lys Gly Val Ile Ser Asp Ile Leu Asp Trp Lys Thr Ser Arg
    850                 855                 860

Thr Phe Phe Tyr Trp Arg Leu Arg Arg Leu Leu Leu Glu Asp Leu Val
865                 870                 875                 880

Lys Lys Lys Ile His Asn Ala Asn Pro Glu Leu Thr Asp Gly Gln Ile
```

```
                885                 890                 895

Gln Ala Met Leu Arg Arg Trp Phe Val Glu Val Glu Gly Thr Val Lys
            900                 905                 910

Ala Tyr Val Trp Asp Asn Asn Lys Asp Leu Ala Glu Trp Leu Glu Lys
        915                 920                 925

Gln Leu Thr Glu Glu Asp Gly Val His Ser Val Ile Glu Glu Asn Ile
    930                 935                 940

Lys Cys Ile Ser Arg Asp Tyr Val Leu Lys Gln Ile Arg Ser Leu Val
945                 950                 955                 960

Gln Ala Asn Pro Glu Val Ala Met Asp Ser Ile Ile His Met Thr Gln
                965                 970                 975

His Ile Ser Pro Thr Gln Arg Ala Glu Val Ile Arg Ile Leu Ser Thr
            980                 985                 990

Met Asp Ser Pro Ser Thr
        995


<210> 1286
<211> 2458
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 386; "

<220>
<221> source
<223> /note="Gene Symbol: ACACB; "

<220>
<221> source
<223> /note="Gene Name:
      acetyl-CoA carboxylase beta; "

<220>
<221> source
<223> /note="Uniprot ID:  O00763; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000341044"
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<400> 1286
Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
1 5 10 15

Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
20 25 30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
35 40 45

Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly
50 55 60

His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys
65 70 75 80

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
85 90 95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser
100 105 110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr
115 120 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala
130 135 140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln
145 150 155 160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
165 170 175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser
180 185 190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly
195 200 205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu
210 215 220

```
His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg
225                 230                 235                 240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly
                245                 250                 255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala
            260                 265                 270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg
        275                 280                 285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu
    290                 295                 300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val
305                 310                 315                 320

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val
                325                 330                 335

Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly
            340                 345                 350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly
        355                 360                 365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp
    370                 375                 380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu
385                 390                 395                 400

Pro Trp Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu
                405                 410                 415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly
            420                 425                 430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
        435                 440                 445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
```

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    450                 455                 460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val
465                 470                 475                 480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln
                485                 490                 495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn
            500                 505                 510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln
        515                 520                 525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe
    530                 535                 540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr
545                 550                 555                 560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe
                565                 570                 575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr
            580                 585                 590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala
        595                 600                 605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly
    610                 615                 620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn
625                 630                 635                 640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu
                645                 650                 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu
            660                 665                 670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala
        675                 680                 685
```

```
Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe
    690                 695                 700

Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala
705                 710                 715                 720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
                725                 730                 735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
            740                 745                 750

Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Ala Glu Lys
        755                 760                 765

Pro Asp Ile Met Leu Gly Val Val Cys Gly Ala Leu Asn Val Ala Asp
    770                 775                 780

Ala Met Phe Arg Thr Cys Met Thr Asp Phe Leu His Ser Leu Glu Arg
785                 790                 795                 800

Gly Gln Val Leu Pro Ala Asp Ser Leu Leu Asn Leu Val Asp Val Glu
                805                 810                 815

Leu Ile Tyr Gly Gly Val Lys Tyr Ile Leu Lys Val Ala Arg Gln Ser
            820                 825                 830

Leu Thr Met Phe Val Leu Ile Met Asn Gly Cys His Ile Glu Ile Asp
        835                 840                 845

Ala His Arg Leu Asn Asp Gly Gly Leu Leu Leu Ser Tyr Asn Gly Asn
    850                 855                 860

Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Ser Tyr Arg Ile Thr
865                 870                 875                 880

Ile Gly Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp Pro Thr Val
                885                 890                 895

Leu Arg Ser Pro Ser Ala Gly Lys Leu Thr Gln Tyr Thr Val Glu Asp
            900                 905                 910
```

```
Gly Gly His Val Glu Ala Gly Ser Ser Tyr Ala Glu Met Glu Val Met
        915                 920                 925

Lys Met Ile Met Thr Leu Asn Val Gln Glu Arg Gly Arg Val Lys Tyr
    930                 935                 940

Ile Lys Arg Pro Gly Ala Val Leu Glu Ala Gly Cys Val Val Ala Arg
945                 950                 955                 960

Leu Glu Leu Asp Asp Pro Ser Lys Val His Pro Ala Glu Pro Phe Thr
                965                 970                 975

Gly Glu Leu Pro Ala Gln Gln Thr Leu Pro Ile Leu Gly Glu Lys Leu
            980                 985                 990

His Gln Val Phe His Ser Val Leu  Glu Asn Leu Thr Asn  Val Met
Ser
        995                 1000                1005

Gly Phe  Cys Leu Pro Glu Pro  Val Phe Ser Ile Lys  Leu Lys Glu
    1010                1015                1020

Trp Val  Gln Lys Leu Met Met  Thr Leu Arg His Pro  Ser Leu Pro
    1025                1030                1035

Leu Leu  Glu Leu Gln Glu Ile  Met Thr Ser Val Ala  Gly Arg Ile
    1040                1045                1050

Pro Ala  Pro Val Glu Lys Ser  Val Arg Arg Val Met  Ala Gln Tyr
    1055                1060                1065

Ala Ser  Asn Ile Thr Ser Val  Leu Cys Gln Phe Pro  Ser Gln Gln
    1070                1075                1080

Ile Ala  Thr Ile Leu Asp Cys  His Ala Ala Thr Leu  Gln Arg Lys
    1085                1090                1095

Ala Asp  Arg Glu Val Phe Phe  Ile Asn Thr Gln Ser  Ile Val Gln
    1100                1105                1110

Leu Val  Gln Arg Tyr Arg Ser  Gly Ile Arg Gly Tyr  Met Lys Thr
    1115                1120                1125
```

Val Val Leu Asp Leu Leu Arg Arg Tyr Leu Arg Val Glu His His
1130 1135 1140

Phe Gln Gln Ala His Tyr Asp Lys Cys Val Ile Asn Leu Arg Glu
1145 1150 1155

Gln Phe Lys Pro Asp Met Ser Gln Val Leu Asp Cys Ile Phe Ser
1160 1165 1170

His Ala Gln Val Ala Lys Lys Asn Gln Leu Val Ile Met Leu Ile
1175 1180 1185

Asp Glu Leu Cys Gly Pro Asp Pro Ser Leu Ser Asp Glu Leu Ile
1190 1195 1200

Ser Ile Leu Asn Glu Leu Thr Gln Leu Ser Lys Ser Glu His Cys
1205 1210 1215

Lys Val Ala Leu Arg Ala Arg Gln Ile Leu Ile Ala Ser His Leu
1220 1225 1230

Pro Ser Tyr Glu Leu Arg His Asn Gln Val Glu Ser Ile Phe Leu
1235 1240 1245

Ser Ala Ile Asp Met Tyr Gly His Gln Phe Cys Pro Glu Asn Leu
1250 1255 1260

Lys Lys Leu Ile Leu Ser Glu Thr Thr Ile Phe Asp Val Leu Pro
1265 1270 1275

Thr Phe Phe Tyr His Ala Asn Lys Val Val Cys Met Ala Ser Leu
1280 1285 1290

Glu Val Tyr Val Arg Arg Gly Tyr Ile Ala Tyr Glu Leu Asn Ser
1295 1300 1305

Leu Gln His Arg Gln Leu Pro Asp Gly Thr Cys Val Val Glu Phe
1310 1315 1320

Gln Phe Met Leu Pro Ser Ser His Pro Asn Arg Met Thr Val Pro
1325 1330 1335

```
Ile Ser  Ile Thr Asn Pro Asp  Leu Leu Arg His Ser  Thr Glu Leu
    1340                1345                1350

Phe Met  Asp Ser Gly Phe Ser  Pro Leu Cys Gln Arg  Met Gly Ala
    1355                1360                1365

Met Val  Ala Phe Arg Arg Phe  Glu Asp Phe Thr Arg  Asn Phe Asp
    1370                1375                1380

Glu Val  Ile Ser Cys Phe Ala  Asn Val Pro Lys Asp  Thr Pro Leu
    1385                1390                1395

Phe Ser  Glu Ala Arg Thr Ser  Leu Tyr Ser Glu Asp  Asp Cys Lys
    1400                1405                1410

Ser Leu  Arg Glu Glu Pro Ile  His Ile Leu Asn Val  Ser Ile Gln
    1415                1420                1425

Cys Ala  Asp His Leu Glu Asp  Glu Ala Leu Val Pro  Ile Leu Arg
    1430                1435                1440

Thr Phe  Val Gln Ser Lys Lys  Asn Ile Leu Val Asp  Tyr Gly Leu
    1445                1450                1455

Arg Arg  Ile Thr Phe Leu Ile  Ala Gln Glu Lys Glu  Phe Pro Lys
    1460                1465                1470

Phe Phe  Thr Phe Arg Ala Arg  Asp Glu Phe Ala Glu  Asp Arg Ile
    1475                1480                1485

Tyr Arg  His Leu Glu Pro Ala  Leu Ala Phe Gln Leu  Glu Leu Asn
    1490                1495                1500

Arg Met  Arg Asn Phe Asp Leu  Thr Ala Val Pro Cys  Ala Asn His
    1505                1510                1515

Lys Met  His Leu Tyr Leu Gly  Ala Ala Lys Val Lys  Glu Gly Val
    1520                1525                1530

Glu Val  Thr Asp His Arg Phe  Phe Ile Arg Ala Ile  Ile Arg His
    1535                1540                1545

Ser Asp  Leu Ile Thr Lys Glu  Ala Ser Phe Glu Tyr  Leu Gln Asn
```

1550 1555 1560

Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp Glu Leu Glu Val
1565 1570 1575

Ala Phe Asn Asn Thr Ser Val Arg Thr Asp Cys Asn His Ile Phe
1580 1585 1590

Leu Asn Phe Val Pro Thr Val Ile Met Asp Pro Phe Lys Ile Glu
1595 1600 1605

Glu Ser Val Arg Tyr Met Val Met Arg Tyr Gly Ser Arg Leu Trp
1610 1615 1620

Lys Leu Arg Val Leu Gln Ala Glu Val Lys Ile Asn Ile Arg Gln
1625 1630 1635

Thr Thr Thr Gly Ser Ala Val Pro Ile Arg Leu Phe Ile Thr Asn
1640 1645 1650

Glu Ser Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr
1655 1660 1665

Asp Ser Arg Ser Gly Asn Ile Met Phe His Ser Phe Gly Asn Lys
1670 1675 1680

Gln Gly Pro Gln His Gly Met Leu Ile Asn Thr Pro Tyr Val Thr
1685 1690 1695

Lys Asp Leu Leu Gln Ala Lys Arg Phe Gln Ala Gln Thr Leu Gly
1700 1705 1710

Thr Thr Tyr Ile Tyr Asp Phe Pro Glu Met Phe Arg Gln Ala Leu
1715 1720 1725

Phe Lys Leu Trp Gly Ser Pro Asp Lys Tyr Pro Lys Asp Ile Leu
1730 1735 1740

Thr Tyr Thr Glu Leu Val Leu Asp Ser Gln Gly Gln Leu Val Glu
1745 1750 1755

Met Asn Arg Leu Pro Gly Gly Asn Glu Val Gly Met Val Ala Phe
1760 1765 1770

Lys Met Arg Phe Lys Thr Gln Glu Tyr Pro Glu Gly Arg Asp Val
1775 1780 1785

Ile Val Ile Gly Asn Asp Ile Thr Phe Arg Ile Gly Ser Phe Gly
1790 1795 1800

Pro Gly Glu Asp Leu Leu Tyr Leu Arg Ala Ser Glu Met Ala Arg
1805 1810 1815

Ala Glu Gly Ile Pro Lys Ile Tyr Val Ala Ala Asn Ser Gly Ala
1820 1825 1830

Arg Ile Gly Met Ala Glu Glu Ile Lys His Met Phe His Val Ala
1835 1840 1845

Trp Val Asp Pro Glu Asp Pro His Lys Gly Phe Lys Tyr Leu Tyr
1850 1855 1860

Leu Thr Pro Gln Asp Tyr Thr Arg Ile Ser Ser Leu Asn Ser Val
1865 1870 1875

His Cys Lys His Ile Glu Glu Gly Gly Glu Ser Arg Tyr Met Ile
1880 1885 1890

Thr Asp Ile Ile Gly Lys Asp Asp Gly Leu Gly Val Glu Asn Leu
1895 1900 1905

Arg Gly Ser Gly Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr Glu
1910 1915 1920

Glu Ile Val Thr Ile Ser Leu Val Thr Cys Arg Ala Ile Gly Ile
1925 1930 1935

Gly Ala Tyr Leu Val Arg Leu Gly Gln Arg Val Ile Gln Val Glu
1940 1945 1950

Asn Ser His Ile Ile Leu Thr Gly Ala Ser Ala Leu Asn Lys Val
1955 1960 1965

Leu Gly Arg Glu Val Tyr Thr Ser Asn Asn Gln Leu Gly Gly Val
1970 1975 1980

```
Gln Ile  Met His Tyr Asn Gly  Val Ser His Ile Thr  Val Pro Asp
    1985                1990                1995

Asp Phe  Glu Gly Val Tyr Thr  Ile Leu Glu Trp Leu  Ser Tyr Met
    2000                2005                2010

Pro Lys  Asp Asn His Ser Pro  Val Pro Ile Ile Thr  Pro Thr Asp
    2015                2020                2025

Pro Ile  Asp Arg Glu Ile Glu  Phe Leu Pro Ser Arg  Ala Pro Tyr
    2030                2035                2040

Asp Pro  Arg Trp Met Leu Ala  Gly Arg Pro His Pro  Thr Leu Lys
    2045                2050                2055

Gly Thr  Trp Gln Ser Gly Phe  Phe Asp His Gly Ser  Phe Lys Glu
    2060                2065                2070

Ile Met  Ala Pro Trp Ala Gln  Thr Val Val Thr Gly  Arg Ala Arg
    2075                2080                2085

Leu Gly  Gly Ile Pro Val Gly  Val Ile Ala Val Glu  Thr Arg Thr
    2090                2095                2100

Val Glu  Val Ala Val Pro Ala  Asp Pro Ala Asn Leu  Asp Ser Glu
    2105                2110                2115

Ala Lys  Ile Ile Gln Gln Ala  Gly Gln Val Trp Phe  Pro Asp Ser
    2120                2125                2130

Ala Tyr  Lys Thr Ala Gln Ala  Val Lys Asp Phe Asn  Arg Glu Lys
    2135                2140                2145

Leu Pro  Leu Met Ile Phe Ala  Asn Trp Arg Gly Phe  Ser Gly Gly
    2150                2155                2160

Met Lys  Asp Met Tyr Asp Gln  Val Leu Lys Phe Gly  Ala Tyr Ile
    2165                2170                2175

Val Asp  Gly Leu Arg Gln Tyr  Lys Gln Pro Ile Leu  Ile Tyr Ile
    2180                2185                2190
```

Pro Pro Tyr Ala Glu Leu Arg Gly Gly Ser Trp Val Val Ile Asp
2195 2200 2205

Ala Thr Ile Asn Pro Leu Cys Ile Glu Met Tyr Ala Asp Lys Glu
2210 2215 2220

Ser Arg Gly Gly Val Leu Glu Pro Glu Gly Thr Val Glu Ile Lys
2225 2230 2235

Phe Arg Lys Lys Asp Leu Ile Lys Ser Met Arg Arg Ile Asp Pro
2240 2245 2250

Ala Tyr Lys Lys Leu Met Glu Gln Leu Gly Glu Pro Asp Leu Ser
2255 2260 2265

Asp Lys Asp Arg Lys Asp Leu Glu Gly Arg Leu Lys Ala Arg Glu
2270 2275 2280

Asp Leu Leu Leu Pro Ile Tyr His Gln Val Ala Val Gln Phe Ala
2285 2290 2295

Asp Phe His Asp Thr Pro Gly Arg Met Leu Glu Lys Gly Val Ile
2300 2305 2310

Ser Asp Ile Leu Glu Trp Lys Thr Ala Arg Thr Phe Leu Tyr Trp
2315 2320 2325

Arg Leu Arg Arg Leu Leu Leu Glu Asp Gln Val Lys Gln Glu Ile
2330 2335 2340

Leu Gln Ala Ser Gly Glu Leu Ser His Val His Ile Gln Ser Met
2345 2350 2355

Leu Arg Arg Trp Phe Val Glu Thr Glu Gly Ala Val Lys Ala Tyr
2360 2365 2370

Leu Trp Asp Asn Asn Gln Val Val Val Gln Trp Leu Glu Gln His
2375 2380 2385

Trp Gln Ala Gly Asp Gly Pro Arg Ser Thr Ile Arg Glu Asn Ile
2390 2395 2400

Thr Tyr Leu Lys His Asp Ser Val Leu Lys Thr Ile Arg Gly Leu

```
    2405                2410                2415

Val Glu  Glu Asn Pro Glu Val  Ala Val Asp Cys Val  Ile Tyr Leu
    2420                2425                2430

Ser Gln  His Ile Ser Pro Ala  Glu Arg Ala Gln Val  Val His Leu
    2435                2440                2445

Leu Ser  Thr Met Asp Ser Pro  Ala Ser Thr
    2450                2455


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Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
            20                  25                  30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
        35                  40                  45

Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly
    50                  55                  60
```

```
His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys
65                  70                  75                  80

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
                85                  90                  95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser
            100                 105                 110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr
        115                 120                 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala
    130                 135                 140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln
145                 150                 155                 160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
                165                 170                 175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser
            180                 185                 190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly
        195                 200                 205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu
    210                 215                 220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg
225                 230                 235                 240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly
                245                 250                 255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala
            260                 265                 270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg
        275                 280                 285
```

```
Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu
    290                 295                 300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val
305                 310                 315                 320

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val
                325                 330                 335

Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly
            340                 345                 350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly
        355                 360                 365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp
    370                 375                 380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu
385                 390                 395                 400

Pro Trp Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu
                405                 410                 415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly
            420                 425                 430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
        435                 440                 445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
    450                 455                 460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val
465                 470                 475                 480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln
                485                 490                 495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn
            500                 505                 510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln
```

```
        515                 520                 525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe
    530                 535                 540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr
545                 550                 555                 560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe
                565                 570                 575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr
            580                 585                 590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala
        595                 600                 605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly
    610                 615                 620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn
625                 630                 635                 640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu
                645                 650                 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu
            660                 665                 670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala
        675                 680                 685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe
    690                 695                 700

Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala
705                 710                 715                 720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
                725                 730                 735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
            740                 745                 750
```

```
Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Ala Glu Lys
        755                 760                 765

Pro Asp Ile Met Leu Gly Val Val Cys Gly Ala Leu Asn Val Ala Asp
    770                 775                 780

Ala Met Phe Arg Thr Cys Met Thr Asp Phe Leu His Ser Leu Glu Arg
785                 790                 795                 800

Gly Gln Val Leu Pro Ala Asp Ser Leu Leu Asn Leu Val Asp Val Glu
                805                 810                 815

Leu Ile Tyr Gly Gly Val Lys Tyr Ile Leu Lys Val Ala Arg Gln Ser
            820                 825                 830

Leu Thr Met Phe Val Leu Ile Met Asn Gly Cys His Ile Glu Ile Asp
        835                 840                 845

Ala His Arg Leu Asn Asp Gly Gly Leu Leu Leu Ser Tyr Asn Gly Asn
    850                 855                 860

Ser Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Ser Tyr Arg Ile Thr
865                 870                 875                 880

Ile Gly Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp Pro Thr Val
                885                 890                 895

Leu Arg Ser Pro Ser Ala Gly Lys Leu Thr Gln Tyr Thr Val Glu Asp
            900                 905                 910

Gly Gly His Val Glu Ala Gly Ser Ser Tyr Ala Glu Met Glu Val Met
        915                 920                 925

Lys Met Ile Met Thr Leu Asn Val Gln Glu Arg Gly Arg Val Lys Tyr
    930                 935                 940

Ile Lys Arg Pro Gly Ala Val Leu Glu Ala Gly Cys Val Val Ala Arg
945                 950                 955                 960

Leu Glu Leu Asp Asp Pro Ser Lys Val His Pro Ala Glu Pro Phe Thr
                965                 970                 975
```

```
Gly Glu Leu Pro Ala Gln Gln Thr Leu Pro Ile Leu Gly Glu Lys Leu
            980                 985                 990

His Gln Val Phe His Ser Val Leu  Glu Asn Leu Thr Asn  Val Met
Ser
        995                1000                1005

Gly Phe  Cys Leu Pro Glu Pro  Val Phe Ser Ile Lys  Leu Lys Glu
    1010                1015                1020

Trp Val  Gln Lys Leu Met Met  Thr Leu Arg His Pro  Ser Leu Pro
    1025                1030                1035

Leu Leu  Glu Leu Gln Glu Ile  Met Thr Ser Val Ala  Gly Arg Ile
    1040                1045                1050

Pro Ala  Pro Val Glu Lys Ser  Val Arg Arg Val Met  Ala Gln Tyr
    1055                1060                1065

Ala Ser  Asn Ile Thr Ser Val  Leu Cys Gln Phe Pro  Ser Gln Gln
    1070                1075                1080

Ile Ala  Thr Ile Leu Asp Cys  His Ala Ala Thr Leu  Gln Arg Lys
    1085                1090                1095

Ala Asp  Arg Glu Val Phe Phe  Ile Asn Thr Gln Ser  Ile Val Gln
    1100                1105                1110

Leu Val  Gln Arg Tyr Arg Ser  Gly Ile Arg Gly Tyr  Met Lys Thr
    1115                1120                1125

Val Val  Leu Asp Leu Leu Arg  Arg Tyr Leu Arg Val  Glu His His
    1130                1135                1140

Phe Gln  Gln Ala His Tyr Asp  Lys Cys Val Ile Asn  Leu Arg Glu
    1145                1150                1155

Gln Phe  Lys Pro Asp Met Ser  Gln Val Leu Asp Cys  Ile Phe Ser
    1160                1165                1170

His Ala  Gln Val Ala Lys Lys  Asn Gln Leu Val Ile  Met Leu Ile
    1175                1180                1185
```

Asp Glu Leu Cys Gly Pro Asp Pro Ser Leu Ser Asp Glu Leu Ile
1190 1195 1200

Ser Ile Leu Asn Glu Leu Thr Gln Leu Ser Lys Ser Glu His Cys
1205 1210 1215

Lys Val Ala Leu Arg Ala Arg Gln Ile Leu Ile Ala Ser His Leu
1220 1225 1230

Pro Ser Tyr Glu Leu Arg His Asn Gln Val Glu Ser Ile Phe Leu
1235 1240 1245

Ser Ala Ile Asp Met Tyr Gly His Gln Phe Cys Pro Glu Asn Leu
1250 1255 1260

Lys Lys Leu Ile Leu Ser Glu Thr Thr Ile Phe Asp Val Leu Pro
1265 1270 1275

Thr Phe Phe Tyr His Ala Asn Lys Val Val Cys Met Ala Ser Leu
1280 1285 1290

Glu Val Tyr Val Arg Arg Gly Tyr Ile Ala Tyr Glu Leu Asn Ser
1295 1300 1305

Leu Gln His Arg Gln Leu Pro Asp Gly Thr Cys Val Val Glu Phe
1310 1315 1320

Gln Phe Met Leu Pro Ser Ser His Pro Asn Arg Met Thr Val Pro
1325 1330 1335

Ile Ser Ile Thr Asn Pro Asp Leu Leu Arg His Ser Thr Glu Leu
1340 1345 1350

Phe Met Asp Ser Gly Phe Ser Pro Leu Cys Gln Arg Met Gly Ala
1355 1360 1365

Met Val Ala Phe Arg Arg Phe Glu Asp Phe Thr Arg Asn Phe Asp
1370 1375 1380

Glu Val Ile Ser Cys Phe Ala Asn Val Pro Lys Asp Thr Pro Leu
1385 1390 1395

```
Phe Ser  Glu Ala Arg Thr Ser  Leu Tyr Ser Glu Asp  Asp Cys Lys
    1400                 1405                 1410

Ser Leu  Arg Glu Glu Pro Ile  His Ile Leu Asn Val  Ser Ile Gln
    1415                 1420                 1425

Cys Ala  Asp His Leu Glu Asp  Glu Ala Leu Val Pro  Ile Leu Arg
    1430                 1435                 1440

Thr Phe  Val Gln Ser Lys Lys  Asn Ile Leu Val Asp  Tyr Gly Leu
    1445                 1450                 1455

Arg Arg  Ile Thr Phe Leu Ile  Ala Gln Glu Lys Glu  Phe Pro Lys
    1460                 1465                 1470

Phe Phe  Thr Phe Arg Ala Arg  Asp Glu Phe Ala Glu  Asp Arg Ile
    1475                 1480                 1485

Tyr Arg  His Leu Glu Pro Ala  Leu Ala Phe Gln Leu  Glu Leu Asn
    1490                 1495                 1500

Arg Met  Arg Asn Phe Asp Leu  Thr Ala Val Pro Cys  Ala Asn His
    1505                 1510                 1515

Lys Met  His Leu Tyr Leu Gly  Ala Ala Lys Val Lys  Glu Gly Val
    1520                 1525                 1530

Glu Val  Thr Asp His Arg Phe  Phe Ile Arg Ala Ile  Ile Arg His
    1535                 1540                 1545

Ser Asp  Leu Ile Thr Lys Glu  Ala Ser Phe Glu Tyr  Leu Gln Asn
    1550                 1555                 1560

Glu Gly  Glu Arg Leu Leu Leu  Glu Ala Met Asp Glu  Leu Glu Val
    1565                 1570                 1575

Ala Phe  Asn Asn Thr Ser Val  Arg Thr Asp Cys Asn  His Ile Phe
    1580                 1585                 1590

Leu Asn  Phe Val Pro Thr Val  Ile Met Asp Pro Phe  Lys Ile Glu
    1595                 1600                 1605

Glu Ser  Val Arg Tyr Met Val  Met Arg Tyr Gly Ser  Arg Leu Trp
```

1610 1615 1620

Lys Leu Arg Val Leu Gln Ala Glu Val Lys Ile Asn Ile Arg Gln
1625 1630 1635

Thr Thr Thr Gly Ser Ala Val Pro Ile Arg Leu Phe Ile Thr Asn
1640 1645 1650

Glu Ser Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr
1655 1660 1665

Asp Ser Arg Ser Gly Asn Ile Met Phe His Ser Phe Gly Asn Lys
1670 1675 1680

Gln Gly Pro Gln His Gly Met Leu Ile Asn Thr Pro Tyr Val Thr
1685 1690 1695

Lys Asp Leu Leu Gln Ala Lys Arg Phe Gln Ala Gln Thr Leu Gly
1700 1705 1710

Thr Thr Tyr Ile Tyr Asp Phe Pro Glu Met Phe Arg Gln Ala Leu
1715 1720 1725

Phe Lys Leu Trp Gly Ser Pro Asp Lys Tyr Pro Lys Asp Ile Leu
1730 1735 1740

Thr Tyr Thr Glu Leu Val Leu Asp Ser Gln Gly Gln Leu Val Glu
1745 1750 1755

Met Asn Arg Leu Pro Gly Gly Asn Glu Val Gly Met Val Ala Phe
1760 1765 1770

Lys Met Arg Phe Lys Thr Gln Glu Tyr Pro Glu Gly Arg Asp Val
1775 1780 1785

Ile Val Ile Gly Asn Asp Ile Thr Phe Arg Ile Gly Ser Phe Gly
1790 1795 1800

Pro Gly Glu Asp Leu Leu Tyr Leu Arg Ala Ser Glu Met Ala Arg
1805 1810 1815

Ala Glu Gly Ile Pro Lys Ile Tyr Val Ala Ala Asn Ser Gly Ala
1820 1825 1830

```
Arg Ile  Gly Met Ala Glu Glu  Ile Lys His Met Phe  His Val Ala
    1835                1840                1845

Trp Val  Asp Pro Glu Asp Pro  His Lys Gly Phe Lys  Tyr Leu Tyr
    1850                1855                1860

Leu Thr  Pro Gln Asp Tyr Thr  Arg Ile Ser Ser Leu  Asn Ser Val
    1865                1870                1875

His Cys  Lys His Ile Glu Glu  Gly Gly Glu Ser Arg  Tyr Met Ile
    1880                1885                1890

Thr Asp  Ile Ile Gly Lys Asp  Asp Gly Leu Gly Val  Glu Asn Leu
    1895                1900                1905

Arg Gly  Ser Gly Met Ile Ala  Gly Glu Ser Ser Leu  Ala Tyr Glu
    1910                1915                1920

Glu Ile  Val Thr Ile Ser Leu  Val Thr Cys Arg Ala  Ile Gly Ile
    1925                1930                1935

Gly Ala  Tyr Leu Val Arg Leu  Gly Gln Arg Val Ile  Gln Val Glu
    1940                1945                1950

Asn Ser  His Ile Ile Leu Thr  Gly Ala Ser Ala Leu  Asn Lys Val
    1955                1960                1965

Leu Gly  Arg Glu Val Tyr Thr  Ser Asn Asn Gln Leu  Gly Gly Val
    1970                1975                1980

Gln Ile  Met His Tyr Asn Gly  Val Ser His Ile Thr  Val Pro Asp
    1985                1990                1995

Asp Phe  Glu Gly Val Tyr Thr  Ile Leu Glu Trp Leu  Ser Tyr Met
    2000                2005                2010

Pro Lys  Asp Asn His Ser Pro  Val Pro Ile Ile Thr  Pro Thr Asp
    2015                2020                2025

Pro Ile  Asp Arg Glu Ile Glu  Phe Leu Pro Ser Arg  Ala Pro Tyr
    2030                2035                2040
```

Asp Pro Arg Trp Met Leu Ala Gly Arg Pro His Pro Thr Leu Lys
2045 2050 2055

Gly Thr Trp Gln Ser Gly Phe Phe Asp His Gly Ser Phe Lys Glu
2060 2065 2070

Ile Met Ala Pro Trp Ala Gln Thr Val Val Thr Gly Arg Ala Arg
2075 2080 2085

Leu Gly Gly Ile Pro Val Gly Val Ile Ala Val Glu Thr Arg Thr
2090 2095 2100

Val Glu Val Ala Val Pro Ala Asp Pro Ala Asn Leu Asp Ser Glu
2105 2110 2115

Ala Lys Ile Ile Gln Gln Ala Gly Gln Val Trp Phe Pro Asp Ser
2120 2125 2130

Ala Tyr Lys Thr Ala Gln Ala Val Lys Asp Phe Asn Arg Glu Lys
2135 2140 2145

Leu Pro Leu Met Ile Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly
2150 2155 2160

Met Lys Asp Met Tyr Asp Gln Val Leu Lys Phe Gly Ala Tyr Ile
2165 2170 2175

Val Asp Gly Leu Arg Gln Tyr Lys Gln Pro Ile Leu Ile Tyr Ile
2180 2185 2190

Pro Pro Tyr Ala Glu Leu Arg Gly Gly Ser Trp Val Val Ile Asp
2195 2200 2205

Ala Thr Ile Asn Pro Leu Cys Ile Glu Met Tyr Ala Asp Lys Glu
2210 2215 2220

Ser Arg Gly Gly Val Leu Glu Pro Glu Gly Thr Val Glu Ile Lys
2225 2230 2235

Phe Arg Lys Lys Asp Leu Ile Lys Ser Met Arg Arg Ile Asp Pro
2240 2245 2250

Ala Tyr Lys Lys Leu Met Glu Gln Leu Gly Glu Pro Asp Leu Ser
2255 2260 2265

Asp Lys Asp Arg Lys Asp Leu Glu Gly Arg Leu Lys Ala Arg Glu
2270 2275 2280

Asp Leu Leu Leu Pro Ile Tyr His Gln Val Ala Val Gln Phe Ala
2285 2290 2295

Asp Phe His Asp Thr Pro Gly Arg Met Leu Glu Lys Gly Val Ile
2300 2305 2310

Ser Asp Ile Leu Glu Trp Lys Thr Ala Arg Thr Phe Leu Tyr Trp
2315 2320 2325

Arg Leu Arg Arg Leu Leu Leu Glu Asp Gln Val Lys Gln Glu Ile
2330 2335 2340

Leu Gln Ala Ser Gly Glu Leu Ser His Val His Ile Gln Ser Met
2345 2350 2355

Leu Arg Arg Trp Phe Val Glu Thr Glu Gly Ala Val Lys Ala Tyr
2360 2365 2370

Leu Trp Asp Asn Asn Gln Val Val Val Gln Trp Leu Glu Gln His
2375 2380 2385

Trp Gln Ala Gly Asp Gly Pro Arg Ser Thr Ile Arg Glu Asn Ile
2390 2395 2400

Thr Tyr Leu Lys His Asp Ser Val Leu Lys Thr Ile Arg Gly Leu
2405 2410 2415

Val Glu Glu Asn Pro Glu Val Ala Val Asp Cys Val Ile Tyr Leu
2420 2425 2430

Ser Gln His Ile Ser Pro Ala Glu Arg Ala Gln Val Val His Leu
2435 2440 2445

Leu Ser Thr Met Asp Ser Pro Ala Ser Thr
2450 2455

<210> 1288

<211> 858
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 386; "

<220>
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<220>
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<223> /note="Gene Name:
acetyl-CoA carboxylase beta; "

<220>
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<223> /note="ENSP ID: ENSP00000367085"

<400> 1288

Met	Thr	Val	Pro	Ile	Ser	Ile	Thr	Asn	Pro	Asp	Leu	Leu	Arg	His	Ser
1				5				10						15	

Thr	Glu	Leu	Phe	Met	Asp	Ser	Gly	Phe	Ser	Pro	Leu	Cys	Gln	Arg	Met
			20					25					30		

Gly	Ala	Met	Val	Ala	Phe	Arg	Arg	Phe	Glu	Asp	Phe	Thr	Arg	Asn	Phe
		35					40					45			

Asp	Glu	Val	Ile	Ser	Cys	Phe	Ala	Asn	Val	Pro	Lys	Asp	Thr	Pro	Leu
	50					55					60				

Phe	Ser	Glu	Ala	Arg	Thr	Ser	Leu	Tyr	Ser	Glu	Asp	Asp	Cys	Lys	Ser
65					70					75					80

Leu	Arg	Glu	Glu	Pro	Ile	His	Ile	Leu	Asn	Val	Ser	Ile	Gln	Cys	Ala
				85					90					95	

Asp	His	Leu	Glu	Asp	Glu	Ala	Leu	Val	Pro	Ile	Leu	Arg	Thr	Phe	Val
			100					105					110		

Gln	Ser	Lys	Lys	Asn	Ile	Leu	Val	Asp	Tyr	Gly	Leu	Arg	Arg	Ile	Thr
		115					120					125			

Phe	Leu	Ile	Ala	Gln	Glu	Lys	Glu	Phe	Pro	Lys	Phe	Phe	Thr	Phe	Arg
	130					135					140				

```
Ala Arg Asp Glu Phe Ala Glu Asp Arg Ile Tyr Arg His Leu Glu Pro
145                 150                 155                 160

Ala Leu Ala Phe Gln Leu Glu Leu Asn Arg Met Arg Asn Phe Asp Leu
                165                 170                 175

Thr Ala Val Pro Cys Ala Asn His Lys Met His Leu Tyr Leu Gly Ala
            180                 185                 190

Ala Lys Val Lys Glu Gly Val Glu Val Thr Asp His Arg Phe Phe Ile
        195                 200                 205

Arg Ala Ile Ile Arg His Ser Asp Leu Ile Thr Lys Glu Ala Ser Phe
    210                 215                 220

Glu Tyr Leu Gln Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met Asp
225                 230                 235                 240

Glu Leu Glu Val Ala Phe Asn Asn Thr Ser Val Arg Thr Asp Cys Asn
                245                 250                 255

His Ile Phe Leu Asn Phe Val Pro Thr Val Ile Met Asp Pro Phe Lys
            260                 265                 270

Ile Glu Glu Ser Val Arg Tyr Met Val Met Arg Tyr Gly Ser Arg Leu
        275                 280                 285

Trp Lys Leu Arg Val Leu Gln Ala Glu Val Lys Ile Asn Ile Arg Gln
    290                 295                 300

Thr Thr Thr Gly Ser Ala Val Pro Ile Arg Leu Phe Ile Thr Asn Glu
305                 310                 315                 320

Ser Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr Asp Ser
                325                 330                 335

Arg Ser Gly Asn Ile Met Phe His Ser Phe Gly Asn Lys Gln Gly Pro
            340                 345                 350

Gln His Gly Met Leu Ile Asn Thr Pro Tyr Val Thr Lys Asp Leu Leu
        355                 360                 365
```

```
Gln Ala Lys Arg Phe Gln Ala Gln Thr Leu Gly Thr Thr Tyr Ile Tyr
    370                 375                 380

Asp Phe Pro Glu Met Phe Arg Gln Ala Leu Phe Lys Leu Trp Gly Ser
385                 390                 395                 400

Pro Asp Lys Tyr Pro Lys Asp Ile Leu Thr Tyr Thr Glu Leu Val Leu
                405                 410                 415

Asp Ser Gln Gly Gln Leu Val Glu Met Asn Arg Leu Pro Gly Gly Asn
            420                 425                 430

Glu Val Gly Met Val Ala Phe Lys Met Arg Phe Lys Thr Gln Glu Tyr
        435                 440                 445

Pro Glu Gly Arg Asp Val Ile Val Ile Gly Asn Asp Ile Thr Phe Arg
    450                 455                 460

Ile Gly Ser Phe Gly Pro Gly Glu Asp Leu Leu Tyr Leu Arg Ala Ser
465                 470                 475                 480

Glu Met Ala Arg Ala Glu Gly Ile Pro Lys Ile Tyr Val Ala Ala Asn
                485                 490                 495

Ser Gly Ala Arg Ile Gly Met Ala Glu Glu Ile Lys His Met Phe His
            500                 505                 510

Val Ala Trp Val Asp Pro Glu Asp Pro His Lys Gly Phe Lys Tyr Leu
        515                 520                 525

Tyr Leu Thr Pro Gln Asp Tyr Thr Arg Ile Ser Ser Leu Asn Ser Val
    530                 535                 540

His Cys Lys His Ile Glu Glu Gly Gly Glu Ser Arg Tyr Met Ile Thr
545                 550                 555                 560

Asp Ile Ile Gly Lys Asp Asp Gly Leu Gly Val Glu Asn Leu Arg Gly
                565                 570                 575

Ser Gly Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr Glu Glu Ile Val
            580                 585                 590

Thr Ile Ser Leu Val Thr Cys Arg Ala Ile Gly Ile Gly Ala Tyr Leu
```

595 600 605

Val Arg Leu Gly Gln Arg Val Ile Gln Val Glu Asn Ser His Ile Ile
610 615 620

Leu Thr Gly Ala Ser Ala Leu Asn Lys Val Leu Gly Arg Glu Val Tyr
625 630 635 640

Thr Ser Asn Asn Gln Leu Gly Gly Val Gln Ile Met His Tyr Asn Gly
645 650 655

Val Ser His Ile Thr Val Pro Asp Asp Phe Glu Gly Val Tyr Thr Ile
660 665 670

Leu Glu Trp Leu Ser Tyr Met Pro Lys Asp Asn His Ser Pro Val Pro
675 680 685

Ile Ile Thr Pro Thr Asp Pro Ile Asp Arg Glu Ile Glu Phe Leu Pro
690 695 700

Ser Arg Ala Pro Tyr Asp Pro Arg Trp Met Leu Ala Gly Arg Pro His
705 710 715 720

Pro Thr Leu Lys Gly Thr Trp Gln Ser Gly Phe Phe Asp His Gly Ser
725 730 735

Phe Lys Glu Ile Met Ala Pro Trp Ala Gln Thr Val Val Thr Gly Arg
740 745 750

Ala Arg Leu Gly Gly Ile Pro Val Gly Val Ile Ala Val Glu Thr Arg
755 760 765

Thr Val Glu Val Ala Val Pro Ala Asp Pro Ala Asn Leu Asp Ser Glu
770 775 780

Ala Lys Ile Ile Gln Gln Ala Gly Gln Val Trp Phe Pro Asp Ser Ala
785 790 795 800

Tyr Lys Thr Ala Gln Ala Val Lys Asp Phe Asn Arg Glu Lys Leu Pro
805 810 815

Leu Met Ile Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly Met Lys Gly
820 825 830

```
Cys Leu Gly Thr Trp Arg Asp Val Ser Trp Trp Lys Ile Arg Ala Met
        835                 840                 845


Leu Pro Met His Ile Gly Glu Gly Ser Val
    850                 855


<210> 1289
<211> 859
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 386; "

<220>
<221> source
<223> /note="Gene Symbol: ACACB; "

<220>
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<223> /note="Gene Name:
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<220>
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 1289
Xaa Met Thr Val Pro Ile Ser Ile Thr Asn Pro Asp Leu Leu Arg His
1               5                  10                  15


Ser Thr Glu Leu Phe Met Asp Ser Gly Phe Ser Pro Leu Cys Gln Arg
            20                  25                  30


Met Gly Ala Met Val Ala Phe Arg Arg Phe Glu Asp Phe Thr Arg Asn
        35                  40                  45


Phe Asp Glu Val Ile Ser Cys Phe Ala Asn Val Pro Lys Asp Thr Pro
    50                  55                  60


Leu Phe Ser Glu Ala Arg Thr Ser Leu Tyr Ser Glu Asp Asp Cys Lys
65                  70                  75                  80
```

```
Ser Leu Arg Glu Glu Pro Ile His Ile Leu Asn Val Ser Ile Gln Cys
                85                  90                  95

Ala Asp His Leu Glu Asp Glu Ala Leu Val Pro Ile Leu Arg Thr Phe
            100                 105                 110

Val Gln Ser Lys Lys Asn Ile Leu Val Asp Tyr Gly Leu Arg Arg Ile
        115                 120                 125

Thr Phe Leu Ile Ala Gln Glu Lys Glu Phe Pro Lys Phe Phe Thr Phe
    130                 135                 140

Arg Ala Arg Asp Glu Phe Ala Glu Asp Arg Ile Tyr Arg His Leu Glu
145                 150                 155                 160

Pro Ala Leu Ala Phe Gln Leu Glu Leu Asn Arg Met Arg Asn Phe Asp
                165                 170                 175

Leu Thr Ala Val Pro Cys Ala Asn His Lys Met His Leu Tyr Leu Gly
            180                 185                 190

Ala Ala Lys Val Lys Glu Gly Val Glu Val Thr Asp His Arg Phe Phe
        195                 200                 205

Ile Arg Ala Ile Ile Arg His Ser Asp Leu Ile Thr Lys Glu Ala Ser
    210                 215                 220

Phe Glu Tyr Leu Gln Asn Glu Gly Glu Arg Leu Leu Leu Glu Ala Met
225                 230                 235                 240

Asp Glu Leu Glu Val Ala Phe Asn Asn Thr Ser Val Arg Thr Asp Cys
                245                 250                 255

Asn His Ile Phe Leu Asn Phe Val Pro Thr Val Ile Met Asp Pro Phe
            260                 265                 270

Lys Ile Glu Glu Ser Val Arg Tyr Met Val Met Arg Tyr Gly Ser Arg
        275                 280                 285

Leu Trp Lys Leu Arg Val Leu Gln Ala Glu Val Lys Ile Asn Ile Arg
    290                 295                 300
```

```
Gln Thr Thr Thr Gly Ser Ala Val Pro Ile Arg Leu Phe Ile Thr Asn
305                 310                 315                 320

Glu Ser Gly Tyr Tyr Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr Asp
                325                 330                 335

Ser Arg Ser Gly Asn Ile Met Phe His Ser Phe Gly Asn Lys Gln Gly
            340                 345                 350

Pro Gln His Gly Met Leu Ile Asn Thr Pro Tyr Val Thr Lys Asp Leu
        355                 360                 365

Leu Gln Ala Lys Arg Phe Gln Ala Gln Thr Leu Gly Thr Thr Tyr Ile
    370                 375                 380

Tyr Asp Phe Pro Glu Met Phe Arg Gln Ala Leu Phe Lys Leu Trp Gly
385                 390                 395                 400

Ser Pro Asp Lys Tyr Pro Lys Asp Ile Leu Thr Tyr Thr Glu Leu Val
                405                 410                 415

Leu Asp Ser Gln Gly Gln Leu Val Glu Met Asn Arg Leu Pro Gly Gly
            420                 425                 430

Asn Glu Val Gly Met Val Ala Phe Lys Met Arg Phe Lys Thr Gln Glu
        435                 440                 445

Tyr Pro Glu Gly Arg Asp Val Ile Val Ile Gly Asn Asp Ile Thr Phe
    450                 455                 460

Arg Ile Gly Ser Phe Gly Pro Gly Glu Asp Leu Leu Tyr Leu Arg Ala
465                 470                 475                 480

Ser Glu Met Ala Arg Ala Glu Gly Ile Pro Lys Ile Tyr Val Ala Ala
                485                 490                 495

Asn Ser Gly Ala Arg Ile Gly Met Ala Glu Glu Ile Lys His Met Phe
            500                 505                 510

His Val Ala Trp Val Asp Pro Glu Asp Pro His Lys Gly Phe Lys Tyr
        515                 520                 525
```

```
Leu Tyr Leu Thr Pro Gln Asp Tyr Thr Arg Ile Ser Ser Leu Asn Ser
    530                 535                 540

Val His Cys Lys His Ile Glu Glu Gly Gly Glu Ser Arg Tyr Met Ile
545                 550                 555                 560

Thr Asp Ile Ile Gly Lys Asp Asp Gly Leu Gly Val Glu Asn Leu Arg
                565                 570                 575

Gly Ser Gly Met Ile Ala Gly Glu Ser Ser Leu Ala Tyr Glu Glu Ile
            580                 585                 590

Val Thr Ile Ser Leu Val Thr Cys Arg Ala Ile Gly Ile Gly Ala Tyr
        595                 600                 605

Leu Val Arg Leu Gly Gln Arg Val Ile Gln Val Glu Asn Ser His Ile
    610                 615                 620

Ile Leu Thr Gly Ala Ser Ala Leu Asn Lys Val Leu Gly Arg Glu Val
625                 630                 635                 640

Tyr Thr Ser Asn Asn Gln Leu Gly Gly Val Gln Ile Met His Tyr Asn
                645                 650                 655

Gly Val Ser His Ile Thr Val Pro Asp Asp Phe Glu Gly Val Tyr Thr
            660                 665                 670

Ile Leu Glu Trp Leu Ser Tyr Met Pro Lys Asp Asn His Ser Pro Val
        675                 680                 685

Pro Ile Ile Thr Pro Thr Asp Pro Ile Asp Arg Glu Ile Glu Phe Leu
    690                 695                 700

Pro Ser Arg Ala Pro Tyr Asp Pro Arg Trp Met Leu Ala Gly Arg Pro
705                 710                 715                 720

His Pro Thr Leu Lys Gly Thr Trp Gln Ser Gly Phe Phe Asp His Gly
                725                 730                 735

Ser Phe Lys Glu Ile Met Ala Pro Trp Ala Gln Thr Val Val Thr Gly
            740                 745                 750

Arg Ala Arg Leu Gly Gly Ile Pro Val Gly Val Ile Ala Val Glu Thr
```

```
        755                 760                 765

Arg Thr Val Glu Val Ala Val Pro Ala Asp Pro Ala Asn Leu Asp Ser
    770                 775                 780

Glu Ala Lys Ile Ile Gln Gln Ala Gly Gln Val Trp Phe Pro Asp Ser
785                 790                 795                 800

Ala Tyr Lys Thr Ala Gln Ala Val Lys Asp Phe Asn Arg Glu Lys Leu
                805                 810                 815

Pro Leu Met Ile Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly Met Lys
            820                 825                 830

Gly Cys Leu Gly Thr Trp Arg Asp Val Ser Trp Trp Lys Ile Arg Ala
        835                 840                 845

Met Leu Pro Met His Ile Gly Glu Gly Ser Val
    850                 855


<210> 1290
<211> 143
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<220>
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<220>
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<400> 1290
Met Thr Asp Ser Lys Pro Ile Thr Lys Ser Lys Ser Glu Ala Asn Leu
1               5                   10                  15

Ile Pro Ser Gln Glu Pro Phe Pro Ala Ser Asp Asn Ser Gly Glu Thr
            20                  25                  30
```

```
Pro Gln Arg Asn Gly Glu Gly His Thr Leu Pro Lys Thr Pro Ser Gln
        35                  40                  45

Ala Glu Pro Ala Ser His Lys Gly Pro Lys Asp Ala Gly Arg Arg Arg
    50                  55                  60

Asn Ser Leu Pro Pro Ser His Gln Lys Pro Pro Arg Asn Pro Leu Ser
65                  70                  75                  80

Ser Ser Asp Ala Ala Pro Ser Pro Glu Leu Gln Ala Asn Gly Thr Gly
                85                  90                  95

Thr Gln Gly Leu Glu Ala Thr Asp Thr Asn Gly Leu Ser Ser Ser Ala
            100                 105                 110

Arg Pro Gln Gly Gln Gln Ala Gly Ser Pro Ser Lys Glu Asp Lys Lys
        115                 120                 125

Gln Ala Asn Ile Lys Arg Gln Leu Met Thr Asn Phe Ile Leu Gly
    130                 135                 140


<210> 1291
<211> 155
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000474680"

<400> 1291
Met Ser Pro Ala Lys Cys Lys Ile Cys Phe Pro Asp Arg Glu Val Lys
1               5                   10                  15

Pro Ser Met Ser Gly Leu His Leu Val Lys Arg Gly Arg Glu His Lys
```

```
            20                  25                  30

Lys Leu Asp Leu His Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe
        35                  40                  45

Val Thr Arg Phe Gly Gly Asp Arg Val Ile Glu Lys Val Leu Ile Ala
    50                  55                  60

Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp
65                  70                  75                  80

Ala Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met
                85                  90                  95

Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala
            100                 105                 110

Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala
        115                 120                 125

Asn Val Glu Leu Ile Val Asp Ile Ala Lys Arg Ile Pro Val Gln Ala
    130                 135                 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn
145                 150                 155


<210> 1292
<211> 112
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000478488"
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 1292
Xaa Val Glu Met Asn Arg Leu Pro Gly Gly Asn Glu Val Gly Met Val
1   5   10   15

Ala Phe Lys Met Arg Phe Lys Thr Gln Glu Tyr Pro Glu Gly Arg Asp
            20   25   30

Val Ile Val Ile Gly Asn Asp Ile Thr Phe Arg Ile Gly Ser Phe Gly
        35   40   45

Pro Gly Glu Asp Leu Leu Tyr Leu Arg Ala Ser Glu Met Ala Arg Ala
    50   55   60

Glu Gly Ile Pro Lys Ile Tyr Val Ala Ala Asn Ser Gly Ala Arg Ile
65   70   75   80

Gly Met Ala Glu Glu Ile Lys His Met Phe His Val Ala Trp Val Asp
                85   90   95

Pro Glu Asp Pro His Lys Ile His Asp His Gly Tyr His Arg Glu Gly
            100   105   110

<210> 1293
<211> 345
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ASMT; "

<220>
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<223> /note="Gene Name:
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      methyltransferase; "

<220>
<221> source
<223> /note="Uniprot ID: P46597; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370627"

<400> 1293
Met Gly Ser Ser Glu Asp Gln Ala Tyr Arg Leu Leu Asn Asp Tyr Ala
1   5   10   15

Asn Gly Phe Met Val Ser Gln Val Leu Phe Ala Ala Cys Glu Leu Gly
            20   25   30

Val Phe Asp Leu Leu Ala Glu Ala Pro Gly Pro Leu Asp Val Ala Ala
        35   40   45

Val Ala Ala Gly Val Arg Ala Ser Ala His Gly Thr Glu Leu Leu Leu
    50   55   60

Asp Ile Cys Val Ser Leu Lys Leu Leu Lys Val Glu Thr Arg Gly Gly
65   70   75   80

Lys Ala Phe Tyr Arg Asn Thr Glu Leu Ser Ser Asp Tyr Leu Thr Thr
                85   90   95

Val Ser Pro Thr Ser Gln Cys Ser Met Leu Lys Tyr Met Gly Arg Thr
            100   105   110

Ser Tyr Arg Cys Trp Gly His Leu Ala Asp Ala Val Arg Glu Gly Arg
        115   120   125

Asn Gln Tyr Leu Glu Thr Phe Gly Val Pro Ala Glu Glu Leu Phe Thr
    130   135   140

Ala Ile Tyr Arg Ser Glu Gly Glu Arg Leu Gln Phe Met Gln Ala Leu
145   150   155   160

Gln Glu Val Trp Ser Val Asn Gly Arg Ser Val Leu Thr Ala Phe Asp
                165   170   175

Leu Ser Val Phe Pro Leu Met Cys Asp Leu Gly Gly Gly Ala Gly Ala
            180   185   190

Leu Ala Lys Glu Cys Met Ser Leu Tyr Pro Gly Cys Lys Ile Thr Val
        195   200   205

```
Phe Asp Ile Pro Glu Val Val Trp Thr Ala Lys Gln His Phe Ser Phe
    210                 215                 220

Gln Glu Glu Glu Gln Ile Asp Phe Gln Glu Gly Asp Phe Phe Lys Asp
225                 230                 235                 240

Pro Leu Pro Glu Ala Asp Leu Tyr Ile Leu Ala Arg Val Leu His Asp
                245                 250                 255

Trp Ala Asp Gly Lys Cys Ser His Leu Leu Glu Arg Ile Tyr His Thr
            260                 265                 270

Cys Lys Pro Gly Gly Gly Ile Leu Val Ile Glu Ser Leu Leu Asp Glu
        275                 280                 285

Asp Arg Arg Gly Pro Leu Leu Thr Gln Leu Tyr Ser Leu Asn Met Leu
    290                 295                 300

Val Gln Thr Glu Gly Gln Glu Arg Thr Pro Thr His Tyr His Met Leu
305                 310                 315                 320

Leu Ser Ser Ala Gly Phe Arg Asp Phe Gln Phe Lys Lys Thr Gly Ala
                325                 330                 335

Ile Tyr Asp Ala Ile Leu Ala Arg Lys
            340                 345


<210> 1294
<211> 298
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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      methyltransferase; "

<220>
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<221> source
<223> /note="Uniprot ID: P46597; "

<220>
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<223> /note="ENSP ID: ENSP00000370631"

<400> 1294

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Met Gly Ser Ser Glu Asp Gln Ala Tyr Arg Leu Leu Asn Asp Tyr Ala
1               5                  10                  15

Asn Gly Phe Met Val Ser Gln Val Leu Phe Ala Ala Cys Glu Leu Gly
            20                  25                  30

Val Phe Asp Leu Leu Ala Glu Ala Pro Gly Pro Leu Asp Val Ala Ala
        35                  40                  45

Val Ala Ala Gly Val Arg Ala Ser Ala His Gly Thr Glu Leu Leu Leu
    50                  55                  60

Asp Ile Cys Val Ser Leu Lys Leu Leu Lys Val Glu Thr Arg Gly Gly
65                  70                  75                  80

Lys Ala Phe Tyr Arg Asn Thr Glu Leu Ser Ser Asp Tyr Leu Thr Thr
                85                  90                  95

Val Ser Pro Thr Ser Gln Cys Ser Met Leu Lys Tyr Met Gly Arg Thr
            100                 105                 110

Ser Tyr Arg Cys Trp Gly His Leu Ala Asp Ala Val Arg Glu Gly Arg
        115                 120                 125

Asn Gln Tyr Leu Glu Thr Phe Gly Val Pro Ala Glu Glu Leu Phe Thr
    130                 135                 140

Ala Ile Tyr Arg Ser Glu Gly Glu Arg Leu Gln Phe Met Gln Ala Leu
145                 150                 155                 160

Gln Glu Val Trp Ser Val Asn Gly Arg Ser Val Leu Thr Ala Phe Asp
                165                 170                 175

Leu Ser Val Phe Pro Leu Met Cys Asp Leu Gly Gly Asp Phe Phe Lys
            180                 185                 190

Asp Pro Leu Pro Glu Ala Asp Leu Tyr Ile Leu Ala Arg Val Leu His
```

```
        195                 200                 205

Asp Trp Ala Asp Gly Lys Cys Ser His Leu Leu Glu Arg Ile Tyr His
    210                 215                 220

Thr Cys Lys Pro Gly Gly Gly Ile Leu Val Ile Glu Ser Leu Leu Asp
225                 230                 235                 240

Glu Asp Arg Arg Gly Pro Leu Leu Thr Gln Leu Tyr Ser Leu Asn Met
                245                 250                 255

Leu Val Gln Thr Glu Gly Gln Glu Arg Thr Pro Thr His Tyr His Met
            260                 265                 270

Leu Leu Ser Ser Ala Gly Phe Arg Asp Phe Gln Phe Lys Lys Thr Gly
        275                 280                 285

Ala Ile Tyr Asp Ala Ile Leu Ala Arg Lys
    290                 295


<210> 1295
<211> 373
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 387; "

<220>
<221> source
<223> /note="Gene Symbol: ASMT; "

<220>
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<223> /note="Gene Name:
      acetylserotonin O-
      methyltransferase; "

<220>
<221> source
<223> /note="Uniprot ID:  P46597; "

<220>
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<223> /note="ENSP ID: ENSP00000370639"

<400> 1295
Met Gly Ser Ser Glu Asp Gln Ala Tyr Arg Leu Leu Asn Asp Tyr Ala
1               5                   10                  15
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Asn Gly Phe Met Val Ser Gln Val Leu Phe Ala Ala Cys Glu Leu Gly
            20                  25                  30

Val Phe Asp Leu Leu Ala Glu Ala Pro Gly Pro Leu Asp Val Ala Ala
        35                  40                  45

Val Ala Ala Gly Val Arg Ala Ser Ala His Gly Thr Glu Leu Leu Leu
    50                  55                  60

Asp Ile Cys Val Ser Leu Lys Leu Leu Lys Val Glu Thr Arg Gly Gly
65                  70                  75                  80

Lys Ala Phe Tyr Arg Asn Thr Glu Leu Ser Ser Asp Tyr Leu Thr Thr
                85                  90                  95

Val Ser Pro Thr Ser Gln Cys Ser Met Leu Lys Tyr Met Gly Arg Thr
            100                 105                 110

Ser Tyr Arg Cys Trp Gly His Leu Ala Asp Ala Val Arg Glu Gly Arg
        115                 120                 125

Asn Gln Tyr Leu Glu Thr Phe Gly Val Pro Ala Glu Glu Leu Phe Thr
    130                 135                 140

Ala Ile Tyr Arg Ser Glu Gly Glu Arg Leu Gln Phe Met Gln Ala Leu
145                 150                 155                 160

Gln Glu Val Trp Ser Val Asn Gly Arg Ser Val Leu Thr Ala Phe Asp
                165                 170                 175

Leu Ser Val Phe Pro Leu Met Cys Asp Leu Gly Gly Thr Trp Ile Lys
            180                 185                 190

Leu Glu Thr Ile Ile Leu Ser Lys Leu Ser Gln Gly Gln Lys Thr Lys
        195                 200                 205

His Arg Val Phe Ser Leu Ile Gly Gly Ala Gly Ala Leu Ala Lys Glu
    210                 215                 220

Cys Met Ser Leu Tyr Pro Gly Cys Lys Ile Thr Val Phe Asp Ile Pro
225                 230                 235                 240
```

```
Glu Val Val Trp Thr Ala Lys Gln His Phe Ser Phe Gln Glu Glu Glu
                245                 250                 255

Gln Ile Asp Phe Gln Glu Gly Asp Phe Phe Lys Asp Pro Leu Pro Glu
            260                 265                 270

Ala Asp Leu Tyr Ile Leu Ala Arg Val Leu His Asp Trp Ala Asp Gly
        275                 280                 285

Lys Cys Ser His Leu Leu Glu Arg Ile Tyr His Thr Cys Lys Pro Gly
    290                 295                 300

Gly Gly Ile Leu Val Ile Glu Ser Leu Leu Asp Glu Asp Arg Arg Gly
305                 310                 315                 320

Pro Leu Leu Thr Gln Leu Tyr Ser Leu Asn Met Leu Val Gln Thr Glu
                325                 330                 335

Gly Gln Glu Arg Thr Pro Thr His Tyr His Met Leu Leu Ser Ser Ala
            340                 345                 350

Gly Phe Arg Asp Phe Gln Phe Lys Lys Thr Gly Ala Ile Tyr Asp Ala
        355                 360                 365

Ile Leu Ala Arg Lys
    370


<210> 1296
<211> 124
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 387; "

<220>
<221> source
<223> /note="Gene Symbol: ASMT; "

<220>
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<223> /note="Gene Name:
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      methyltransferase; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000392053"

<400> 1296
Asp Cys Arg Leu Thr Ser Val Cys Leu Pro Cys Val Pro Gly Asp Phe
1   5   10   15

Phe Lys Asp Pro Leu Pro Glu Ala Asp Leu Tyr Ile Leu Ala Arg Val
            20   25   30

Leu His Asp Trp Ala Asp Gly Lys Cys Ser His Leu Leu Glu Arg Ile
        35   40   45

Tyr His Thr Cys Lys Pro Gly Gly Gly Ile Leu Val Ile Glu Ser Leu
    50   55   60

Leu Asp Glu Asp Arg Arg Gly Pro Leu Leu Thr Gln Leu Tyr Ser Leu
65   70   75   80

Asn Met Leu Val Gln Thr Glu Gly Gln Glu Arg Thr Pro Thr His Tyr
                85   90   95

His Met Leu Leu Ser Ser Ala Gly Phe Arg Asp Phe Gln Phe Lys Lys
            100   105   110

Thr Gly Ala Ile Tyr Asp Ala Ile Leu Ala Arg Lys
        115   120

<210> 1297
<211> 621
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 388; "

<220>
<221> source
<223> /note="Gene Symbol: ASMTL; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID: O95671; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370718"

<400> 1297
Met Val Leu Cys Pro Val Ile Gly Lys Leu Leu His Lys Arg Val Val
1   5   10   15

Leu Ala Ser Ala Ser Pro Arg Arg Gln Glu Ile Leu Ser Asn Ala Gly
            20   25   30

Leu Arg Phe Glu Val Val Pro Ser Lys Phe Lys Glu Lys Leu Asp Lys
        35   40   45

Ala Ser Phe Ala Thr Pro Tyr Gly Tyr Ala Met Glu Thr Ala Lys Gln
    50   55   60

Lys Ala Leu Glu Val Ala Asn Arg Leu Tyr Gln Lys Asp Leu Arg Ala
65   70   75   80

Pro Asp Val Val Ile Gly Ala Asp Thr Ile Val Thr Val Gly Gly Leu
                85   90   95

Ile Leu Glu Lys Pro Val Asp Lys Gln Asp Ala Tyr Arg Met Leu Ser
            100   105   110

Arg Leu Ser Gly Arg Glu His Ser Val Phe Thr Gly Val Ala Ile Val
        115   120   125

His Cys Ser Ser Lys Asp His Gln Leu Asp Thr Arg Val Ser Glu Phe
    130   135   140

Tyr Glu Glu Thr Lys Val Lys Phe Ser Glu Leu Ser Glu Glu Leu Leu
145   150   155   160

Trp Glu Tyr Val His Ser Gly Glu Pro Met Asp Lys Ala Gly Gly Tyr
                165   170   175

Gly Ile Gln Ala Leu Gly Gly Met Leu Val Glu Ser Val His Gly Asp
            180   185   190

Phe Leu Asn Val Val Gly Phe Pro Leu Asn His Phe Cys Lys Gln Leu
        195   200   205

```
Val Lys Leu Tyr Tyr Pro Pro Arg Pro Glu Asp Leu Arg Arg Ser Val
    210                 215                 220

Lys His Asp Ser Ile Pro Ala Ala Asp Thr Phe Glu Asp Leu Ser Asp
225                 230                 235                 240

Val Glu Gly Gly Gly Ser Glu Pro Thr Gln Arg Asp Ala Gly Ser Arg
                245                 250                 255

Asp Glu Lys Ala Glu Ala Gly Glu Ala Gly Gln Ala Thr Ala Glu Ala
            260                 265                 270

Glu Cys His Arg Thr Arg Glu Thr Leu Pro Pro Phe Pro Thr Arg Leu
        275                 280                 285

Leu Glu Leu Ile Glu Gly Phe Met Leu Ser Lys Gly Leu Leu Thr Ala
    290                 295                 300

Cys Lys Leu Lys Val Phe Asp Leu Leu Lys Asp Glu Ala Pro Gln Lys
305                 310                 315                 320

Ala Ala Asp Ile Ala Ser Lys Val Asp Ala Ser Ala Cys Gly Met Glu
                325                 330                 335

Arg Leu Leu Asp Ile Cys Ala Ala Met Gly Leu Leu Glu Lys Thr Glu
            340                 345                 350

Gln Gly Tyr Ser Asn Thr Glu Thr Ala Asn Val Tyr Leu Ala Ser Asp
        355                 360                 365

Gly Glu Tyr Ser Leu His Gly Phe Ile Met His Asn Asn Asp Leu Thr
    370                 375                 380

Trp Asn Leu Phe Thr Tyr Leu Glu Phe Ala Ile Arg Glu Gly Thr Asn
385                 390                 395                 400

Gln His His Arg Ala Leu Gly Lys Lys Ala Glu Asp Leu Phe Gln Asp
                405                 410                 415

Ala Tyr Tyr Gln Ser Pro Glu Thr Arg Leu Arg Phe Met Arg Ala Met
            420                 425                 430
```

```
His Gly Met Thr Lys Leu Thr Ala Cys Gln Val Ala Thr Ala Phe Asn
        435                 440                 445

Leu Ser Arg Phe Ser Ser Ala Cys Asp Val Gly Gly Cys Thr Gly Ala
    450                 455                 460

Leu Ala Arg Glu Leu Ala Arg Glu Tyr Pro Arg Met Gln Val Thr Val
465                 470                 475                 480

Phe Asp Leu Pro Asp Ile Ile Glu Leu Ala Ala His Phe Gln Pro Pro
                485                 490                 495

Gly Pro Gln Ala Val Gln Ile His Phe Ala Ala Gly Asp Phe Phe Arg
            500                 505                 510

Asp Pro Leu Pro Ser Ala Glu Leu Tyr Val Leu Cys Arg Ile Leu His
        515                 520                 525

Asp Trp Pro Asp Asp Lys Val His Lys Leu Leu Ser Arg Val Ala Glu
    530                 535                 540

Ser Cys Lys Pro Gly Ala Gly Leu Leu Leu Val Glu Thr Leu Leu Asp
545                 550                 555                 560

Glu Glu Lys Arg Val Ala Gln Arg Ala Leu Met Gln Ser Leu Asn Met
                565                 570                 575

Leu Val Gln Thr Glu Gly Lys Glu Arg Ser Leu Gly Glu Tyr Gln Cys
            580                 585                 590

Leu Leu Glu Leu His Gly Phe His Gln Val Gln Val Val His Leu Gly
        595                 600                 605

Gly Val Leu Asp Ala Ile Leu Ala Thr Lys Val Ala Pro
    610                 615                 620


<210> 1298
<211> 605
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 388; "
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<220>
<221> source
<223> /note="Gene Symbol: ASMTL; "

<220>
<221> source
<223> /note="Gene Name:
acetylserotonin O-methyltransferase-like; "

<220>
<221> source
<223> /note="Uniprot ID: O95671; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370734"

<400> 1298
Met Val Leu Cys Pro Val Ile Gly Lys Leu Leu His Lys Arg Val Val
1 5 10 15

Leu Ala Ser Ala Ser Pro Arg Arg Gln Glu Ile Leu Ser Asn Ala Gly
20 25 30

Leu Arg Phe Glu Val Val Pro Ser Lys Phe Lys Glu Lys Leu Asp Lys
35 40 45

Ala Ser Phe Ala Thr Pro Tyr Gly Tyr Ala Met Glu Thr Ala Lys Gln
50 55 60

Lys Ala Leu Glu Val Ala Asn Arg Leu Tyr Gln Thr Val Gly Gly Leu
65 70 75 80

Ile Leu Glu Lys Pro Val Asp Lys Gln Asp Ala Tyr Arg Met Leu Ser
85 90 95

Arg Leu Ser Gly Arg Glu His Ser Val Phe Thr Gly Val Ala Ile Val
100 105 110

His Cys Ser Ser Lys Asp His Gln Leu Asp Thr Arg Val Ser Glu Phe
115 120 125

Tyr Glu Glu Thr Lys Val Lys Phe Ser Glu Leu Ser Glu Glu Leu Leu
130 135 140

Trp Glu Tyr Val His Ser Gly Glu Pro Met Asp Lys Ala Gly Gly Tyr
145 150 155 160

```
Gly Ile Gln Ala Leu Gly Gly Met Leu Val Glu Ser Val His Gly Asp
                165                 170                 175

Phe Leu Asn Val Val Gly Phe Pro Leu Asn His Phe Cys Lys Gln Leu
            180                 185                 190

Val Lys Leu Tyr Tyr Pro Pro Arg Pro Glu Asp Leu Arg Arg Ser Val
        195                 200                 205

Lys His Asp Ser Ile Pro Ala Ala Asp Thr Phe Glu Asp Leu Ser Asp
    210                 215                 220

Val Glu Gly Gly Gly Ser Glu Pro Thr Gln Arg Asp Ala Gly Ser Arg
225                 230                 235                 240

Asp Glu Lys Ala Glu Ala Gly Glu Ala Gly Gln Ala Thr Ala Glu Ala
                245                 250                 255

Glu Cys His Arg Thr Arg Glu Thr Leu Pro Pro Phe Pro Thr Arg Leu
            260                 265                 270

Leu Glu Leu Ile Glu Gly Phe Met Leu Ser Lys Gly Leu Leu Thr Ala
        275                 280                 285

Cys Lys Leu Lys Val Phe Asp Leu Leu Lys Asp Glu Ala Pro Gln Lys
    290                 295                 300

Ala Ala Asp Ile Ala Ser Lys Val Asp Ala Ser Ala Cys Gly Met Glu
305                 310                 315                 320

Arg Leu Leu Asp Ile Cys Ala Ala Met Gly Leu Leu Glu Lys Thr Glu
                325                 330                 335

Gln Gly Tyr Ser Asn Thr Glu Thr Ala Asn Val Tyr Leu Ala Ser Asp
            340                 345                 350

Gly Glu Tyr Ser Leu His Gly Phe Ile Met His Asn Asn Asp Leu Thr
        355                 360                 365

Trp Asn Leu Phe Thr Tyr Leu Glu Phe Ala Ile Arg Glu Gly Thr Asn
    370                 375                 380
```

Gln His His Arg Ala Leu Gly Lys Lys Ala Glu Asp Leu Phe Gln Asp
385 390 395 400

Ala Tyr Tyr Gln Ser Pro Glu Thr Arg Leu Arg Phe Met Arg Ala Met
405 410 415

His Gly Met Thr Lys Leu Thr Ala Cys Gln Val Ala Thr Ala Phe Asn
420 425 430

Leu Ser Arg Phe Ser Ser Ala Cys Asp Val Gly Gly Cys Thr Gly Ala
435 440 445

Leu Ala Arg Glu Leu Ala Arg Glu Tyr Pro Arg Met Gln Val Thr Val
450 455 460

Phe Asp Leu Pro Asp Ile Ile Glu Leu Ala Ala His Phe Gln Pro Pro
465 470 475 480

Gly Pro Gln Ala Val Gln Ile His Phe Ala Ala Gly Asp Phe Phe Arg
485 490 495

Asp Pro Leu Pro Ser Ala Glu Leu Tyr Val Leu Cys Arg Ile Leu His
500 505 510

Asp Trp Pro Asp Asp Lys Val His Lys Leu Leu Ser Arg Val Ala Glu
515 520 525

Ser Cys Lys Pro Gly Ala Gly Leu Leu Leu Val Glu Thr Leu Leu Asp
530 535 540

Glu Glu Lys Arg Val Ala Gln Arg Ala Leu Met Gln Ser Leu Asn Met
545 550 555 560

Leu Val Gln Thr Glu Gly Lys Glu Arg Ser Leu Gly Glu Tyr Gln Cys
565 570 575

Leu Leu Glu Leu His Gly Phe His Gln Val Gln Val Val His Leu Gly
580 585 590

Gly Val Leu Asp Ala Ile Leu Ala Thr Lys Val Ala Pro
595 600 605

<210> 1299

<211> 563
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 388; "

<220>
<221> source
<223> /note="Gene Symbol: ASMTL; "

<220>
<221> source
<223> /note="Gene Name:
acetylserotonin O-methyltransferase-like; "

<220>
<221> source
<223> /note="Uniprot ID: O95671; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446410"

<400> 1299

Met	Glu	Thr	Ala	Lys	Gln	Lys	Ala	Leu	Glu	Val	Ala	Asn	Arg	Leu	Tyr
1				5					10						15
Gln	Lys	Asp	Leu	Arg	Ala	Pro	Asp	Val	Val	Ile	Gly	Ala	Asp	Thr	Ile
			20					25					30		
Val	Thr	Val	Gly	Gly	Leu	Ile	Leu	Glu	Lys	Pro	Val	Asp	Lys	Gln	Asp
		35					40					45			
Ala	Tyr	Arg	Met	Leu	Ser	Arg	Leu	Ser	Gly	Arg	Glu	His	Ser	Val	Phe
	50					55					60				
Thr	Gly	Val	Ala	Ile	Val	His	Cys	Ser	Ser	Lys	Asp	His	Gln	Leu	Asp
65				70					75						80
Thr	Arg	Val	Ser	Glu	Phe	Tyr	Glu	Glu	Thr	Lys	Val	Lys	Phe	Ser	Glu
			85					90					95		
Leu	Ser	Glu	Glu	Leu	Leu	Trp	Glu	Tyr	Val	His	Ser	Gly	Glu	Pro	Met
		100					105					110			
Asp	Lys	Ala	Gly	Gly	Tyr	Gly	Ile	Gln	Ala	Leu	Gly	Gly	Met	Leu	Val
	115					120					125				

```
Glu Ser Val His Gly Asp Phe Leu Asn Val Val Gly Phe Pro Leu Asn
    130                 135                 140

His Phe Cys Lys Gln Leu Val Lys Leu Tyr Tyr Pro Pro Arg Pro Glu
145                 150                 155                 160

Asp Leu Arg Arg Ser Val Lys His Asp Ser Ile Pro Ala Ala Asp Thr
                165                 170                 175

Phe Glu Asp Leu Ser Asp Val Glu Gly Gly Gly Ser Glu Pro Thr Gln
            180                 185                 190

Arg Asp Ala Gly Ser Arg Asp Glu Lys Ala Glu Ala Gly Glu Ala Gly
        195                 200                 205

Gln Ala Thr Ala Glu Ala Glu Cys His Arg Thr Arg Glu Thr Leu Pro
    210                 215                 220

Pro Phe Pro Thr Arg Leu Leu Glu Leu Ile Glu Gly Phe Met Leu Ser
225                 230                 235                 240

Lys Gly Leu Leu Thr Ala Cys Lys Leu Lys Val Phe Asp Leu Leu Lys
                245                 250                 255

Asp Glu Ala Pro Gln Lys Ala Ala Asp Ile Ala Ser Lys Val Asp Ala
            260                 265                 270

Ser Ala Cys Gly Met Glu Arg Leu Leu Asp Ile Cys Ala Ala Met Gly
        275                 280                 285

Leu Leu Glu Lys Thr Glu Gln Gly Tyr Ser Asn Thr Glu Thr Ala Asn
    290                 295                 300

Val Tyr Leu Ala Ser Asp Gly Glu Tyr Ser Leu His Gly Phe Ile Met
305                 310                 315                 320

His Asn Asn Asp Leu Thr Trp Asn Leu Phe Thr Tyr Leu Glu Phe Ala
                325                 330                 335

Ile Arg Glu Gly Thr Asn Gln His His Arg Ala Leu Gly Lys Lys Ala
            340                 345                 350
```

Glu Asp Leu Phe Gln Asp Ala Tyr Tyr Gln Ser Pro Glu Thr Arg Leu
355 360 365

Arg Phe Met Arg Ala Met His Gly Met Thr Lys Leu Thr Ala Cys Gln
370 375 380

Val Ala Thr Ala Phe Asn Leu Ser Arg Phe Ser Ser Ala Cys Asp Val
385 390 395 400

Gly Gly Cys Thr Gly Ala Leu Ala Arg Glu Leu Ala Arg Glu Tyr Pro
405 410 415

Arg Met Gln Val Thr Val Phe Asp Leu Pro Asp Ile Ile Glu Leu Ala
420 425 430

Ala His Phe Gln Pro Pro Gly Pro Gln Ala Val Gln Ile His Phe Ala
435 440 445

Ala Gly Asp Phe Phe Arg Asp Pro Leu Pro Ser Ala Glu Leu Tyr Val
450 455 460

Leu Cys Arg Ile Leu His Asp Trp Pro Asp Asp Lys Val His Lys Leu
465 470 475 480

Leu Ser Arg Val Ala Glu Ser Cys Lys Pro Gly Ala Gly Leu Leu Leu
485 490 495

Val Glu Thr Leu Leu Asp Glu Glu Lys Arg Val Ala Gln Arg Ala Leu
500 505 510

Met Gln Ser Leu Asn Met Leu Val Gln Thr Glu Gly Lys Glu Arg Ser
515 520 525

Leu Gly Glu Tyr Gln Cys Leu Leu Glu Leu His Gly Phe His Gln Val
530 535 540

Gln Val Val His Leu Gly Gly Val Leu Asp Ala Ile Leu Ala Thr Lys
545 550 555 560

Val Ala Pro

<210> 1300

<211> 236
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 389; "

<220>
<221> source
<223> /note="Gene Symbol: ASCL1; "

<220>
<221> source
<223> /note="Gene Name:
achaete-scute family bHLH transcription
factor
1; "

<220>
<221> source
<223> /note="Uniprot ID: P50553; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000266744"

<400> 1300
Met Glu Ser Ser Ala Lys Met Glu Ser Gly Gly Ala Gly Gln Gln Pro
1   5   10   15

Gln Pro Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe Phe
            20   25   30

Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln
        35   40   45

Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro
    50   55   60

Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His Lys
65   70   75   80

Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu Leu
                85   90   95

Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu
            100   105   110

Pro Gln Gln Gln Pro Ala Ala Val Ala Arg Arg Asn Glu Arg Glu Arg

```
        115                 120                 125

Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His
    130                 135                 140

Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu
145                 150                 155                 160

Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu
                165                 170                 175

His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr
            180                 185                 190

Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro
        195                 200                 205

Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro
    210                 215                 220

Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn Trp Phe
225                 230                 235


<210> 1301
<211> 193
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 390; "

<220>
<221> source
<223> /note="Gene Symbol: ASCL2; "

<220>
<221> source
<223> /note="Gene Name:
      achaete-scute family bHLH transcription
      factor
      2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99929; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000332293"

<400> 1301

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Met Asp Gly Gly Thr Leu Pro Arg Ser Ala Pro Pro Ala Pro Pro Val
1               5                  10                  15

Pro Val Gly Cys Ala Ala Arg Arg Arg Pro Ala Ser Pro Glu Leu Leu
            20                  25                  30

Arg Cys Ser Arg Arg Arg Arg Pro Ala Thr Ala Glu Thr Gly Gly Gly
        35                  40                  45

Ala Ala Ala Val Ala Arg Arg Asn Glu Arg Glu Arg Asn Arg Val Lys
    50                  55                  60

Leu Val Asn Leu Gly Phe Gln Ala Leu Arg Gln His Val Pro His Gly
65                  70                  75                  80

Gly Ala Ser Lys Lys Leu Ser Lys Val Glu Thr Leu Arg Ser Ala Val
                85                  90                  95

Glu Tyr Ile Arg Ala Leu Gln Arg Leu Leu Ala Glu His Asp Ala Val
            100                 105                 110

Arg Asn Ala Leu Ala Gly Gly Leu Arg Pro Gln Ala Val Arg Pro Ser
        115                 120                 125

Ala Pro Arg Gly Pro Pro Gly Thr Thr Pro Val Ala Ala Ser Pro Ser
    130                 135                 140

Arg Ala Ser Ser Ser Pro Gly Arg Gly Gly Ser Ser Glu Pro Gly Ser
145                 150                 155                 160

Pro Arg Ser Ala Tyr Ser Ser Asp Asp Ser Gly Cys Glu Gly Ala Leu
                165                 170                 175

Ser Pro Ala Glu Arg Glu Leu Leu Asp Phe Ser Ser Trp Leu Gly Gly
            180                 185                 190

Tyr
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<210> 1302
<211> 181

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 391; "

<220>
<221> source
<223> /note="Gene Symbol: ASCL3; "

<220>
<221> source
<223> /note="Gene Name:
achaete-scute family bHLH transcription
factor
3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NQ33; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435770"

<400> 1302

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Met Met Asp Asn Arg Gly Asn Ser Ser Leu Pro Asp Lys Leu Pro Ile
1               5                  10                  15

Phe Pro Asp Ser Ala Arg Leu Pro Leu Thr Arg Ser Phe Tyr Leu Glu
            20                  25                  30

Pro Met Val Thr Phe His Val His Pro Glu Ala Pro Val Ser Ser Pro
        35                  40                  45

Tyr Ser Glu Glu Leu Pro Arg Leu Pro Phe Pro Ser Asp Ser Leu Ile
    50                  55                  60

Leu Gly Asn Tyr Ser Glu Pro Cys Pro Phe Ser Phe Pro Met Pro Tyr
65                  70                  75                  80

Pro Asn Tyr Arg Gly Cys Glu Tyr Ser Tyr Gly Pro Ala Phe Thr Arg
                85                  90                  95

Lys Arg Asn Glu Arg Glu Arg Gln Arg Val Lys Cys Val Asn Glu Gly
            100                 105                 110

Tyr Ala Gln Leu Arg His His Leu Pro Glu Glu Tyr Leu Glu Lys Arg
        115                 120                 125
```

```
Leu Ser Lys Val Glu Thr Leu Arg Ala Ala Ile Lys Tyr Ile Asn Tyr
    130                 135                 140

Leu Gln Ser Leu Leu Tyr Pro Asp Lys Ala Glu Thr Lys Asn Asn Pro
145                 150                 155                 160

Gly Lys Val Ser Ser Met Ile Ala Thr Thr Ser His His Ala Asp Pro
                165                 170                 175

Met Phe Arg Ile Val
            180


<210> 1303
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 392; "

<220>
<221> source
<223> /note="Gene Symbol: ASCL4; "

<220>
<221> source
<223> /note="Gene Name:
      achaete-scute family bHLH transcription
      factor
      4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6XD76; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000345420"

<400> 1303
Met Met Glu Thr Arg Lys Pro Ala Glu Arg Leu Ala Leu Pro Tyr Ser
1               5                   10                  15

Leu Arg Thr Ala Pro Leu Gly Val Pro Gly Thr Leu Pro Gly Leu Pro
            20                  25                  30

Arg Arg Asp Pro Leu Arg Val Ala Leu Arg Leu Asp Ala Ala Cys Trp
        35                  40                  45
```

```
Glu Trp Ala Arg Ser Gly Cys Ala Arg Gly Trp Gln Tyr Leu Pro Val
    50                  55                  60

Pro Leu Asp Ser Ala Phe Glu Pro Ala Phe Leu Arg Lys Arg Asn Glu
65                  70                  75                  80

Arg Glu Arg Gln Arg Val Arg Cys Val Asn Glu Gly Tyr Ala Arg Leu
                85                  90                  95

Arg Asp His Leu Pro Arg Glu Leu Ala Asp Lys Arg Leu Ser Lys Val
            100                 105                 110

Glu Thr Leu Arg Ala Ala Ile Asp Tyr Ile Lys His Leu Gln Glu Leu
        115                 120                 125

Leu Glu Arg Gln Ala Trp Gly Leu Glu Gly Ala Ala Gly Ala Val Pro
    130                 135                 140

Gln Arg Arg Ala Glu Cys Asn Ser Asp Gly Glu Ser Lys Ala Ser Ser
145                 150                 155                 160

Ala Pro Ser Pro Ser Ser Glu Pro Glu Glu Gly Gly Ser
                165                 170


<210> 1304
<211> 206
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 393; "

<220>
<221> source
<223> /note="Gene Symbol: ASCL5; "

<220>
<221> source
<223> /note="Gene Name:
      achaete-scute family bHLH transcription
      factor
      5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q7RTU5; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000469019"

<400> 1304
Met Asn Asn Asn Phe Cys Arg Ala Leu Val Asp Arg Arg Pro Leu Gly
1   5   10   15

Pro Pro Ser Cys Met Gln Leu Gly Val Met Pro Pro Pro Arg Gln Ala
            20   25   30

Pro Leu Pro Pro Ala Glu Pro Leu Gly Asn Val Pro Phe Leu Leu Tyr
        35   40   45

Pro Gly Pro Ala Glu Pro Pro Tyr Tyr Asp Ala Tyr Ala Gly Val Phe
    50   55   60

Pro Tyr Val Pro Phe Pro Gly Ala Phe Gly Val Tyr Glu Tyr Pro Phe
65   70   75   80

Glu Pro Ala Phe Ile Gln Lys Arg Asn Glu Arg Glu Arg Gln Arg Val
                85   90   95

Lys Cys Val Asn Glu Gly Tyr Ala Arg Leu Arg Gly His Leu Pro Gly
            100   105   110

Ala Leu Ala Glu Lys Arg Leu Ser Lys Val Glu Thr Leu Arg Ala Ala
        115   120   125

Ile Arg Tyr Ile Lys Tyr Leu Gln Glu Leu Leu Ser Ser Ala Pro Asp
    130   135   140

Gly Ser Thr Pro Pro Ala Ser Arg Gly Leu Pro Gly Thr Gly Pro Cys
145   150   155   160

Pro Ala Pro Pro Ala Thr Pro Arg Pro Asp Arg Pro Gly Asp Gly Glu
                165   170   175

Ala Arg Ala Pro Ser Ser Leu Val Pro Glu Ser Ser Glu Ser Ser Cys
            180   185   190

Phe Ser Pro Ser Pro Phe Leu Glu Ser Glu Glu Ser Trp His
        195   200   205

<210> 1305
<211> 206
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 393; "

<220>
<221> source
<223> /note="Gene Symbol: ASCL5; "

<220>
<221> source
<223> /note="Gene Name:
achaete-scute family bHLH transcription
factor
5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472681"

<400> 1305
Met Asn Asn Asn Phe Cys Arg Ala Leu Val Asp Arg Arg Pro Leu Gly
1 5 10 15

Pro Pro Ser Cys Met Gln Leu Gly Val Met Pro Pro Pro Arg Gln Ala
20 25 30

Pro Leu Pro Pro Ala Glu Pro Leu Gly Asn Val Pro Phe Leu Leu Tyr
35 40 45

Pro Gly Pro Ala Glu Pro Pro Tyr Tyr Asp Ala Tyr Ala Gly Val Phe
50 55 60

Pro Tyr Val Pro Phe Pro Gly Ala Phe Gly Val Tyr Glu Tyr Pro Phe
65 70 75 80

Glu Pro Ala Phe Ile Gln Lys Arg Asn Glu Arg Glu Arg Gln Arg Val
85 90 95

Lys Cys Val Asn Glu Gly Tyr Ala Arg Leu Arg Gly His Leu Pro Gly
100 105 110

Ala Leu Ala Glu Lys Arg Leu Ser Lys Val Glu Thr Leu Arg Ala Ala
115 120 125

```
Ile Arg Tyr Ile Lys Tyr Leu Gln Glu Leu Leu Ser Ser Ala Pro Asp
    130                 135                 140

Gly Ser Thr Pro Pro Ala Ser Arg Gly Leu Pro Gly Thr Gly Pro Cys
145                 150                 155                 160

Pro Ala Pro Pro Ala Thr Pro Arg Pro Asp Arg Pro Gly Asp Gly Glu
                165                 170                 175

Ala Arg Ala Pro Ser Ser Leu Val Pro Glu Ser Ser Glu Ser Ser Cys
            180                 185                 190

Phe Ser Pro Ser Pro Phe Leu Glu Ser Glu Glu Ser Trp His
        195                 200                 205


<210> 1306
<211> 546
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 394; "

<220>
<221> source
<223> /note="Gene Symbol: AAAS; "

<220>
<221> source
<223> /note="Gene Name:
      achalasia, adrenocortical insufficiency, alacrimia; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NRG9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000209873"

<400> 1306
Met Cys Ser Leu Gly Leu Phe Pro Pro Pro Pro Pro Arg Gly Gln Val
1               5                   10                  15

Thr Leu Tyr Glu His Asn Asn Glu Leu Val Thr Gly Ser Ser Tyr Glu
            20                  25                  30

Ser Pro Pro Pro Asp Phe Arg Gly Gln Trp Ile Asn Leu Pro Val Leu
```

```
        35                  40                  45

Gln Leu Thr Lys Asp Pro Leu Lys Thr Pro Gly Arg Leu Asp His Gly
    50                  55                  60

Thr Arg Thr Ala Phe Ile His His Arg Glu Gln Val Trp Lys Arg Cys
65                  70                  75                  80

Ile Asn Ile Trp Arg Asp Val Gly Leu Phe Gly Val Leu Asn Glu Ile
                85                  90                  95

Ala Asn Ser Glu Glu Glu Val Phe Glu Trp Val Lys Thr Ala Ser Gly
            100                 105                 110

Trp Ala Leu Ala Leu Cys Arg Trp Ala Ser Ser Leu His Gly Ser Leu
        115                 120                 125

Phe Pro His Leu Ser Leu Arg Ser Glu Asp Leu Ile Ala Glu Phe Ala
    130                 135                 140

Gln Val Thr Asn Trp Ser Ser Cys Cys Leu Arg Val Phe Ala Trp His
145                 150                 155                 160

Pro His Thr Asn Lys Phe Ala Val Ala Leu Leu Asp Asp Ser Val Arg
                165                 170                 175

Val Tyr Asn Ala Ser Ser Thr Ile Val Pro Ser Leu Lys His Arg Leu
            180                 185                 190

Gln Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu Ser Ala Ser Val
        195                 200                 205

Leu Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp Thr Leu Asp Pro
    210                 215                 220

Thr Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala Gln Val Leu Ser
225                 230                 235                 240

His Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp Ala Pro Ser Gly
                245                 250                 255

Gly Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala Ile Arg Val Trp
            260                 265                 270
```

```
Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly
        275                 280                 285

Gly Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala
    290                 295                 300

Thr Thr Pro Ser Ala Val Phe Arg Val Trp Glu Ala Gln Met Trp Thr
305                 310                 315                 320

Cys Glu Arg Trp Pro Thr Leu Ser Gly Arg Cys Gln Thr Gly Cys Trp
                325                 330                 335

Ser Pro Asp Gly Ser Arg Leu Leu Phe Thr Val Leu Gly Glu Pro Leu
            340                 345                 350

Ile Tyr Ser Leu Ser Phe Pro Glu Arg Cys Gly Glu Gly Lys Gly Cys
        355                 360                 365

Val Gly Gly Ala Lys Ser Ala Thr Ile Val Ala Asp Leu Ser Glu Thr
    370                 375                 380

Thr Ile Gln Thr Pro Asp Gly Glu Glu Arg Leu Gly Gly Glu Ala His
385                 390                 395                 400

Ser Met Val Trp Asp Pro Ser Gly Glu Arg Leu Ala Val Leu Met Lys
                405                 410                 415

Gly Lys Pro Arg Val Gln Asp Gly Lys Pro Val Ile Leu Leu Phe Arg
            420                 425                 430

Thr Arg Asn Ser Pro Val Phe Glu Leu Leu Pro Cys Gly Ile Ile Gln
        435                 440                 445

Gly Glu Pro Gly Ala Gln Pro Gln Leu Ile Thr Phe His Pro Ser Phe
    450                 455                 460

Asn Lys Gly Ala Leu Leu Ser Val Gly Trp Ser Thr Gly Arg Ile Ala
465                 470                 475                 480

His Ile Pro Leu Tyr Phe Val Asn Ala Gln Phe Pro Arg Phe Ser Pro
                485                 490                 495
```

```
Val Leu Gly Arg Ala Gln Glu Pro Pro Ala Gly Gly Gly Ser Ile
            500                 505                 510

His Asp Leu Pro Leu Phe Thr Glu Thr Ser Pro Thr Ser Ala Pro Trp
        515                 520                 525

Asp Pro Leu Pro Gly Pro Pro Pro Val Leu Pro His Ser Pro His Ser
    530                 535                 540

His Leu
545
```

<210> 1307
<211> 513
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 394; "

<220>
<221> source
<223> /note="Gene Symbol: AAAS; "

<220>
<221> source
<223> /note="Gene Name:
achalasia, adrenocortical insufficiency, alacrimia; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NRG9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377908"

<400> 1307

```
Met Cys Ser Leu Gly Leu Phe Pro Pro Pro Pro Arg Gly Gln Val
1               5                   10                  15

Thr Leu Tyr Glu His Asn Asn Glu Leu Val Thr Gly Ser Ser Tyr Glu
            20                  25                  30

Ser Pro Pro Pro Asp Phe Arg Gly Gln Trp Ile Asn Leu Pro Val Leu
        35                  40                  45

Gln Leu Thr Lys Asp Pro Leu Lys Thr Pro Gly Arg Leu Asp His Gly
```

```
    50                  55                  60

Thr Arg Thr Ala Phe Ile His His Arg Glu Gln Val Trp Lys Arg Cys
65                  70                  75                  80

Ile Asn Ile Trp Arg Asp Val Gly Leu Phe Gly Val Leu Asn Glu Ile
                85                  90                  95

Ala Asn Ser Glu Glu Glu Val Phe Glu Trp Val Lys Thr Ala Ser Gly
            100                 105                 110

Trp Ala Leu Ala Leu Cys Arg Trp Ala Ser Ser Leu His Gly Ser Leu
        115                 120                 125

Phe Pro His Leu Ser Leu Arg Ser Glu Asp Leu Ile Ala Glu Phe Ala
    130                 135                 140

Gln Val Thr Asn Cys Thr Ile Val Pro Ser Leu Lys His Arg Leu Gln
145                 150                 155                 160

Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu Ser Ala Ser Val Leu
                165                 170                 175

Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp Thr Leu Asp Pro Thr
            180                 185                 190

Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala Gln Val Leu Ser His
        195                 200                 205

Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp Ala Pro Ser Gly Gly
    210                 215                 220

Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala Ile Arg Val Trp Asp
225                 230                 235                 240

Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly Gly
                245                 250                 255

Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala Thr
            260                 265                 270

Thr Pro Ser Ala Val Phe Arg Val Trp Glu Ala Gln Met Trp Thr Cys
        275                 280                 285
```

```
Glu Arg Trp Pro Thr Leu Ser Gly Arg Cys Gln Thr Gly Cys Trp Ser
    290                 295                 300

Pro Asp Gly Ser Arg Leu Leu Phe Thr Val Leu Gly Glu Pro Leu Ile
305                 310                 315                 320

Tyr Ser Leu Ser Phe Pro Glu Arg Cys Gly Glu Gly Lys Gly Cys Val
                325                 330                 335

Gly Gly Ala Lys Ser Ala Thr Ile Val Ala Asp Leu Ser Glu Thr Thr
            340                 345                 350

Ile Gln Thr Pro Asp Gly Glu Glu Arg Leu Gly Gly Glu Ala His Ser
        355                 360                 365

Met Val Trp Asp Pro Ser Gly Glu Arg Leu Ala Val Leu Met Lys Gly
    370                 375                 380

Lys Pro Arg Val Gln Asp Gly Lys Pro Val Ile Leu Leu Phe Arg Thr
385                 390                 395                 400

Arg Asn Ser Pro Val Phe Glu Leu Leu Pro Cys Gly Ile Ile Gln Gly
                405                 410                 415

Glu Pro Gly Ala Gln Pro Gln Leu Ile Thr Phe His Pro Ser Phe Asn
            420                 425                 430

Lys Gly Ala Leu Leu Ser Val Gly Trp Ser Thr Gly Arg Ile Ala His
        435                 440                 445

Ile Pro Leu Tyr Phe Val Asn Ala Gln Phe Pro Arg Phe Ser Pro Val
    450                 455                 460

Leu Gly Arg Ala Gln Glu Pro Pro Ala Gly Gly Gly Gly Ser Ile His
465                 470                 475                 480

Asp Leu Pro Leu Phe Thr Glu Thr Ser Pro Thr Ser Ala Pro Trp Asp
                485                 490                 495

Pro Leu Pro Gly Pro Pro Pro Val Leu Pro His Ser Pro His Ser His
            500                 505                 510
```

Leu

<210> 1308
<211> 422
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 394; "

<220>
<221> source
<223> /note="Gene Symbol: AAAS; "

<220>
<221> source
<223> /note="Gene Name:
achalasia, adrenocortical insufficiency, alacrimia; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446885"

<400> 1308
Met Lys Leu Gln Thr Gln Lys Lys Arg Leu Arg Ser Glu Asp Leu Ile
1 5 10 15

Ala Glu Phe Ala Gln Val Thr Asn Trp Ser Ser Cys Cys Leu Arg Val
20 25 30

Phe Ala Trp His Pro His Thr Asn Lys Phe Ala Val Ala Leu Leu Asp
35 40 45

Asp Ser Val Arg Val Tyr Asn Ala Ser Ser Thr Ile Val Pro Ser Leu
50 55 60

Lys His Arg Leu Gln Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu
65 70 75 80

Ser Ala Ser Val Leu Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp
85 90 95

Thr Leu Asp Pro Thr Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala
100 105 110

Gln Val Leu Ser His Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp

```
        115                 120                 125

Ala Pro Ser Gly Gly Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala
    130                 135                 140

Ile Arg Val Trp Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp
145                 150                 155                 160

Phe Arg Gly Gly Gly Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser
                165                 170                 175

Lys Ile Leu Ala Thr Thr Pro Ser Ala Val Phe Arg Val Trp Glu Ala
            180                 185                 190

Gln Met Trp Thr Cys Glu Arg Trp Pro Thr Leu Ser Gly Arg Cys Gln
        195                 200                 205

Thr Gly Cys Trp Ser Pro Asp Gly Ser Arg Leu Leu Phe Thr Val Leu
    210                 215                 220

Gly Glu Pro Leu Ile Tyr Ser Leu Ser Phe Pro Glu Arg Cys Gly Glu
225                 230                 235                 240

Gly Lys Gly Cys Val Gly Gly Ala Lys Ser Ala Thr Ile Val Ala Asp
                245                 250                 255

Leu Ser Glu Thr Thr Ile Gln Thr Pro Asp Gly Glu Glu Arg Leu Gly
            260                 265                 270

Gly Glu Ala His Ser Met Val Trp Asp Pro Ser Gly Glu Arg Leu Ala
        275                 280                 285

Val Leu Met Lys Gly Lys Pro Arg Val Gln Asp Gly Lys Pro Val Ile
    290                 295                 300

Leu Leu Phe Arg Thr Arg Asn Ser Pro Val Phe Glu Leu Leu Pro Cys
305                 310                 315                 320

Gly Ile Ile Gln Gly Glu Pro Gly Ala Gln Pro Gln Leu Ile Thr Phe
                325                 330                 335

His Pro Ser Phe Asn Lys Gly Ala Leu Leu Ser Val Gly Trp Ser Thr
            340                 345                 350
```

```
Gly Arg Ile Ala His Ile Pro Leu Tyr Phe Val Asn Ala Gln Phe Pro
        355                 360                 365

Arg Phe Ser Pro Val Leu Gly Arg Ala Gln Glu Pro Pro Ala Gly Gly
    370                 375                 380

Gly Gly Ser Ile His Asp Leu Pro Leu Phe Thr Glu Thr Ser Pro Thr
385                 390                 395                 400

Ser Ala Pro Trp Asp Pro Leu Pro Gly Pro Pro Pro Val Leu Pro His
                405                 410                 415

Ser Pro His Ser His Leu
            420


<210> 1309
<211> 277
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 394; "

<220>
<221> source
<223> /note="Gene Symbol: AAAS; "

<220>
<221> source
<223> /note="Gene Name:
      achalasia, adrenocortical insufficiency, alacrimia; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448020"

<400> 1309
Met Cys Ser Leu Gly Leu Phe Pro Pro Pro Pro Pro Arg Gly Gln Val
1               5                   10                  15

Thr Leu Tyr Glu His Asn Asn Glu Leu Val Thr Gly Ser Ser Tyr Glu
            20                  25                  30

Ser Pro Pro Pro Asp Phe Arg Gly Gln Trp Ile Asn Leu Pro Val Leu
        35                  40                  45
```

```
Gln Leu Thr Lys Asp Pro Leu Lys Thr Pro Gly Arg Leu Asp His Gly
    50                  55                  60

Thr Arg Thr Ala Phe Ile His His Arg Glu Gln Val Trp Lys Arg Cys
65                  70                  75                  80

Ile Asn Ile Trp Arg Asp Val Gly Leu Phe Gly Val Leu Asn Glu Ile
                85                  90                  95

Ala Asn Ser Glu Glu Glu Val Phe Glu Trp Val Lys Thr Ala Ser Gly
            100                 105                 110

Trp Ala Leu Ala Leu Cys Arg Trp Ala Ser Ser Leu His Gly Ser Leu
        115                 120                 125

Phe Pro His Leu Ser Leu Arg Ser Glu Asp Leu Ile Ala Glu Phe Ala
    130                 135                 140

Gln Val Thr Asn Cys Thr Ile Val Pro Ser Leu Lys His Arg Leu Gln
145                 150                 155                 160

Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu Ser Ala Ser Val Leu
                165                 170                 175

Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp Thr Leu Asp Pro Thr
            180                 185                 190

Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala Gln Val Leu Ser His
        195                 200                 205

Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp Ala Pro Ser Gly Gly
    210                 215                 220

Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala Ile Arg Val Trp Asp
225                 230                 235                 240

Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly Gly
                245                 250                 255

Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala Thr
            260                 265                 270

Thr Pro Ser Ala Val
```

275

<210> 1310
<211> 358
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 394; "

<220>
<221> source
<223> /note="Gene Symbol: AAAS; "

<220>
<221> source
<223> /note="Gene Name:
achalasia, adrenocortical insufficiency, alacrimia; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457518"

<400> 1310
Pro His Thr Asn Lys Phe Ala Val Ala Leu Leu Asp Asp Ser Val Arg
1 5 10 15

Val Tyr Asn Ala Ser Ser Thr Ile Val Pro Ser Leu Lys His Arg Leu
20 25 30

Gln Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu Ser Ala Ser Val
35 40 45

Leu Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp Thr Leu Asp Pro
50 55 60

Thr Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala Gln Val Leu Ser
65 70 75 80

His Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp Ala Pro Ser Gly
85 90 95

Gly Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala Ile Arg Val Trp
100 105 110

Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly
115 120 125

```
Gly Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala
    130                 135                 140

Thr Thr Pro Ser Ala Val Phe Arg Val Trp Glu Ala Gln Met Trp Thr
145                 150                 155                 160

Cys Glu Arg Trp Pro Thr Leu Ser Gly Arg Cys Gln Thr Gly Cys Trp
                165                 170                 175

Ser Pro Asp Gly Ser Arg Leu Leu Phe Thr Val Leu Gly Glu Pro Leu
            180                 185                 190

Ile Tyr Ser Leu Ser Phe Pro Glu Arg Cys Gly Glu Gly Lys Gly Cys
        195                 200                 205

Val Gly Gly Ala Lys Ser Ala Thr Ile Val Ala Asp Leu Ser Glu Thr
    210                 215                 220

Thr Ile Gln Thr Pro Asp Gly Glu Glu Arg Leu Gly Gly Glu Ala His
225                 230                 235                 240

Ser Met Val Trp Asp Pro Ser Gly Glu Arg Leu Ala Val Leu Met Lys
                245                 250                 255

Gly Lys Pro Arg Val Gln Asp Gly Lys Pro Val Ile Leu Leu Phe Arg
            260                 265                 270

Thr Arg Asn Ser Pro Val Phe Glu Leu Leu Pro Trp Ala Gly Pro Gln
        275                 280                 285

Ala Glu Leu Pro Thr Ser Arg Cys Thr Leu Ser Met Pro Ser Phe His
    290                 295                 300

Val Leu Ala Gln Cys Leu Gly Gly Pro Arg Asn Pro Leu Leu Gly Val
305                 310                 315                 320

Glu Ala Leu Phe Met Thr Cys Pro Ser Leu Leu Arg His Pro Gln Pro
                325                 330                 335

Leu Pro Leu Gly Thr Leu Ser Gln Gly His His Leu Phe Cys Pro Thr
            340                 345                 350
```

Pro His Ile Pro Thr Ser
        355

<210> 1311
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="Uniprot ID: P24666; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000272065"

<400> 1311
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1   5   10   15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
            20   25   30

Asp Gln Asn Ile Ser Glu Asn Trp Arg Val Asp Ser Ala Ala Thr Ser
        35   40   45

Gly Tyr Glu Ile Gly Asn Pro Pro Asp Tyr Arg Gly Gln Ser Cys Met
    50   55   60

Lys Arg His Gly Ile Pro Met Ser His Val Ala Arg Gln Ile Thr Lys
65   70   75   80

Glu Asp Phe Ala Thr Phe Asp Tyr Ile Leu Cys Met Asp Glu Ser Asn
                85   90   95

Leu Arg Asp Leu Asn Arg Lys Ser Asn Gln Val Lys Thr Cys Lys Ala
            100   105   110

```
Lys Ile Glu Leu Leu Gly Ser Tyr Asp Pro Gln Lys Gln Leu Ile Ile
        115                 120                 125

Glu Asp Pro Tyr Tyr Gly Asn Asp Ser Asp Phe Glu Thr Val Tyr Gln
    130                 135                 140

Gln Cys Val Arg Cys Cys Arg Ala Phe Leu Glu Lys Ala His
145                 150                 155


<210> 1312
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="Uniprot ID:  P24666; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000272067"

<400> 1312
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1               5                   10                  15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
            20                  25                  30

Asp Gln Asn Ile Ser Glu Asn Trp Val Ile Asp Ser Gly Ala Val Ser
        35                  40                  45

Asp Trp Asn Val Gly Arg Ser Pro Asp Pro Arg Ala Val Ser Cys Leu
    50                  55                  60
```

```
Arg Asn His Gly Ile His Thr Ala His Lys Ala Arg Gln Ile Thr Lys
65                  70                  75                  80


Glu Asp Phe Ala Thr Phe Asp Tyr Ile Leu Cys Met Asp Glu Ser Asn
                85                  90                  95


Leu Arg Asp Leu Asn Arg Lys Ser Asn Gln Val Lys Thr Cys Lys Ala
            100                 105                 110


Lys Ile Glu Leu Leu Gly Ser Tyr Asp Pro Gln Lys Gln Leu Ile Ile
        115                 120                 125


Glu Asp Pro Tyr Tyr Gly Asn Asp Ser Asp Phe Glu Thr Val Tyr Gln
    130                 135                 140


Gln Cys Val Arg Cys Cys Arg Ala Phe Leu Glu Lys Ala His
145                 150                 155


<210> 1313
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384184"

<400> 1313
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Lys
1               5                   10                  15


Ile Phe Tyr Cys Cys Gly Asn Tyr Ser Leu Cys Gly Lys Lys Val Thr
            20                  25                  30


Phe Val Asp His Pro Leu Gln Lys Gln Phe Ser Gly Asn Leu
        35                  40                  45
```

<210> 1314
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384307"

<400> 1314
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1 5 10 15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
20 25 30

Asp Gln Asn Ile Ser Glu Asn Trp Arg Val Asp Ser Ala Ala Thr Ser
35 40 45

Gly Gly Ser Leu Thr Ala Val Leu Phe Leu Thr Gly Thr Trp Ala Gly
50 55 60

Pro Gln Thr Gln Glu Leu
65 70

<210> 1315
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="Uniprot ID: P24666; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000385404"

<400> 1315
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1 5 10 15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
            20 25 30

Asp Gln Asn Ile Ser Glu Asn Trp Arg Val Asp Ser Ala Ala Thr Ser
        35 40 45

Gly Tyr Glu Ile Gly Asn Pro Pro Asp Tyr Arg Gly Gln Ser Cys Met
    50 55 60

Lys Arg His Gly Ile Pro Met Ser His Val Ala Arg Gln Val Pro Ser
65 70 75 80

Leu Asp Leu Lys Leu Cys Val Leu Cys Phe Ser Gly Ser Leu Thr Ala
                85 90 95

Val Leu Phe Leu Thr Gly Thr Trp Ala Gly Pro Gln Thr Gln Glu Leu
            100 105 110

<210> 1316
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>

<221> source
<223> /note="Gene Name:
acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389681"

<400> 1316
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Lys
1 5 10 15

Ile Phe Tyr Cys Cys Gly Asn Tyr Ser Leu Cys Gly Lys Lys Val Thr
20 25 30

Phe Val Asp His Pro Leu Gln Lys Gln Phe Ser Gly Asn Leu
35 40 45

<210> 1317
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408596"

<400> 1317
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1 5 10 15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
20 25 30

Asp Gln Asn Ile Ser Glu Asn Trp Val Ile Asp Ser Gly Ala Val Ser
35 40 45

Asp Trp Asn Val Gly Arg Ser Pro Asp Pro Arg Ala Val Ser Cys Leu

50 55 60

Arg Asn His Gly Ile His Thr Ala His Lys Ala Arg Gln Val Asp Lys
65 70 75 80

Leu Leu Phe Asn Phe
85

<210> 1318
<211> 80
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410331"

<400> 1318
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1 5 10 15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
20 25 30

Asp Gln Asn Ile Ser Glu Asn Trp Arg Val Asp Ser Ala Ala Thr Ser
35 40 45

Gly Tyr Glu Ile Gly Asn Pro Pro Asp Tyr Arg Gly Gln Ser Cys Met
50 55 60

Lys Arg His Gly Ile Pro Met Ser His Val Ala Arg Gln Arg Phe Glu
65 70 75 80

<210> 1319
<211> 70
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 395; "

<220>
<221> source
<223> /note="Gene Symbol: ACP1; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 1, soluble; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000411121"

<400> 1319
Met Ala Glu Gln Ala Thr Lys Ser Val Leu Phe Val Cys Leu Gly Asn
1 5 10 15

Ile Cys Arg Ser Pro Ile Ala Glu Ala Val Phe Arg Lys Leu Val Thr
20 25 30

Asp Gln Asn Ile Ser Glu Asn Trp Arg Val Asp Ser Ala Ala Thr Ser
35 40 45

Gly Gly Ser Leu Thr Ala Val Leu Phe Leu Thr Gly Thr Trp Ala Gly
50 55 60

Pro Gln Thr Gln Glu Leu
65 70

<210> 1320
<211> 423
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
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<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="Uniprot ID: P11117; "

<220>
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<223> /note="ENSP ID: ENSP00000256997"

<400> 1320
Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
1   5   10   15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
            20   25   30

Leu Arg Phe Val Thr Leu Leu Tyr Arg His Gly Asp Arg Ser Pro Val
        35   40   45

Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu Trp Pro Gln Gly
    50   55   60

Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His Trp Glu Leu Gly
65   70   75   80

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
                85   90   95

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
            100   105   110

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
        115   120   125

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
    130   135   140

Pro Ile Thr Glu Asp Arg Leu Leu Lys Phe Pro Leu Gly Pro Cys Pro
145   150   155   160

Arg Tyr Glu Gln Leu Gln Asn Glu Thr Arg Gln Thr Pro Glu Tyr Gln
                165   170   175

Asn Glu Ser Ser Arg Asn Ala Gln Phe Leu Asp Met Val Ala Asn Glu
            180   185   190

```
Thr Gly Leu Thr Asp Leu Thr Leu Glu Thr Val Trp Asn Val Tyr Asp
        195                 200                 205

Thr Leu Phe Cys Glu Gln Thr His Gly Leu Arg Leu Pro Pro Trp Ala
    210                 215                 220

Ser Pro Gln Thr Met Gln Arg Leu Ser Arg Leu Lys Asp Phe Ser Phe
225                 230                 235                 240

Arg Phe Leu Phe Gly Ile Tyr Gln Gln Ala Glu Lys Ala Arg Leu Gln
                245                 250                 255

Gly Gly Val Leu Leu Ala Gln Ile Arg Lys Asn Leu Thr Leu Met Ala
            260                 265                 270

Thr Thr Ser Gln Leu Pro Lys Leu Leu Val Tyr Ser Ala His Asp Thr
        275                 280                 285

Thr Leu Val Ala Leu Gln Met Ala Leu Asp Val Tyr Asn Gly Glu Gln
    290                 295                 300

Ala Pro Tyr Ala Ser Cys His Ile Phe Glu Leu Tyr Gln Glu Asp Ser
305                 310                 315                 320

Gly Asn Phe Ser Val Glu Met Tyr Phe Arg Asn Glu Ser Asp Lys Ala
                325                 330                 335

Pro Trp Pro Leu Ser Leu Pro Gly Cys Pro His Arg Cys Pro Leu Gln
            340                 345                 350

Asp Phe Leu Arg Leu Thr Glu Pro Val Val Pro Lys Asp Trp Gln Gln
        355                 360                 365

Glu Cys Gln Leu Ala Ser Gly Pro Ala Asp Thr Glu Val Ile Val Ala
    370                 375                 380

Leu Ala Val Cys Gly Ser Ile Leu Phe Leu Leu Ile Val Leu Leu Leu
385                 390                 395                 400

Thr Val Leu Phe Arg Met Gln Ala Gln Pro Pro Gly Tyr Arg His Val
                405                 410                 415
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Ala Asp Gly Glu Asp His Ala
420

<210> 1321
<211> 391
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432205"

<400> 1321
Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
1 5 10 15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
20 25 30

Leu Arg Phe Val Thr Leu Glu Gly Met Leu Gln His Trp Glu Leu Gly
35 40 45

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
50 55 60

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
65 70 75 80

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
85 90 95

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
100 105 110

Pro Ile Thr Glu Asp Arg Leu Leu Lys Phe Pro Leu Gly Pro Cys Pro
115 120 125

```
Arg Tyr Glu Gln Leu Gln Asn Glu Thr Arg Gln Thr Pro Glu Tyr Gln
    130                 135                 140

Asn Glu Ser Ser Arg Asn Ala Gln Phe Leu Asp Met Val Ala Asn Glu
145                 150                 155                 160

Thr Gly Leu Thr Asp Leu Thr Leu Glu Thr Val Trp Asn Val Tyr Asp
                165                 170                 175

Thr Leu Phe Cys Glu Gln Thr His Gly Leu Arg Leu Pro Pro Trp Ala
            180                 185                 190

Ser Pro Gln Thr Met Gln Arg Leu Ser Arg Leu Lys Asp Phe Ser Phe
        195                 200                 205

Arg Phe Leu Phe Gly Ile Tyr Gln Gln Ala Glu Lys Ala Arg Leu Gln
    210                 215                 220

Gly Gly Val Leu Leu Ala Gln Ile Arg Lys Asn Leu Thr Leu Met Ala
225                 230                 235                 240

Thr Thr Ser Gln Leu Pro Lys Leu Leu Val Tyr Ser Ala His Asp Thr
                245                 250                 255

Thr Leu Val Ala Leu Gln Met Ala Leu Asp Val Tyr Asn Gly Glu Gln
            260                 265                 270

Ala Pro Tyr Ala Ser Cys His Ile Phe Glu Leu Tyr Gln Glu Asp Ser
        275                 280                 285

Gly Asn Phe Ser Val Glu Met Tyr Phe Arg Asn Glu Ser Asp Lys Ala
    290                 295                 300

Pro Trp Pro Leu Ser Leu Pro Gly Cys Pro His Arg Cys Pro Leu Gln
305                 310                 315                 320

Asp Phe Leu Arg Leu Thr Glu Pro Val Val Pro Lys Asp Trp Gln Gln
                325                 330                 335

Glu Cys Gln Leu Ala Ser Gly Pro Ala Asp Thr Glu Val Ile Val Ala
            340                 345                 350
```

```
Leu Ala Val Cys Gly Ser Ile Leu Phe Leu Leu Ile Val Leu Leu Leu
        355                 360                 365

Thr Val Leu Phe Arg Met Gln Ala Gln Pro Pro Gly Tyr Arg His Val
    370                 375                 380

Ala Asp Gly Glu Asp His Ala
385                 390


<210> 1322
<211> 395
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432439"

<400> 1322
Met Gly Val Arg Met Thr Glu Tyr Val Gly Leu Tyr Arg His Gly Asp
1               5                  10                  15

Arg Ser Pro Val Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu
            20                  25                  30

Trp Pro Gln Gly Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His
        35                  40                  45

Trp Glu Leu Gly Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn
    50                  55                  60

Thr Ser Tyr His Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp
65                  70                  75                  80

Arg Thr Leu Met Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro
```

```
                85                  90                  95

Asn Gly Met Gln Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro
            100                 105                 110

Val His Thr Val Pro Ile Thr Glu Asp Arg Leu Leu Lys Phe Pro Leu
        115                 120                 125

Gly Pro Cys Pro Arg Tyr Glu Gln Leu Gln Asn Glu Thr Arg Gln Thr
    130                 135                 140

Pro Glu Tyr Gln Asn Glu Ser Ser Arg Asn Ala Gln Phe Leu Asp Met
145                 150                 155                 160

Val Ala Asn Glu Thr Gly Leu Thr Asp Leu Thr Leu Glu Thr Val Trp
                165                 170                 175

Asn Val Tyr Asp Thr Leu Phe Cys Glu Gln Thr His Gly Leu Arg Leu
            180                 185                 190

Pro Pro Trp Ala Ser Pro Gln Thr Met Gln Arg Leu Ser Arg Leu Lys
        195                 200                 205

Asp Phe Ser Phe Arg Phe Leu Phe Gly Ile Tyr Gln Gln Ala Glu Lys
    210                 215                 220

Ala Arg Leu Gln Gly Gly Val Leu Leu Ala Gln Ile Arg Lys Asn Leu
225                 230                 235                 240

Thr Leu Met Ala Thr Thr Ser Gln Leu Pro Lys Leu Leu Val Tyr Ser
                245                 250                 255

Ala His Asp Thr Thr Leu Val Ala Leu Gln Met Ala Leu Asp Val Tyr
            260                 265                 270

Asn Gly Glu Gln Ala Pro Tyr Ala Ser Cys His Ile Phe Glu Leu Tyr
        275                 280                 285

Gln Glu Asp Ser Gly Asn Phe Ser Val Glu Met Tyr Phe Arg Asn Glu
    290                 295                 300

Ser Asp Lys Ala Pro Trp Pro Leu Ser Leu Pro Gly Cys Pro His Arg
305                 310                 315                 320
```

```
Cys Pro Leu Gln Asp Phe Leu Arg Leu Thr Glu Pro Val Val Pro Lys
                325                 330                 335

Asp Trp Gln Gln Glu Cys Gln Leu Ala Ser Gly Pro Ala Asp Thr Glu
            340                 345                 350

Val Ile Val Ala Leu Ala Val Cys Gly Ser Ile Leu Phe Leu Leu Ile
        355                 360                 365

Val Leu Leu Leu Thr Val Leu Phe Arg Met Gln Ala Gln Pro Pro Gly
    370                 375                 380

Tyr Arg His Val Ala Asp Gly Glu Asp His Ala
385                 390                 395


<210> 1323
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432466"

<400> 1323
Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
1               5                   10                  15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
            20                  25                  30

Leu Arg Phe Val Thr Leu Leu Tyr Arg His Gly Asp Arg Ser Pro Val
        35                  40                  45
```

```
Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu Trp Pro Gln Gly
    50                  55                  60

Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His Trp Glu Leu Gly
65                  70                  75                  80

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
                85                  90                  95

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
            100                 105                 110

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
        115                 120                 125

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
    130                 135                 140

Pro Ile Thr Glu Asp Arg Ser Arg Thr Glu Thr Leu Ile His Phe Ser
145                 150                 155                 160


<210> 1324
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434205"

<400> 1324
Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
1               5                   10                  15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
            20                  25                  30
```

```
Leu Arg Phe Val Thr Leu Leu Tyr Arg His Gly Asp Arg Ser Pro Val
        35                  40                  45

Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu Trp Pro Gln Gly
    50                  55                  60

Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His Trp Glu Leu Gly
65                  70                  75                  80

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
                85                  90                  95

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
            100                 105                 110

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
        115                 120                 125

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
    130                 135                 140

Pro Ile Thr Glu Asp Arg Gln Ala Gln Val Thr Arg Thr Val Glu His
145                 150                 155                 160

Ser Ala
```

<210> 1325
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 2, lysosomal; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000435261"

<400> 1325
Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
1   5   10   15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
            20   25   30

Leu Arg Phe Val Thr Leu Leu Tyr Arg His Gly Asp Arg Ser Pro Val
        35   40   45

Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu Trp Pro Gln Gly
    50   55   60

Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His Trp Glu Leu Gly
65   70   75   80

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
                85   90   95

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
            100   105   110

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
        115   120   125

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
    130   135   140

Pro Ile Thr Glu Asp Arg Asp
145   150

<210> 1326
<211> 305
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436487"

<400> 1326
Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
1 5 10 15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
20 25 30

Leu Arg Phe Val Thr Leu Leu Tyr Arg His Gly Asp Arg Ser Pro Val
35 40 45

Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu Trp Pro Gln Gly
50 55 60

Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His Trp Glu Leu Gly
65 70 75 80

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
85 90 95

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
100 105 110

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
115 120 125

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
130 135 140

Pro Ile Thr Glu Asp Arg Gln Phe Leu Asp Met Val Ala Asn Glu Thr
145 150 155 160

Gly Leu Thr Asp Leu Thr Leu Glu Thr Val Trp Asn Val Tyr Asp Thr
165 170 175

Leu Phe Cys Glu Gln Thr His Gly Leu Arg Leu Pro Pro Trp Ala Ser
180 185 190

```
Pro Gln Thr Met Gln Arg Leu Ser Arg Leu Lys Asp Phe Ser Phe Arg
        195                 200                 205

Phe Leu Phe Gly Ile Tyr Gln Gln Ala Glu Lys Ala Arg Leu Gln Gly
    210                 215                 220

Gly Val Leu Leu Ala Gln Ile Arg Lys Asn Leu Thr Leu Met Ala Thr
225                 230                 235                 240

Thr Ser Gln Leu Pro Lys Leu Leu Val Tyr Ser Ala His Asp Thr Thr
                245                 250                 255

Leu Val Ala Leu Gln Met Ala Leu Asp Val Tyr Asn Gly Glu Gln Ala
            260                 265                 270

Pro Tyr Ala Ser Cys His Ile Phe Glu Leu Tyr Gln Glu Asp Ser Gly
        275                 280                 285

Asn Phe Ser Val Glu Met Tyr Phe Arg Asn Glu Ser Asp Lys Ala Pro
    290                 295                 300

Trp
305
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<210> 1327
<211> 360
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 396; "

<220>
<221> source
<223> /note="Gene Symbol: ACP2; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 2, lysosomal; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436658"

<400> 1327
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Met Ala Gly Lys Arg Ser Gly Trp Ser Arg Ala Ala Leu Leu Gln Leu
```

```
1               5                   10                  15

Leu Leu Gly Val Asn Leu Val Val Met Pro Pro Thr Arg Ala Arg Ser
            20                  25                  30

Leu Arg Phe Val Thr Leu Leu Tyr Arg His Gly Asp Arg Ser Pro Val
        35                  40                  45

Lys Thr Tyr Pro Lys Asp Pro Tyr Gln Glu Glu Glu Trp Pro Gln Gly
    50                  55                  60

Phe Gly Gln Leu Thr Lys Glu Gly Met Leu Gln His Trp Glu Leu Gly
65                  70                  75                  80

Gln Ala Leu Arg Gln Arg Tyr His Gly Phe Leu Asn Thr Ser Tyr His
                85                  90                  95

Arg Gln Glu Val Tyr Val Arg Ser Thr Asp Phe Asp Arg Thr Leu Met
            100                 105                 110

Ser Ala Glu Ala Asn Leu Ala Gly Leu Phe Pro Pro Asn Gly Met Gln
        115                 120                 125

Arg Phe Asn Pro Asn Ile Ser Trp Gln Pro Ile Pro Val His Thr Val
    130                 135                 140

Pro Ile Thr Glu Asp Arg Gln Thr His Gly Leu Arg Leu Pro Pro Trp
145                 150                 155                 160

Ala Ser Pro Gln Thr Met Gln Arg Leu Ser Arg Leu Lys Asp Phe Ser
                165                 170                 175

Phe Arg Phe Leu Phe Gly Ile Tyr Gln Gln Ala Glu Lys Ala Arg Leu
            180                 185                 190

Gln Gly Gly Val Leu Leu Ala Gln Ile Arg Lys Asn Leu Thr Leu Met
        195                 200                 205

Ala Thr Thr Ser Gln Leu Pro Lys Leu Leu Val Tyr Ser Ala His Asp
    210                 215                 220

Thr Thr Leu Val Ala Leu Gln Met Ala Leu Asp Val Tyr Asn Gly Glu
225                 230                 235                 240
```

```
Gln Ala Pro Tyr Ala Ser Cys His Ile Phe Glu Leu Tyr Gln Glu Asp
                245                 250                 255

Ser Gly Asn Phe Ser Val Glu Met Tyr Phe Arg Asn Glu Ser Asp Lys
            260                 265                 270

Ala Pro Trp Pro Leu Ser Leu Pro Gly Cys Pro His Arg Cys Pro Leu
        275                 280                 285

Gln Asp Phe Leu Arg Leu Thr Glu Pro Val Val Pro Lys Asp Trp Gln
    290                 295                 300

Gln Glu Cys Gln Leu Ala Ser Gly Pro Ala Asp Thr Glu Val Ile Val
305                 310                 315                 320

Ala Leu Ala Val Cys Gly Ser Ile Leu Phe Leu Leu Ile Val Leu Leu
                325                 330                 335

Leu Thr Val Leu Phe Arg Met Gln Ala Gln Pro Pro Gly Tyr Arg His
            340                 345                 350

Val Ala Asp Gly Glu Asp His Ala
        355                 360


<210> 1328
<211> 325
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 397; "

<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
<221> source
<223> /note="Uniprot ID:  P13686; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000218758"

<400> 1328
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1   5   10   15

Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
            20   25   30

Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
        35   40   45

Ala Asn Ala Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp
    50   55   60

Phe Ile Leu Ser Leu Gly Asp Asn Phe Tyr Phe Thr Gly Val Gln Asp
65   70   75   80

Ile Asn Asp Lys Arg Phe Gln Glu Thr Phe Glu Asp Val Phe Ser Asp
                85   90   95

Arg Ser Leu Arg Lys Val Pro Trp Tyr Val Leu Ala Gly Asn His Asp
            100   105   110

His Leu Gly Asn Val Ser Ala Gln Ile Ala Tyr Ser Lys Ile Ser Lys
        115   120   125

Arg Trp Asn Phe Pro Ser Pro Phe Tyr Arg Leu His Phe Lys Ile Pro
    130   135   140

Gln Thr Asn Val Ser Val Ala Ile Phe Met Leu Asp Thr Val Thr Leu
145   150   155   160

Cys Gly Asn Ser Asp Asp Phe Leu Ser Gln Gln Pro Glu Arg Pro Arg
                165   170   175

Asp Val Lys Leu Ala Arg Thr Gln Leu Ser Trp Leu Lys Lys Gln Leu
            180   185   190

Ala Ala Ala Arg Glu Asp Tyr Val Leu Val Ala Gly His Tyr Pro Val
        195   200   205

Trp Ser Ile Ala Glu His Gly Pro Thr His Cys Leu Val Lys Gln Leu

```
    210                 215                 220

Arg Pro Leu Leu Ala Thr Tyr Gly Val Thr Ala Tyr Leu Cys Gly His
225                 230                 235                 240

Asp His Asn Leu Gln Tyr Leu Gln Asp Glu Asn Gly Val Gly Tyr Val
                245                 250                 255

Leu Ser Gly Ala Gly Asn Phe Met Asp Pro Ser Lys Arg His Gln Arg
            260                 265                 270

Lys Val Pro Asn Gly Tyr Leu Arg Phe His Tyr Gly Thr Glu Asp Ser
        275                 280                 285

Leu Gly Gly Phe Ala Tyr Val Glu Ile Ser Ser Lys Glu Met Thr Val
    290                 295                 300

Thr Tyr Ile Glu Ala Ser Gly Lys Ser Leu Phe Lys Thr Arg Leu Pro
305                 310                 315                 320

Arg Arg Ala Arg Pro
                325


<210> 1329
<211> 325
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 397; "

<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
<221> source
<223> /note="Uniprot ID:  P13686; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392374"
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<400> 1329
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1 5 10 15

Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
20 25 30

Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
35 40 45

Ala Asn Ala Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp
50 55 60

Phe Ile Leu Ser Leu Gly Asp Asn Phe Tyr Phe Thr Gly Val Gln Asp
65 70 75 80

Ile Asn Asp Lys Arg Phe Gln Glu Thr Phe Glu Asp Val Phe Ser Asp
85 90 95

Arg Ser Leu Arg Lys Val Pro Trp Tyr Val Leu Ala Gly Asn His Asp
100 105 110

His Leu Gly Asn Val Ser Ala Gln Ile Ala Tyr Ser Lys Ile Ser Lys
115 120 125

Arg Trp Asn Phe Pro Ser Pro Phe Tyr Arg Leu His Phe Lys Ile Pro
130 135 140

Gln Thr Asn Val Ser Val Ala Ile Phe Met Leu Asp Thr Val Thr Leu
145 150 155 160

Cys Gly Asn Ser Asp Asp Phe Leu Ser Gln Gln Pro Glu Arg Pro Arg
165 170 175

Asp Val Lys Leu Ala Arg Thr Gln Leu Ser Trp Leu Lys Lys Gln Leu
180 185 190

Ala Ala Ala Arg Glu Asp Tyr Val Leu Val Ala Gly His Tyr Pro Val
195 200 205

Trp Ser Ile Ala Glu His Gly Pro Thr His Cys Leu Val Lys Gln Leu
210 215 220

```
Arg Pro Leu Leu Ala Thr Tyr Gly Val Thr Ala Tyr Leu Cys Gly His
225                 230                 235                 240

Asp His Asn Leu Gln Tyr Leu Gln Asp Glu Asn Gly Val Gly Tyr Val
                245                 250                 255

Leu Ser Gly Ala Gly Asn Phe Met Asp Pro Ser Lys Arg His Gln Arg
            260                 265                 270

Lys Val Pro Asn Gly Tyr Leu Arg Phe His Tyr Gly Thr Glu Asp Ser
        275                 280                 285

Leu Gly Gly Phe Ala Tyr Val Glu Ile Ser Ser Lys Glu Met Thr Val
    290                 295                 300

Thr Tyr Ile Glu Ala Ser Gly Lys Ser Leu Phe Lys Thr Arg Leu Pro
305                 310                 315                 320

Arg Arg Ala Arg Pro
                325


<210> 1330
<211> 325
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 397; "

<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
<221> source
<223> /note="Uniprot ID:  P13686; "

<220>
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<400> 1330
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1               5                   10                  15
```

```
Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
            20                  25                  30

Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
        35                  40                  45

Ala Asn Ala Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp
    50                  55                  60

Phe Ile Leu Ser Leu Gly Asp Asn Phe Tyr Phe Thr Gly Val Gln Asp
65                  70                  75                  80

Ile Asn Asp Lys Arg Phe Gln Glu Thr Phe Glu Asp Val Phe Ser Asp
                85                  90                  95

Arg Ser Leu Arg Lys Val Pro Trp Tyr Val Leu Ala Gly Asn His Asp
            100                 105                 110

His Leu Gly Asn Val Ser Ala Gln Ile Ala Tyr Ser Lys Ile Ser Lys
        115                 120                 125

Arg Trp Asn Phe Pro Ser Pro Phe Tyr Arg Leu His Phe Lys Ile Pro
    130                 135                 140

Gln Thr Asn Val Ser Val Ala Ile Phe Met Leu Asp Thr Val Thr Leu
145                 150                 155                 160

Cys Gly Asn Ser Asp Asp Phe Leu Ser Gln Gln Pro Glu Arg Pro Arg
                165                 170                 175

Asp Val Lys Leu Ala Arg Thr Gln Leu Ser Trp Leu Lys Lys Gln Leu
            180                 185                 190

Ala Ala Ala Arg Glu Asp Tyr Val Leu Val Ala Gly His Tyr Pro Val
        195                 200                 205

Trp Ser Ile Ala Glu His Gly Pro Thr His Cys Leu Val Lys Gln Leu
    210                 215                 220

Arg Pro Leu Leu Ala Thr Tyr Gly Val Thr Ala Tyr Leu Cys Gly His
225                 230                 235                 240
```

```
Asp His Asn Leu Gln Tyr Leu Gln Asp Glu Asn Gly Val Gly Tyr Val
                245                 250                 255

Leu Ser Gly Ala Gly Asn Phe Met Asp Pro Ser Lys Arg His Gln Arg
            260                 265                 270

Lys Val Pro Asn Gly Tyr Leu Arg Phe His Tyr Gly Thr Glu Asp Ser
        275                 280                 285

Leu Gly Gly Phe Ala Tyr Val Glu Ile Ser Ser Lys Glu Met Thr Val
    290                 295                 300

Thr Tyr Ile Glu Ala Ser Gly Lys Ser Leu Phe Lys Thr Arg Leu Pro
305                 310                 315                 320

Arg Arg Ala Arg Pro
                325


<210> 1331
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 397; "

<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
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<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
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<223> /note="ENSP ID: ENSP00000464831"

<400> 1331
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1               5                   10                  15

Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
            20                  25                  30

Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
```

```
        35                  40                  45

Ala Asn Ala Lys
    50


<210> 1332
<211> 124
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACP5; "

<220>
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<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
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<223> /note="ENSP ID: ENSP00000465127"

<400> 1332
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1               5                  10                  15


Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
            20                  25                  30


Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
        35                  40                  45


Ala Asn Ala Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp
    50                  55                  60


Phe Ile Leu Ser Leu Gly Asp Asn Phe Tyr Phe Thr Gly Val Gln Asp
65                  70                  75                  80


Ile Asn Asp Lys Arg Phe Gln Glu Thr Phe Glu Asp Val Phe Ser Asp
                85                  90                  95


Arg Ser Leu Arg Lys Val Pro Trp Tyr Val Leu Ala Gly Asn His Asp
            100                 105                 110
```

```
His Leu Gly Asn Val Ser Ala Gln Ile Ala Tyr Ser
        115                 120


<210> 1333
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
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<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
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<223> /note="ENSP ID: ENSP00000465498"

<400> 1333
Met Asp Met Trp Thr
1               5


<210> 1334
<211> 59
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468509"

<400> 1334
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1               5                   10                  15
```

```
Ser Leu Gly Ile Ser Trp Thr Pro Gln Ser Gly Thr Ser Ala Arg Ser
            20                  25                  30

Pro Thr Ala Ile Cys Ala Ser Thr Met Gly Leu Lys Thr His Trp Val
        35                  40                  45

Ala Leu Pro Met Trp Arg Ser Ala Pro Lys Arg
    50                  55

<210> 1335
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 397; "

<220>
<221> source
<223> /note="Gene Symbol: ACP5; "

<220>
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<223> /note="Gene Name:
      acid phosphatase 5, tartrate resistant; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468685"

<400> 1335
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1               5                   10                  15

Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
            20                  25                  30

Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
        35                  40                  45

Ala Asn Ala Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp
    50                  55                  60

Phe Ile Leu Ser Leu Gly Asp Asn Phe Tyr
65                  70
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<210> 1336
<211> 325
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 397; "

<220>
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<223> /note="Gene Symbol: ACP5; "

<220>
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<223> /note="Gene Name:
acid phosphatase 5, tartrate resistant; "

<220>
<221> source
<223> /note="Uniprot ID: P13686; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468767"

<400> 1336
Met Asp Met Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro
1   5   10   15

Ser Leu Ala Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly
            20   25   30

Asp Trp Gly Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met
        35   40   45

Ala Asn Ala Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp
    50   55   60

Phe Ile Leu Ser Leu Gly Asp Asn Phe Tyr Phe Thr Gly Val Gln Asp
65   70   75   80

Ile Asn Asp Lys Arg Phe Gln Glu Thr Phe Glu Asp Val Phe Ser Asp
                85   90   95

Arg Ser Leu Arg Lys Val Pro Trp Tyr Val Leu Ala Gly Asn His Asp
            100   105   110

His Leu Gly Asn Val Ser Ala Gln Ile Ala Tyr Ser Lys Ile Ser Lys
        115   120   125

```
Arg Trp Asn Phe Pro Ser Pro Phe Tyr Arg Leu His Phe Lys Ile Pro
    130                 135                 140

Gln Thr Asn Val Ser Val Ala Ile Phe Met Leu Asp Thr Val Thr Leu
145                 150                 155                 160

Cys Gly Asn Ser Asp Asp Phe Leu Ser Gln Gln Pro Glu Arg Pro Arg
                165                 170                 175

Asp Val Lys Leu Ala Arg Thr Gln Leu Ser Trp Leu Lys Lys Gln Leu
            180                 185                 190

Ala Ala Ala Arg Glu Asp Tyr Val Leu Val Ala Gly His Tyr Pro Val
        195                 200                 205

Trp Ser Ile Ala Glu His Gly Pro Thr His Cys Leu Val Lys Gln Leu
    210                 215                 220

Arg Pro Leu Leu Ala Thr Tyr Gly Val Thr Ala Tyr Leu Cys Gly His
225                 230                 235                 240

Asp His Asn Leu Gln Tyr Leu Gln Asp Glu Asn Gly Val Gly Tyr Val
                245                 250                 255

Leu Ser Gly Ala Gly Asn Phe Met Asp Pro Ser Lys Arg His Gln Arg
            260                 265                 270

Lys Val Pro Asn Gly Tyr Leu Arg Phe His Tyr Gly Thr Glu Asp Ser
        275                 280                 285

Leu Gly Gly Phe Ala Tyr Val Glu Ile Ser Ser Lys Glu Met Thr Val
    290                 295                 300

Thr Tyr Ile Glu Ala Ser Gly Lys Ser Leu Phe Lys Thr Arg Leu Pro
305                 310                 315                 320

Arg Arg Ala Arg Pro
                325


<210> 1337
<211> 228
<212> PRT
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<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 6, lysophosphatidic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376714"

<400> 1337

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Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1               5                  10                  15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
            20                  25                  30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
        35                  40                  45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
    50                  55                  60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Gly Gly Met Phe Ala Gly Gln
65                  70                  75                  80

Leu Thr Lys Val Gly Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu
                85                  90                  95

Arg Lys Asn Tyr Val Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn
            100                 105                 110

Pro Gln Glu Val Phe Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu
        115                 120                 125

Ser Thr Arg Cys Leu Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly
    130                 135                 140

Pro Ile Ile Ile His Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro
```

145 150 155 160

Asn Tyr Gln Ser Cys Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg
165 170 175

Gln Thr Ala Ser Leu Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val
180 185 190

Lys Asp Arg Met Gly Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile
195 200 205

Leu Leu Asp Asn Val Ala Ala Glu Gln Glu Lys Met Gly Ser Cys Arg
210 215 220

Phe His Gly Ser
225

<210> 1338
<211> 428
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 6, lysophosphatidic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463574"

<400> 1338
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
35 40 45

```
Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
    50                  55                  60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
65                  70                  75                  80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
                85                  90                  95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
            100                 105                 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
        115                 120                 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
    130                 135                 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145                 150                 155                 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
                165                 170                 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
            180                 185                 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
        195                 200                 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
    210                 215                 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
225                 230                 235                 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
                245                 250                 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
            260                 265                 270
```

```
Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
        275                 280                 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
    290                 295                 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
305                 310                 315                 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
                325                 330                 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
            340                 345                 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
        355                 360                 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
    370                 375                 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
385                 390                 395                 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
                405                 410                 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
            420                 425


<210> 1339
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 6, lysophosphatidic; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000477476"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1339
Xaa Arg Cys Leu Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro
1 5 10 15

Ile Ile Ile His Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn
20 25 30

Tyr Gln Ser Cys Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln
35 40 45

Thr Ala Ser Leu Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys
50 55 60

Asp Arg Met Gly Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu
65 70 75 80

Leu Asp Asn Val Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro
85 90 95

Met Leu Lys Arg Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr
100 105 110

Ser Leu Tyr Ile Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala
115 120 125

Val Gly Pro Phe Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met
130 135 140

Asp Ser Ala Thr Ala Pro Asp Lys Ile Arg Thr Cys Arg
145 150 155

<210> 1340
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 6, lysophosphatidic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479906"

<400> 1340
Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro Leu Lys Pro
1 5 10 15

Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu Leu Glu Val
20 25 30

Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu Ala Gly Gly
35 40 45

Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu Thr Thr Leu
50 55 60

Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly Met Gln Gln
65 70 75 80

Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val Glu Asp Ile
85 90 95

Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe Ile Arg Ser
100 105 110

Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu Leu Ala Gly
115 120 125

Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His Thr Asp
130 135 140

<210> 1341
<211> 77
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 6, lysophosphatidic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480100"

<400> 1341
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Tyr Ser Phe His
65 70 75

<210> 1342
<211> 271
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase 6, lysophosphatidic; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NPH0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481777"

<400> 1342
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1   5   10   15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
            20   25   30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
        35   40   45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
    50   55   60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
65   70   75   80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
                85   90   95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
            100   105   110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
        115   120   125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
    130   135   140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145   150   155   160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
                165   170   175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
            180   185   190

```
Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
        195                 200                 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
    210                 215                 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
225                 230                 235                 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
                245                 250                 255

Ala Ala Glu Gln Glu Lys Met Gly Ser Cys Arg Phe His Gly Ser
            260                 265                 270


<210> 1343
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 398; "

<220>
<221> source
<223> /note="Gene Symbol: ACP6; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase 6, lysophosphatidic; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482100"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1343
Xaa Asp Ser Gln Tyr His Glu Thr Thr Leu Lys Gly Gly Met Phe Ala
1               5                   10                  15

Gly Gln Leu Thr Lys Val Gly Met Gln Gln Met Phe Ala Leu Gly Glu
            20                  25                  30
```

```
Arg Leu Arg Lys Asn Tyr Val Glu Asp Ile Pro Phe Leu Ser Pro Thr
        35                  40                  45

Phe Asn Pro Gln Glu Val Phe Ile Arg Ser Thr Asn Ile Phe Arg Asn
    50                  55                  60

Leu Glu Ser Thr Arg Cys Leu Leu Ala Gly Leu Phe Gln Cys Gln Lys
65                  70                  75                  80

Glu Gly Pro Ile Ile Ile His Thr Asp Glu Ala Asp Ser Glu Val Leu
                85                  90                  95

Tyr Pro Asn Tyr Gln Ser Cys Trp Ser Leu Arg Gln Arg Thr Arg Gly
            100                 105                 110

Arg Arg Gln Thr Ala Ser Leu Gln Pro Gly Ile Ser Glu Asp Leu Lys
        115                 120                 125

Lys Val Lys Asp Arg Met Gly Ile Asp Ser Ser Asp Lys Val Asp Phe
    130                 135                 140

Phe Ile Leu Leu Asp Asn Val Ala Ala Glu Gln Glu Lys Met Gly Ser
145                 150                 155                 160

Cys Arg Phe His Gly Ser
                165


<210> 1344
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 399; "

<220>
<221> source
<223> /note="Gene Symbol: ACPP; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase, prostate; "

<220>
<221> source
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<223> /note="Uniprot ID: P15309; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000323036"

<400> 1344

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Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
1               5                  10                  15

Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
            20                  25                  30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
        35                  40                  45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
    50                  55                  60

Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
65                  70                  75                  80

Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
                85                  90                  95

Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
            100                 105                 110

Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
        115                 120                 125

Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
    130                 135                 140

Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
145                 150                 155                 160

Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
                165                 170                 175

Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
            180                 185                 190

Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
        195                 200                 205
```

Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro
210 215 220

Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu
225 230 235 240

Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser
245 250 255

Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys
260 265 270

Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala
275 280 285

His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn
290 295 300

Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe
305 310 315 320

Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln
325 330 335

His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro
340 345 350

Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp
355 360 365

Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Val Leu Lys Val Ile
370 375 380

Phe Ala Val Ala Phe Cys Leu Ile Ser Ala Val Leu Met Val Leu Leu
385 390 395 400

Phe Ile His Ile Arg Arg Gly Leu Cys Trp Gln Arg Glu Ser Tyr Gly
405 410 415

Asn Ile

<210> 1345
<211> 386
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 399; "

<220>
<221> source
<223> /note="Gene Symbol: ACPP; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase, prostate; "

<220>
<221> source
<223> /note="Uniprot ID: P15309; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000337471"

<400> 1345
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
1 5 10 15

Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
20 25 30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
35 40 45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
50 55 60

Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
65 70 75 80

Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
85 90 95

Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
100 105 110

Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly

```
        115                 120                 125

Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
    130                 135                 140

Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
145                 150                 155                 160

Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
                165                 170                 175

Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
            180                 185                 190

Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
        195                 200                 205

Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro
    210                 215                 220

Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu
225                 230                 235                 240

Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser
                245                 250                 255

Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys
            260                 265                 270

Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala
        275                 280                 285

His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn
    290                 295                 300

Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe
305                 310                 315                 320

Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln
                325                 330                 335

His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro
            340                 345                 350
```

```
Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp
        355                 360                 365

Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly Thr Glu Asp Ser
    370                 375                 380

Thr Asp
385
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<210> 1346
<211> 353
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 399; "

<220>
<221> source
<223> /note="Gene Symbol: ACPP; "

<220>
<221> source
<223> /note="Gene Name:
acid phosphatase, prostate; "

<220>
<221> source
<223> /note="Uniprot ID: P15309; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417744"

<400> 1346

```
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
1               5                  10                  15

Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
            20                  25                  30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
        35                  40                  45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
    50                  55                  60
```

```
Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
65                  70                  75                  80

Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
                85                  90                  95

Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
            100                 105                 110

Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
        115                 120                 125

Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
    130                 135                 140

Thr Val Pro Leu Ser Glu Asp Gln Asp Phe Ile Ala Thr Leu Gly Lys
145                 150                 155                 160

Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys Val
                165                 170                 175

Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro Ser
            180                 185                 190

Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu Leu
        195                 200                 205

Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser Arg
    210                 215                 220

Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys Arg
225                 230                 235                 240

Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala His
                245                 250                 255

Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn Gly
            260                 265                 270

Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe Glu
        275                 280                 285

Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln His
```

```
    290                 295                 300

Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro Leu
305                 310                 315                 320

Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp Ser
                325                 330                 335

Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly Thr Glu Asp Ser Thr
            340                 345                 350

Asp



<210> 1347
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 399; "

<220>
<221> source
<223> /note="Gene Symbol: ACPP; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase, prostate; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418366"

<400> 1347
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
1               5                   10                  15

Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
            20                  25                  30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
        35                  40                  45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
    50                  55                  60
```

```
Gln Gly Phe Gly Gln Leu Thr Gln Val Tyr Ile Arg Ser Thr Asp Val
65                  70                  75                  80

Asp Arg Thr Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro
                85                  90                  95

Pro Glu Gly Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile
            100                 105                 110

Pro Val His Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro
        115                 120                 125

Phe Arg Asn Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys
    130                 135                 140

Ser Glu Glu Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala
145                 150                 155                 160

Thr Leu Gly Lys Leu
                165


<210> 1348
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 399; "

<220>
<221> source
<223> /note="Gene Symbol: ACPP; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase, prostate; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422036"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid
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<400> 1348
Xaa Glu Leu Tyr Phe Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr
1   5   10   15

Arg Asn Glu Thr Gln His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys
            20   25   30

Ser Pro Ser Cys Pro Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val
        35   40   45

Ile Pro Gln Asp Trp Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln
    50   55   60

Gly Pro Ala Glu Thr Ala His Ser Ala Arg Arg Asn His Asp Ile Ala
65   70   75   80

Leu Pro Cys Gly Arg Ser Thr Cys Leu Glu Asn Thr Val Leu Tyr Tyr
                85   90   95

His Tyr Gly

<210> 1349
<211> 426
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 400; "

<220>
<221> source
<223> /note="Gene Symbol: ACPT; "

<220>
<221> source
<223> /note="Gene Name:
      acid phosphatase, testicular; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BZG2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000270593"

<400> 1349
Met Ala Gly Leu Gly Phe Trp Gly His Pro Ala Gly Pro Leu Leu Leu

```
1               5                   10                  15

Leu Leu Leu Leu Val Leu Pro Pro Arg Ala Leu Pro Glu Gly Pro Leu
            20                  25                  30

Val Phe Val Ala Leu Val Phe Arg His Gly Asp Arg Ala Pro Leu Ala
        35                  40                  45

Ser Tyr Pro Met Asp Pro His Lys Glu Val Ala Ser Thr Leu Trp Pro
    50                  55                  60

Arg Gly Leu Gly Gln Leu Thr Thr Glu Gly Val Arg Gln Gln Leu Glu
65                  70                  75                  80

Leu Gly Arg Phe Leu Arg Ser Arg Tyr Glu Ala Phe Leu Ser Pro Glu
                85                  90                  95

Tyr Arg Arg Glu Glu Val Tyr Ile Arg Ser Thr Asp Phe Asp Arg Thr
            100                 105                 110

Leu Glu Ser Ala Gln Ala Asn Leu Ala Gly Leu Phe Pro Glu Ala Ala
        115                 120                 125

Pro Gly Ser Pro Glu Ala Arg Trp Arg Pro Ile Pro Val His Thr Val
    130                 135                 140

Pro Val Ala Glu Asp Lys Leu Leu Arg Phe Pro Met Arg Ser Cys Pro
145                 150                 155                 160

Arg Tyr His Glu Leu Leu Arg Glu Ala Thr Glu Ala Ala Glu Tyr Gln
                165                 170                 175

Glu Ala Leu Glu Gly Trp Thr Gly Phe Leu Ser Arg Leu Glu Asn Phe
            180                 185                 190

Thr Gly Leu Ser Leu Val Gly Glu Pro Leu Arg Arg Ala Trp Lys Val
        195                 200                 205

Leu Asp Thr Leu Met Cys Gln Gln Ala His Gly Leu Pro Leu Pro Ala
    210                 215                 220

Trp Ala Ser Pro Asp Val Leu Arg Thr Leu Ala Gln Ile Ser Ala Leu
225                 230                 235                 240
```

```
Asp Ile Gly Ala His Val Gly Pro Pro Arg Ala Ala Glu Lys Ala Gln
                245                 250                 255

Leu Thr Gly Gly Ile Leu Leu Asn Ala Ile Leu Ala Asn Phe Ser Arg
            260                 265                 270

Val Gln Arg Leu Gly Leu Pro Leu Lys Met Val Met Tyr Ser Ala His
        275                 280                 285

Asp Ser Thr Leu Leu Ala Leu Gln Gly Ala Leu Gly Leu Tyr Asp Gly
    290                 295                 300

His Thr Pro Pro Tyr Ala Ala Cys Leu Gly Phe Glu Phe Arg Lys His
305                 310                 315                 320

Leu Gly Asn Pro Ala Lys Asp Gly Gly Asn Val Thr Val Ser Leu Phe
                325                 330                 335

Tyr Arg Asn Asp Ser Ala His Leu Pro Leu Pro Leu Ser Leu Pro Gly
            340                 345                 350

Cys Pro Ala Pro Cys Pro Leu Gly Arg Phe Tyr Gln Leu Thr Ala Pro
        355                 360                 365

Ala Arg Pro Pro Ala His Gly Val Ser Cys His Gly Pro Tyr Glu Ala
    370                 375                 380

Ala Ile Pro Pro Ala Pro Val Val Pro Leu Leu Ala Gly Ala Val Ala
385                 390                 395                 400

Val Leu Val Ala Leu Ser Leu Gly Leu Gly Leu Leu Ala Trp Arg Pro
                405                 410                 415

Gly Cys Leu Arg Ala Leu Gly Gly Pro Val
            420                 425
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<210> 1350
<211> 574
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 401; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC1; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 1; "

<220>
<221> source
<223> /note="Uniprot ID: P78348; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000228468"

<400> 1350
Met Glu Leu Lys Ala Glu Glu Glu Glu Val Gly Gly Val Gln Pro Val
1 5 10 15

Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Leu Ala His
20 25 30

Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp Ala Leu
35 40 45

Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu Arg
50 55 60

Val Gln Tyr Tyr Phe His Tyr His His Val Thr Lys Leu Asp Glu Val
65 70 75 80

Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Leu Asn
85 90 95

Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala Gly
100 105 110

Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp Thr Gln
115 120 125

Met Ala Asp Glu Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala Asn Phe
130 135 140

Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr Asp Arg

145 150 155 160

Ala Gly His Asp Ile Arg Asp Met Leu Leu Ser Cys His Phe Arg Gly
165 170 175

Glu Val Cys Ser Ala Glu Asp Phe Lys Val Val Phe Thr Arg Tyr Gly
180 185 190

Lys Cys Tyr Thr Phe Asn Ser Gly Arg Asp Gly Arg Pro Arg Leu Lys
195 200 205

Thr Met Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile
210 215 220

Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr Ser
225 230 235 240

Phe Glu Ala Gly Ile Lys Val Gln Ile His Ser Gln Asp Glu Pro Pro
245 250 255

Phe Ile Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr Phe
260 265 270

Val Ala Cys Gln Glu Gln Arg Leu Ile Tyr Leu Pro Pro Pro Trp Gly
275 280 285

Thr Cys Lys Ala Val Thr Met Asp Ser Asp Leu Asp Phe Phe Asp Ser
290 295 300

Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Leu Val
305 310 315 320

Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr
325 330 335

Cys Thr Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe
340 345 350

Leu Val Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn
355 360 365

Leu Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys
370 375 380

Ala Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr
385 390 395 400

Ile Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn
405 410 415

Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu
420 425 430

Gly Glu Leu Leu Met Thr Pro Val Pro Phe Ser Cys His Gly His Gly
435 440 445

Val Ala Pro Tyr His Pro Lys Ala Gly Cys Ser Leu Leu Ser His Glu
450 455 460

Gly Pro Pro Pro Gln Arg Pro Phe Pro Lys Pro Cys Cys Leu Gly Asp
465 470 475 480

Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr Val
485 490 495

Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Lys Leu Cys
500 505 510

Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp Lys
515 520 525

Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys Glu
530 535 540

Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile Leu
545 550 555 560

Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys
565 570

<210> 1351
<211> 528
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 401; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC1; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 1; "

<220>
<221> source
<223> /note="Uniprot ID: P78348; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000400228"

<400> 1351
Met Glu Leu Lys Ala Glu Glu Glu Glu Val Gly Gly Val Gln Pro Val
1 5 10 15

Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Leu Ala His
20 25 30

Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp Ala Leu
35 40 45

Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu Arg
50 55 60

Val Gln Tyr Tyr Phe His Tyr His His Val Thr Lys Leu Asp Glu Val
65 70 75 80

Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Leu Asn
85 90 95

Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala Gly
100 105 110

Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp Thr Gln
115 120 125

Met Ala Asp Glu Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala Asn Phe
130 135 140

Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr Asp Arg

145 150 155 160

Ala Gly His Asp Ile Arg Asp Met Leu Leu Ser Cys His Phe Arg Gly
165 170 175

Glu Val Cys Ser Ala Glu Asp Phe Lys Val Val Phe Thr Arg Tyr Gly
180 185 190

Lys Cys Tyr Thr Phe Asn Ser Gly Arg Asp Gly Arg Pro Arg Leu Lys
195 200 205

Thr Met Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile
210 215 220

Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr Ser
225 230 235 240

Phe Glu Ala Gly Ile Lys Val Gln Ile His Ser Gln Asp Glu Pro Pro
245 250 255

Phe Ile Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr Phe
260 265 270

Val Ala Cys Gln Glu Gln Arg Leu Ile Tyr Leu Pro Pro Pro Trp Gly
275 280 285

Thr Cys Lys Ala Val Thr Met Asp Ser Asp Leu Asp Phe Phe Asp Ser
290 295 300

Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Leu Val
305 310 315 320

Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr
325 330 335

Cys Thr Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe
340 345 350

Leu Val Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn
355 360 365

Leu Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys
370 375 380

```
Ala Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr
385                 390                 395                 400

Ile Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn
                405                 410                 415

Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu
            420                 425                 430

Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu
        435                 440                 445

Thr Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Lys
    450                 455                 460

Leu Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala
465                 470                 475                 480

Asp Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro
                485                 490                 495

Cys Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn
            500                 505                 510

Ile Leu Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys
        515                 520                 525


<210> 1352
<211> 396
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 401; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC1; "

<220>
<221> source
<223> /note="Gene Name:
      acid sensing (proton gated) ion channel 1; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000402896"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1352
Xaa Ile Arg Asp Met Leu Leu Ser Cys His Phe Arg Gly Glu Val Cys
1 5 10 15

Ser Ala Glu Asp Phe Lys Val Lys Pro Met Gln Val Ala Lys Glu Leu
20 25 30

Arg Arg Cys Thr Leu Pro Gly Thr Val Phe Gln Gly Thr Gln Arg Ala
35 40 45

Arg Lys Gly Glu Lys Gln Val Phe Thr Arg Tyr Gly Lys Cys Tyr Thr
50 55 60

Phe Asn Ser Gly Arg Asp Gly Arg Pro Arg Leu Lys Thr Met Lys Gly
65 70 75 80

Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile Gln Gln Asp Glu
85 90 95

Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr Ser Phe Glu Ala Gly
100 105 110

Ile Lys Val Gln Ile His Ser Gln Asp Glu Pro Pro Phe Ile Asp Gln
115 120 125

Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr Phe Val Ala Cys Gln
130 135 140

Glu Gln Arg Leu Ile Tyr Leu Pro Pro Pro Trp Gly Thr Cys Lys Ala
145 150 155 160

Val Thr Met Asp Ser Asp Leu Asp Phe Phe Asp Ser Tyr Ser Ile Thr
165 170 175

Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Leu Val Glu Asn Cys Asn
180 185 190

```
Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr Cys Thr Pro Glu
        195                 200                 205

Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe Leu Val Glu Lys
    210                 215                 220

Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn Leu Thr Arg Tyr
225                 230                 235                 240

Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Ala Ser Ala Lys
                245                 250                 255

Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile Gly Glu Asn
            260                 265                 270

Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr Glu Thr Ile
        275                 280                 285

Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly Asp Ile Gly
    290                 295                 300

Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr Val Leu Glu
305                 310                 315                 320

Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Lys Leu Cys Arg Arg
                325                 330                 335

Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp Lys Gly Val
            340                 345                 350

Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys Glu Ser Leu
        355                 360                 365

Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile Leu Pro His
    370                 375                 380

His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys
385                 390                 395
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<210> 1353
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 401; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC1; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446863"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1353
Xaa Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr
1 5 10 15

Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly
20 25 30

Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr
35 40 45

Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Lys Leu
50 55 60

Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp
65 70 75 80

Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys
85 90 95

Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile
100 105 110

Leu Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys
115 120 125

<210> 1354
<211> 263
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 401; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC1; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448263"

<400> 1354
Met Glu Leu Lys Ala Glu Glu Glu Glu Val Gly Gly Val Gln Pro Val
1 5 10 15

Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Leu Ala His
20 25 30

Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp Ala Leu
35 40 45

Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu Arg
50 55 60

Val Gln Tyr Tyr Phe His Tyr His His Val Thr Lys Leu Asp Glu Val
65 70 75 80

Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Leu Asn
85 90 95

Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala Gly
100 105 110

Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp Thr Gln
115 120 125

Met Ala Asp Glu Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala Asn Phe
130 135 140

```
Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr Asp Arg
145                 150                 155                 160

Ala Gly His Asp Ile Arg Asp Met Leu Leu Ser Cys His Phe Arg Gly
                165                 170                 175

Glu Val Cys Ser Ala Glu Asp Phe Lys Val Lys Pro Met Gln Val Ala
            180                 185                 190

Lys Glu Leu Arg Arg Cys Thr Leu Pro Gly Thr Val Phe Gln Gly Thr
        195                 200                 205

Gln Arg Ala Arg Lys Gly Leu His Thr Leu Trp Lys Val Leu His Val
    210                 215                 220

Gln Leu Gly Pro Arg Trp Ala Ala Ala Ala Glu Asp His Glu Gly Trp
225                 230                 235                 240

Asp Gly Gln Trp Ala Gly Asn His Ala Gly His Pro Ala Gly Arg Val
                245                 250                 255

Pro Ala Cys Val Gly Gly Asp
            260


<210> 1355
<211> 562
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 401; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC1; "

<220>
<221> source
<223> /note="Gene Name:
      acid sensing (proton gated) ion channel 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P78348; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000450247"

<400> 1355
Met Pro Ile Gln Ile Phe Cys Ser Met Ser Phe Ser Ser Gly Glu Glu
1 5 10 15

Ala Pro Gly Pro Leu Gly Asp Ile Trp Gly Pro His His His Gln Gln
20 25 30

Gln Gln Asp Ile Ser Glu Ser Glu Glu Glu Glu Glu Lys Glu Lys
35 40 45

Glu Ala Val Arg Lys Glu Ala Ser Glu Gly His Ser Pro Met Asp Leu
50 55 60

Val Ala Phe Ala Asn Ser Cys Thr Leu His Gly Thr Asn His Ile Phe
65 70 75 80

Val Glu Gly Gly Pro Gly Pro Arg Gln Val Leu Trp Ala Val Ala Phe
85 90 95

Val Leu Ala Leu Gly Ala Phe Leu Cys Gln Val Gly Asp Arg Val Ala
100 105 110

Tyr Tyr Leu Ser Tyr Pro His Val Thr Leu Leu Asn Glu Val Ala Thr
115 120 125

Thr Glu Leu Ala Phe Pro Ala Val Thr Leu Cys Asn Thr Asn Ala Val
130 135 140

Arg Leu Ser Gln Leu Ser Tyr Pro Asp Leu Leu Tyr Leu Ala Pro Met
145 150 155 160

Leu Gly Leu Asp Glu Ser Asp Asp Pro Gly Val Pro Leu Ala Pro Pro
165 170 175

Gly Pro Glu Ala Phe Ser Gly Glu Pro Phe Asn Leu His Arg Phe Tyr
180 185 190

Asn Arg Ser Cys His Arg Leu Glu Asp Met Leu Leu Tyr Cys Ser Tyr
195 200 205

Gln Gly Gly Pro Cys Gly Pro His Asn Phe Ser Val Val Phe Thr Arg

```
    210                 215                 220

Tyr Gly Lys Cys Tyr Thr Phe Asn Ser Gly Arg Asp Gly Arg Pro Arg
225                 230                 235                 240

Leu Lys Thr Met Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu
                245                 250                 255

Asp Ile Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu
            260                 265                 270

Thr Ser Phe Glu Ala Gly Ile Lys Val Gln Ile His Ser Gln Asp Glu
        275                 280                 285

Pro Pro Phe Ile Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln
    290                 295                 300

Thr Phe Val Ala Cys Gln Glu Gln Arg Leu Ile Tyr Leu Pro Pro Pro
305                 310                 315                 320

Trp Gly Thr Cys Lys Ala Val Thr Met Asp Ser Asp Leu Asp Phe Phe
                325                 330                 335

Asp Ser Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr
            340                 345                 350

Leu Val Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala
        355                 360                 365

Pro Tyr Cys Thr Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu
    370                 375                 380

Asp Phe Leu Val Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro
385                 390                 395                 400

Cys Asn Leu Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro
                405                 410                 415

Ser Lys Ala Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu
            420                 425                 430

Gln Tyr Ile Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val
        435                 440                 445
```

```
Leu Asn Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly
    450                 455                 460

Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser
465                 470                 475                 480

Ile Leu Thr Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys
                485                 490                 495

His Lys Leu Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser
            500                 505                 510

Ser Ala Asp Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His
        515                 520                 525

Asn Pro Cys Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala
    530                 535                 540

Ala Asn Ile Leu Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe
545                 550                 555                 560

Thr Cys
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<210> 1356
<211> 563
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 402; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC2; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q16515; "

<220>

<221> source
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Met Ser Arg Ile Gly Gly Ala Gly Leu Pro Ala Ala Ala Leu Thr Gly
1 5 10 15

Pro Gly Arg Phe Arg Met Ala Arg Glu Glu Pro Ala Pro Ala Ala Leu
20 25 30

Ala Ala Ala Gly Gln Pro Gly Gly Gly Arg Gly Gly Glu Arg Ala Leu
35 40 45

Gln Gly Pro Gly Val Ala Arg Arg Gly Arg Pro Ser Leu Ser Arg Ala
50 55 60

Lys Leu His Gly Leu Arg His Met Cys Ala Gly Arg Thr Ala Ala Gly
65 70 75 80

Gly Ser Phe Gln Arg Arg Ala Leu Trp Val Leu Ala Phe Cys Thr Ser
85 90 95

Phe Gly Leu Leu Leu Ser Trp Ser Ser Asn Arg Leu Leu Tyr Trp Leu
100 105 110

Ser Phe Pro Ser His Thr Arg Val His Arg Glu Trp Ser Arg Gln Leu
115 120 125

Pro Phe Pro Ala Val Thr Val Cys Asn Asn Asn Pro Leu Arg Phe Pro
130 135 140

Arg Leu Ser Lys Gly Asp Leu Tyr Tyr Ala Gly His Trp Leu Gly Leu
145 150 155 160

Leu Leu Pro Asn Arg Thr Ala Arg Pro Leu Val Ser Glu Leu Leu Arg
165 170 175

Gly Asp Glu Pro Arg Arg Gln Trp Phe Arg Lys Leu Ala Asp Phe Arg
180 185 190

Leu Phe Leu Pro Pro Arg His Phe Glu Gly Ile Ser Ala Ala Phe Met
195 200 205

Asp Arg Leu Gly His Gln Leu Glu Asp Met Leu Leu Ser Cys Lys Tyr

```
    210                 215                 220

Arg Gly Glu Leu Cys Gly Pro His Asn Phe Ser Ser Val Phe Thr Lys
225                 230                 235                 240

Tyr Gly Lys Cys Tyr Met Phe Asn Ser Gly Glu Asp Gly Lys Pro Leu
                245                 250                 255

Leu Thr Thr Val Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu
            260                 265                 270

Asp Ile Gln Gln Asp Glu Tyr Leu Pro Ile Trp Gly Glu Thr Glu Glu
        275                 280                 285

Thr Thr Phe Glu Ala Gly Val Lys Val Gln Ile His Ser Gln Ser Glu
    290                 295                 300

Pro Pro Phe Ile Gln Glu Leu Gly Phe Gly Val Ala Pro Gly Phe Gln
305                 310                 315                 320

Thr Phe Val Ala Thr Gln Glu Gln Arg Leu Thr Tyr Leu Pro Pro Pro
                325                 330                 335

Trp Gly Glu Cys Arg Ser Ser Glu Met Gly Leu Asp Phe Phe Pro Val
            340                 345                 350

Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Ile Val
        355                 360                 365

Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Phe
    370                 375                 380

Cys Thr Pro Glu Gln His Lys Glu Cys Ala Glu Pro Ala Leu Gly Leu
385                 390                 395                 400

Leu Ala Glu Lys Asp Ser Asn Tyr Cys Leu Cys Arg Thr Pro Cys Asn
                405                 410                 415

Leu Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys
            420                 425                 430

Thr Ser Ala Lys Tyr Leu Glu Lys Lys Phe Asn Lys Ser Glu Lys Tyr
        435                 440                 445
```

```
Ile Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Ala Leu Asn
    450                 455                 460

Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val Ala Ala Leu Leu
465                 470                 475                 480

Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu
                485                 490                 495

Thr Ile Leu Glu Leu Phe Asp Tyr Ile Tyr Glu Leu Ile Lys Glu Lys
            500                 505                 510

Leu Leu Asp Leu Leu Gly Lys Glu Glu Asp Glu Gly Ser His Asp Glu
        515                 520                 525

Asn Val Ser Thr Cys Asp Thr Met Pro Asn His Ser Glu Thr Ile Ser
    530                 535                 540

His Thr Val Asn Val Pro Leu Gln Thr Thr Leu Gly Thr Leu Glu Glu
545                 550                 555                 560

Ile Ala Cys
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<210> 1357
<211> 512
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Uniprot ID: Q16515; "

<220>

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<400> 1357
Met Asp Leu Lys Glu Ser Pro Ser Glu Gly Ser Leu Gln Pro Ser Ser
1 5 10 15

Ile Gln Ile Phe Ala Asn Thr Ser Thr Leu His Gly Ile Arg His Ile
20 25 30

Phe Val Tyr Gly Pro Leu Thr Ile Arg Arg Val Leu Trp Ala Val Ala
35 40 45

Phe Val Gly Ser Leu Gly Leu Leu Leu Val Glu Ser Ser Glu Arg Val
50 55 60

Ser Tyr Tyr Phe Ser Tyr Gln His Val Thr Lys Val Asp Glu Val Val
65 70 75 80

Ala Gln Ser Leu Val Phe Pro Ala Val Thr Leu Cys Asn Leu Asn Gly
85 90 95

Phe Arg Phe Ser Arg Leu Thr Thr Asn Asp Leu Tyr His Ala Gly Glu
100 105 110

Leu Leu Ala Leu Leu Asp Val Asn Leu Gln Ile Pro Asp Pro His Leu
115 120 125

Ala Asp Pro Ser Val Leu Glu Ala Leu Arg Gln Lys Ala Asn Phe Lys
130 135 140

His Tyr Lys Pro Lys Gln Phe Ser Met Leu Glu Phe Leu His Arg Val
145 150 155 160

Gly His Asp Leu Lys Asp Met Met Leu Tyr Cys Lys Phe Lys Gly Gln
165 170 175

Glu Cys Gly His Gln Asp Phe Thr Thr Val Phe Thr Lys Tyr Gly Lys
180 185 190

Cys Tyr Met Phe Asn Ser Gly Glu Asp Gly Lys Pro Leu Leu Thr Thr
195 200 205

Val Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile Gln

```
    210                 215                 220

Gln Asp Glu Tyr Leu Pro Ile Trp Gly Glu Thr Glu Glu Thr Thr Phe
225                 230                 235                 240

Glu Ala Gly Val Lys Val Gln Ile His Ser Gln Ser Glu Pro Pro Phe
                245                 250                 255

Ile Gln Glu Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr Phe Val
            260                 265                 270

Ala Thr Gln Glu Gln Arg Leu Thr Tyr Leu Pro Pro Pro Trp Gly Glu
        275                 280                 285

Cys Arg Ser Ser Glu Met Gly Leu Asp Phe Phe Pro Val Tyr Ser Ile
    290                 295                 300

Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Ile Val Glu Asn Cys
305                 310                 315                 320

Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Phe Cys Thr Pro
                325                 330                 335

Glu Gln His Lys Glu Cys Ala Glu Pro Ala Leu Gly Leu Leu Ala Glu
            340                 345                 350

Lys Asp Ser Asn Tyr Cys Leu Cys Arg Thr Pro Cys Asn Leu Thr Arg
        355                 360                 365

Tyr Asn Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Thr Ser Ala
    370                 375                 380

Lys Tyr Leu Glu Lys Lys Phe Asn Lys Ser Glu Lys Tyr Ile Ser Glu
385                 390                 395                 400

Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Ala Leu Asn Tyr Glu Thr
                405                 410                 415

Ile Glu Gln Lys Lys Ala Tyr Glu Val Ala Ala Leu Leu Gly Asp Ile
            420                 425                 430

Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr Ile Leu
        435                 440                 445
```

```
Glu Leu Phe Asp Tyr Ile Tyr Glu Leu Ile Lys Glu Lys Leu Leu Asp
    450                 455                 460

Leu Leu Gly Lys Glu Glu Asp Glu Gly Ser His Asp Glu Asn Val Ser
465                 470                 475                 480

Thr Cys Asp Thr Met Pro Asn His Ser Glu Thr Ile Ser His Thr Val
                485                 490                 495

Asn Val Pro Leu Gln Thr Thr Leu Gly Thr Leu Glu Glu Ile Ala Cys
            500                 505                 510


<210> 1358
<211> 549
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<223> /note="Uniprot ID:  Q9UHC3; "

<220>
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<223> /note="ENSP ID: ENSP00000297512"

<400> 1358
Met Lys Pro Thr Ser Gly Pro Glu Glu Ala Arg Arg Pro Ala Ser Asp
1               5                   10                  15

Ile Arg Val Phe Ala Ser Asn Cys Ser Met His Gly Leu Gly His Val
            20                  25                  30

Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg Gly Met Trp Ala Ala Ala
        35                  40                  45
```

```
Val Val Leu Ser Val Ala Thr Phe Leu Tyr Gln Val Ala Glu Arg Val
    50                  55                  60

Arg Tyr Tyr Arg Glu Phe His His Gln Thr Ala Leu Asp Glu Arg Glu
65                  70                  75                  80

Ser His Arg Leu Ile Phe Pro Ala Val Thr Leu Cys Asn Ile Asn Pro
                85                  90                  95

Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly Ser
            100                 105                 110

Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Phe Leu Arg Ala
        115                 120                 125

Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
    130                 135                 140

Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
145                 150                 155                 160

Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro Glu Asn Phe
                165                 170                 175

Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
            180                 185                 190

Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
        195                 200                 205

Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
    210                 215                 220

Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
225                 230                 235                 240

Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
                245                 250                 255

Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Gln Leu
            260                 265                 270

Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
```

```
        275                 280                 285

Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
    290                 295                 300

Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
305                 310                 315                 320

Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
                325                 330                 335

Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His
            340                 345                 350

Pro Ala Ile Asp Ala Met Leu Arg Lys Asp Ser Cys Ala Cys Pro Asn
        355                 360                 365

Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu Leu Ser Met Val Arg Ile
    370                 375                 380

Pro Ser Arg Ala Ala Ala Arg Phe Leu Ala Arg Lys Leu Asn Arg Ser
385                 390                 395                 400

Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala Leu Asp Ile Phe Phe Glu
                405                 410                 415

Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys Lys Ala Tyr Glu Met Ser
            420                 425                 430

Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala
        435                 440                 445

Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe
    450                 455                 460

Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn Arg Gln His Ser Gln Arg
465                 470                 475                 480

His Ser Ser Thr Asn Leu Leu Gln Glu Gly Leu Gly Ser His Arg Thr
                485                 490                 495

Gln Val Pro His Leu Ser Leu Gly Pro Ser Thr Leu Leu Cys Ser Glu
            500                 505                 510
```

Asp Leu Pro Pro Leu Pro Val Pro Ser Pro Arg Leu Ser Pro Pro Pro
        515   520   525

Thr Ala Pro Ala Thr Leu Ser His Ser Ser Arg Pro Ala Val Cys Val
    530   535   540

Leu Gly Ala Pro Pro
545

<210> 1359
<211> 531
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 403; "

<220>
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      acid sensing (proton gated) ion channel 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UHC3; "

<220>
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<223> /note="ENSP ID: ENSP00000344838"

<400> 1359
Met Lys Pro Thr Ser Gly Pro Glu Glu Ala Arg Arg Pro Ala Ser Asp
1   5   10   15

Ile Arg Val Phe Ala Ser Asn Cys Ser Met His Gly Leu Gly His Val
            20   25   30

Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg Gly Met Trp Ala Ala Ala
        35   40   45

Val Val Leu Ser Val Ala Thr Phe Leu Tyr Gln Val Ala Glu Arg Val
    50   55   60

```
Arg Tyr Tyr Arg Glu Phe His His Gln Thr Ala Leu Asp Glu Arg Glu
65                  70                  75                  80

Ser His Arg Leu Ile Phe Pro Ala Val Thr Leu Cys Asn Ile Asn Pro
                85                  90                  95

Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly Ser
            100                 105                 110

Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Phe Leu Arg Ala
        115                 120                 125

Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
    130                 135                 140

Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
145                 150                 155                 160

Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro Glu Asn Phe
                165                 170                 175

Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
            180                 185                 190

Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
        195                 200                 205

Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
    210                 215                 220

Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
225                 230                 235                 240

Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
                245                 250                 255

Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Gln Leu
            260                 265                 270

Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
        275                 280                 285

Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
```

290 295 300

Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
305 310 315 320

Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
325 330 335

Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His
340 345 350

Pro Ala Ile Asp Ala Met Leu Arg Lys Asp Ser Cys Ala Cys Pro Asn
355 360 365

Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu Leu Ser Met Val Arg Ile
370 375 380

Pro Ser Arg Ala Ala Ala Arg Phe Leu Ala Arg Lys Leu Asn Arg Ser
385 390 395 400

Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala Leu Asp Ile Phe Phe Glu
405 410 415

Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys Lys Ala Tyr Glu Met Ser
420 425 430

Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala
435 440 445

Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe
450 455 460

Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn Arg Gln His Ser Gln Arg
465 470 475 480

His Ser Ser Thr Asn Leu Leu Gln Glu Gly Leu Gly Ser His Arg Thr
485 490 495

Gln Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Pro Pro Cys
500 505 510

Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr Leu Val
515 520 525

Thr Gln Leu
530

<210> 1360
<211> 543
<212> PRT
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<220>
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<220>
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<223> /note="Uniprot ID: Q9UHC3; "

<220>
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<400> 1360
Met Lys Pro Thr Ser Gly Pro Glu Glu Ala Arg Arg Pro Ala Ser Asp
1 5 10 15

Ile Arg Val Phe Ala Ser Asn Cys Ser Met His Gly Leu Gly His Val
20 25 30

Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg Gly Met Trp Ala Ala Ala
35 40 45

Val Val Leu Ser Val Ala Thr Phe Leu Tyr Gln Val Ala Glu Arg Val
50 55 60

Arg Tyr Tyr Arg Glu Phe His His Gln Thr Ala Leu Asp Glu Arg Glu
65 70 75 80

Ser His Arg Leu Ile Phe Pro Ala Val Thr Leu Cys Asn Ile Asn Pro
85 90 95

```
Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly Ser
            100                 105                 110

Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Phe Leu Arg Ala
        115                 120                 125

Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
    130                 135                 140

Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
145                 150                 155                 160

Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro Glu Asn Phe
                165                 170                 175

Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
            180                 185                 190

Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
        195                 200                 205

Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
    210                 215                 220

Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
225                 230                 235                 240

Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
                245                 250                 255

Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Gln Leu
            260                 265                 270

Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
        275                 280                 285

Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
    290                 295                 300

Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
305                 310                 315                 320

Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
```

325 330 335

Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His
340 345 350

Pro Ala Ile Asp Ala Met Leu Arg Lys Asp Ser Cys Ala Cys Pro Asn
355 360 365

Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu Leu Ser Met Val Arg Ile
370 375 380

Pro Ser Arg Ala Ala Ala Arg Phe Leu Ala Arg Lys Leu Asn Arg Ser
385 390 395 400

Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala Leu Asp Ile Phe Phe Glu
405 410 415

Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys Lys Ala Tyr Glu Met Ser
420 425 430

Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala
435 440 445

Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe
450 455 460

Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn Arg Gln His Ser Gln Arg
465 470 475 480

His Ser Ser Thr Asn Leu Thr Ser His Pro Ser Leu Cys Arg His Gln
485 490 495

Asp Ser Leu Arg Leu Pro Pro His Leu Leu Pro Cys His Thr Ala Leu
500 505 510

Asp Leu Leu Ser Val Ser Ser Glu Pro Arg Pro Asp Ile Leu Asp Met
515 520 525

Pro Ser Leu His Val Ala Phe Pro Ser Ser Pro Gln Ile Lys Ser
530 535 540

<210> 1361
<211> 407

<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000367136"

<400> 1361

Met	Lys	Pro	Thr	Ser	Gly	Pro	Glu	Glu	Ala	Arg	Arg	Pro	Ala	Ser	Asp
1				5				10						15	
Ile	Arg	Val	Phe	Ala	Ser	Asn	Cys	Ser	Met	His	Gly	Leu	Gly	His	Val
			20					25					30		
Phe	Gly	Pro	Gly	Ser	Leu	Ser	Leu	Arg	Arg	Gly	Met	Trp	Ala	Ala	Ala
		35					40					45			
Val	Val	Leu	Ser	Val	Ala	Thr	Phe	Leu	Tyr	Gln	Val	Ala	Glu	Arg	Val
	50					55					60				
Arg	Tyr	Tyr	Arg	Glu	Phe	His	His	Gln	Thr	Ala	Leu	Asp	Glu	Arg	Glu
65					70					75					80
Ser	His	Arg	Leu	Ile	Phe	Pro	Ala	Val	Thr	Leu	Cys	Asn	Ile	Asn	Pro
				85					90					95	
Leu	Arg	Arg	Ser	Arg	Leu	Thr	Pro	Asn	Asp	Leu	His	Trp	Ala	Gly	Ser
			100					105					110		
Ala	Leu	Leu	Gly	Leu	Asp	Pro	Ala	Glu	His	Ala	Ala	Phe	Leu	Arg	Ala
		115					120					125			

```
Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
    130                 135                 140

Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
145                 150                 155                 160

Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro Glu Asn Phe
                165                 170                 175

Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
            180                 185                 190

Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
        195                 200                 205

Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
    210                 215                 220

Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
225                 230                 235                 240

Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
                245                 250                 255

Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Gln Leu
            260                 265                 270

Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
        275                 280                 285

Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
    290                 295                 300

Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
305                 310                 315                 320

Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
                325                 330                 335

Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His
            340                 345                 350

Pro Ala Ile Gly Arg Thr Cys Trp Pro Trp Thr Ser Ser Leu Arg Pro
```

```
        355                 360                 365

Ser Thr Met Arg Pro Trp Ser Arg Arg Arg Pro Met Arg Cys Gln Ser
    370                 375                 380

Cys Leu Val Thr Leu Gly Ala Arg Trp Gly Cys Ser Ser Gly Pro Ala
385                 390                 395                 400

Cys Ser Pro Ser Ser Arg Ser
                405
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<210> 1362
<211> 149
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000418361"

<400> 1362

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Cys Ala Ser Thr Arg Tyr Ala Lys Glu Leu Ser Met Val Arg Ile Pro
1               5                   10                  15

Ser Arg Ala Ala Ala Arg Phe Leu Ala Arg Lys Leu Asn Arg Ser Glu
            20                  25                  30

Ala Tyr Ile Ala Glu Asn Val Leu Ala Leu Asp Ile Phe Phe Glu Ala
        35                  40                  45

Leu Asn Tyr Glu Thr Val Glu Gln Lys Lys Ala Tyr Glu Met Ser Glu
    50                  55                  60

Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser
65                  70                  75                  80
```

```
Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe Arg
                85                  90                  95

Asp Lys Val Leu Gly Tyr Phe Trp Asn Arg Gln His Ser Gln Arg His
            100                 105                 110

Ser Ser Thr Asn Leu Leu Gln Glu Gly Leu Gly Ser His Arg Thr Gln
        115                 120                 125

Val Pro His Leu Ser Leu Gly Pro Ser Ser Arg Pro Ala Val Cys Val
    130                 135                 140

Leu Gly Ala Pro Pro
145
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<210> 1363
<211> 407
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 403; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC3; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UHC3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418605"

<400> 1363

```
Met Lys Pro Thr Ser Gly Pro Glu Glu Ala Arg Arg Pro Ala Ser Asp
1               5                   10                  15

Ile Arg Val Phe Ala Ser Asn Cys Ser Met His Gly Leu Gly His Val
            20                  25                  30

Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg Gly Met Trp Ala Ala Ala
```

```
        35                  40                  45

Val Val Leu Ser Val Ala Thr Phe Leu Tyr Gln Val Ala Glu Arg Val
    50                  55                  60

Arg Tyr Tyr Arg Glu Phe His His Gln Thr Ala Leu Asp Glu Arg Glu
65                  70                  75                  80

Ser His Arg Leu Ile Phe Pro Ala Val Thr Leu Cys Asn Ile Asn Pro
                85                  90                  95

Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly Ser
            100                 105                 110

Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Phe Leu Arg Ala
        115                 120                 125

Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
    130                 135                 140

Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
145                 150                 155                 160

Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro Glu Asn Phe
                165                 170                 175

Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
            180                 185                 190

Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
        195                 200                 205

Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
    210                 215                 220

Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
225                 230                 235                 240

Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
                245                 250                 255

Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Gln Leu
            260                 265                 270
```

```
Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
        275                 280                 285

Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
    290                 295                 300

Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
305                 310                 315                 320

Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
                325                 330                 335

Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His
            340                 345                 350

Pro Ala Ile Gly Arg Thr Cys Trp Pro Trp Thr Ser Ser Leu Arg Pro
        355                 360                 365

Ser Thr Met Arg Pro Trp Ser Arg Arg Arg Pro Met Arg Cys Gln Ser
    370                 375                 380

Cys Leu Val Thr Leu Gly Ala Arg Trp Gly Cys Ser Ser Gly Pro Ala
385                 390                 395                 400

Cys Ser Pro Ser Ser Arg Ser
                405
```

<210> 1364
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 403; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC3; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel 3; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000420371"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1364
Xaa Glu Val Arg Leu Pro Asn Gly Val His Ala Arg Arg Arg Ala Ser
1 5 10 15

Val Gln Pro Pro Ala Val Gln Glu Leu Cys Pro Pro Gly His Arg Glu
20 25 30

Asn Val Leu Ala Leu Asp Ile Phe Phe Glu Ala Leu Asn Tyr Glu Thr
35 40 45

Val Glu Gln Lys Lys Ala Tyr Glu Met Ser Glu Leu Leu Gly Asp Ile
50 55 60

Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Leu Leu Thr Ile Leu
65 70 75 80

Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe Arg Asp Lys Val Leu Gly
85 90 95

Tyr Phe Trp Asn Arg Gln His Ser Gln Arg His Ser Ser Thr Asn Leu
100 105 110

Leu Gln Glu Gly Leu Gly Ser His Arg Thr Gln Val Pro His Leu Ser
115 120 125

Leu Gly Pro Ser Ser Arg Pro Ala Val Cys Val Leu Gly Ala Pro Pro
130 135 140

<210> 1365
<211> 647
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 404; "

<220>
<221> source

<223> /note="Gene Symbol: ASIC4; "

<220>
<221> source
<223> /note="Gene Name:
acid sensing (proton gated) ion channel family
member 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q96FT7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000326627"

<400> 1365

```
Met Leu Ser Gly Ala Ala Gly Ala Ala Arg Arg Gly Gly Ala Ala Leu
1               5                  10                  15

Ala Pro Ser Leu Thr Arg Ser Leu Ala Gly Thr His Ala Gly Ala Asp
            20                  25                  30

Ser Cys Ala Gly Ala Asp Lys Gly Ser His Lys Glu Thr Ile Glu Glu
        35                  40                  45

Arg Asp Lys Arg Gln Gln Arg Gln Gln Arg Gln Arg Gln His Gln Gly
    50                  55                  60

Cys Gly Ala Ala Gly Ser Gly Ser Asp Ser Pro Thr Ser Gly Pro His
65                  70                  75                  80

Pro Val Pro Val Leu Phe Pro Leu Ala Leu Ser Leu Glu Glu Gln Pro
                85                  90                  95

Leu Pro Pro Leu Pro Leu Gly Arg Ala Pro Gly Leu Leu Ala Arg Glu
            100                 105                 110

Gly Gln Gly Arg Glu Ala Leu Ala Ser Pro Ser Ser Arg Gly Gln Met
        115                 120                 125

Pro Ile Glu Ile Val Cys Lys Ile Lys Phe Ala Glu Glu Asp Ala Lys
    130                 135                 140

Pro Lys Glu Lys Glu Ala Gly Asp Glu Gln Ser Leu Leu Gly Ala Val
145                 150                 155                 160
```

```
Ala Pro Gly Ala Ala Pro Arg Asp Leu Ala Thr Phe Ala Ser Thr Ser
                165                 170                 175

Thr Leu His Gly Leu Gly Arg Ala Cys Gly Pro Gly Pro His Gly Leu
            180                 185                 190

Arg Arg Thr Leu Trp Ala Leu Ala Leu Leu Thr Ser Leu Ala Ala Phe
        195                 200                 205

Leu Tyr Gln Ala Ala Gly Leu Ala Arg Gly Tyr Leu Thr Arg Pro His
    210                 215                 220

Leu Val Ala Met Asp Pro Ala Ala Pro Ala Pro Val Ala Gly Phe Pro
225                 230                 235                 240

Ala Val Thr Leu Cys Asn Ile Asn Arg Phe Arg His Ser Ala Leu Ser
                245                 250                 255

Asp Ala Asp Ile Phe His Leu Ala Asn Leu Thr Gly Leu Pro Pro Lys
            260                 265                 270

Asp Arg Asp Gly His Arg Ala Ala Gly Leu Arg Tyr Pro Glu Pro Asp
        275                 280                 285

Met Val Asp Ile Leu Asn Arg Thr Gly His Gln Leu Ala Asp Met Leu
    290                 295                 300

Lys Ser Cys Asn Phe Ser Gly His His Cys Ser Ala Ser Asn Phe Ser
305                 310                 315                 320

Val Val Tyr Thr Arg Tyr Gly Lys Cys Tyr Thr Phe Asn Ala Asp Pro
                325                 330                 335

Arg Ser Ser Leu Pro Ser Arg Ala Gly Gly Met Gly Ser Gly Leu Glu
            340                 345                 350

Ile Met Leu Asp Ile Gln Gln Glu Glu Tyr Leu Pro Ile Trp Arg Glu
        355                 360                 365

Thr Asn Glu Thr Ser Phe Glu Ala Gly Ile Arg Val Gln Ile His Ser
    370                 375                 380

Gln Glu Glu Pro Pro Tyr Ile His Gln Leu Gly Phe Gly Val Ser Pro
```

385 390 395 400

Gly Phe Gln Thr Phe Val Ser Cys Gln Glu Gln Arg Leu Thr Tyr Leu
405 410 415

Pro Gln Pro Trp Gly Asn Cys Arg Ala Glu Ser Glu Leu Arg Glu Pro
420 425 430

Glu Leu Gln Gly Tyr Ser Ala Tyr Ser Val Ser Ala Cys Arg Leu Arg
435 440 445

Cys Glu Lys Glu Ala Val Leu Gln Arg Cys His Cys Arg Met Val His
450 455 460

Met Pro Asp Ser Leu Gly Gly Gly Pro Glu Gly Pro Cys Phe Cys Pro
465 470 475 480

Thr Pro Cys Asn Leu Thr Arg Tyr Gly Lys Glu Ile Ser Met Val Arg
485 490 495

Ile Pro Asn Arg Gly Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn Arg
500 505 510

Asn Glu Thr Tyr Ile Arg Glu Asn Phe Leu Val Leu Asp Val Phe Phe
515 520 525

Glu Ala Leu Thr Ser Glu Ala Met Glu Gln Arg Ala Ala Tyr Gly Leu
530 535 540

Ser Ala Leu Leu Gly Asp Leu Gly Gly Gln Met Gly Leu Phe Ile Gly
545 550 555 560

Ala Ser Ile Leu Thr Leu Leu Glu Ile Leu Asp Tyr Ile Tyr Glu Val
565 570 575

Ser Trp Asp Arg Leu Lys Arg Val Trp Arg Arg Pro Lys Thr Pro Leu
580 585 590

Arg Thr Ser Thr Gly Gly Ile Ser Thr Leu Gly Leu Gln Glu Leu Lys
595 600 605

Glu Gln Ser Pro Cys Pro Ser Arg Gly Arg Val Glu Gly Gly Gly Val
610 615 620

```
Ser Ser Leu Leu Pro Asn His His His Pro His Gly Pro Pro Gly Gly
625                 630                 635                 640


Leu Phe Glu Asp Phe Ala Cys
                645


<210> 1366
<211> 666
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 404; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC4; "

<220>
<221> source
<223> /note="Gene Name:
      acid sensing (proton gated) ion channel family
      member 4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96FT7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000350786"

<400> 1366
Met Leu Ser Gly Ala Ala Gly Ala Ala Arg Arg Gly Gly Ala Ala Leu
1               5                   10                  15


Ala Pro Ser Leu Thr Arg Ser Leu Ala Gly Thr His Ala Gly Ala Asp
            20                  25                  30


Ser Cys Ala Gly Ala Asp Lys Gly Ser His Lys Glu Thr Ile Glu Glu
        35                  40                  45


Arg Asp Lys Arg Gln Gln Arg Gln Gln Arg Gln Arg Gln His Gln Gly
    50                  55                  60


Cys Gly Ala Ala Gly Ser Gly Ser Asp Ser Pro Thr Ser Gly Pro His
65                  70                  75                  80
```

```
Pro Val Pro Val Leu Phe Pro Leu Ala Leu Ser Leu Glu Glu Gln Pro
                85                  90                  95

Leu Pro Pro Leu Pro Leu Gly Arg Ala Pro Gly Leu Leu Ala Arg Glu
            100                 105                 110

Gly Gln Gly Arg Glu Ala Leu Ala Ser Pro Ser Ser Arg Gly Gln Met
        115                 120                 125

Pro Ile Glu Ile Val Cys Lys Ile Lys Phe Ala Glu Glu Asp Ala Lys
    130                 135                 140

Pro Lys Glu Lys Glu Ala Gly Asp Glu Gln Ser Leu Leu Gly Ala Val
145                 150                 155                 160

Ala Pro Gly Ala Ala Pro Arg Asp Leu Ala Thr Phe Ala Ser Thr Ser
                165                 170                 175

Thr Leu His Gly Leu Gly Arg Ala Cys Gly Pro Gly Pro His Gly Leu
            180                 185                 190

Arg Arg Thr Leu Trp Ala Leu Ala Leu Leu Thr Ser Leu Ala Ala Phe
        195                 200                 205

Leu Tyr Gln Ala Ala Gly Leu Ala Arg Gly Tyr Leu Thr Arg Pro His
    210                 215                 220

Leu Val Ala Met Asp Pro Ala Ala Pro Ala Pro Val Ala Gly Phe Pro
225                 230                 235                 240

Ala Val Thr Leu Cys Asn Ile Asn Arg Phe Arg His Ser Ala Leu Ser
                245                 250                 255

Asp Ala Asp Ile Phe His Leu Ala Asn Leu Thr Gly Leu Pro Pro Lys
            260                 265                 270

Asp Arg Asp Gly His Arg Ala Ala Gly Leu Arg Tyr Pro Glu Pro Asp
        275                 280                 285

Met Val Asp Ile Leu Asn Arg Thr Gly His Gln Leu Ala Asp Met Leu
    290                 295                 300
```

```
Lys Ser Cys Asn Phe Ser Gly His His Cys Ser Ala Ser Asn Phe Ser
305                 310                 315                 320

Val Val Tyr Thr Arg Tyr Gly Lys Cys Tyr Thr Phe Asn Ala Asp Pro
                325                 330                 335

Arg Ser Ser Leu Pro Ser Arg Ala Gly Gly Met Gly Ser Gly Leu Glu
            340                 345                 350

Ile Met Leu Asp Ile Gln Gln Glu Glu Tyr Leu Pro Ile Trp Arg Glu
        355                 360                 365

Thr Asn Glu Thr Ser Phe Glu Ala Gly Ile Arg Val Gln Ile His Ser
    370                 375                 380

Gln Glu Glu Pro Pro Tyr Ile His Gln Leu Gly Phe Gly Val Ser Pro
385                 390                 395                 400

Gly Phe Gln Thr Phe Val Ser Cys Gln Glu Gln Arg Leu Thr Tyr Leu
                405                 410                 415

Pro Gln Pro Trp Gly Asn Cys Arg Ala Glu Ser Glu Leu Arg Glu Pro
            420                 425                 430

Glu Leu Gln Gly Tyr Ser Ala Tyr Ser Val Ser Ala Cys Arg Leu Arg
        435                 440                 445

Cys Glu Lys Glu Ala Val Leu Gln Arg Cys His Cys Arg Met Val His
    450                 455                 460

Met Pro Gly Asn Glu Thr Ile Cys Pro Pro Asn Ile Tyr Ile Glu Cys
465                 470                 475                 480

Ala Asp His Thr Leu Asp Ser Leu Gly Gly Gly Pro Glu Gly Pro Cys
                485                 490                 495

Phe Cys Pro Thr Pro Cys Asn Leu Thr Arg Tyr Gly Lys Glu Ile Ser
            500                 505                 510

Met Val Arg Ile Pro Asn Arg Gly Ser Ala Arg Tyr Leu Ala Arg Lys
        515                 520                 525

Tyr Asn Arg Asn Glu Thr Tyr Ile Arg Glu Asn Phe Leu Val Leu Asp
```

```
    530                 535                 540

Val Phe Phe Glu Ala Leu Thr Ser Glu Ala Met Glu Gln Arg Ala Ala
545                 550                 555                 560

Tyr Gly Leu Ser Ala Leu Leu Gly Asp Leu Gly Gly Gln Met Gly Leu
                565                 570                 575

Phe Ile Gly Ala Ser Ile Leu Thr Leu Leu Glu Ile Leu Asp Tyr Ile
            580                 585                 590

Tyr Glu Val Ser Trp Asp Arg Leu Lys Arg Val Trp Arg Arg Pro Lys
        595                 600                 605

Thr Pro Leu Arg Thr Ser Thr Gly Gly Ile Ser Thr Leu Gly Leu Gln
    610                 615                 620

Glu Leu Lys Glu Gln Ser Pro Cys Pro Ser Arg Gly Arg Val Glu Gly
625                 630                 635                 640

Gly Gly Val Ser Ser Leu Leu Pro Asn His His His Pro His Gly Pro
                645                 650                 655

Pro Gly Gly Leu Phe Glu Asp Phe Ala Cys
            660                 665


<210> 1367
<211> 505
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 405; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC5; "

<220>
<221> source
<223> /note="Gene Name:
      acid sensing (proton gated) ion channel family
      member 5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NY37; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000442477"

<400> 1367
Met Glu Gln Thr Glu Lys Ser Lys Val Tyr Ala Glu Asn Gly Leu Leu
1 5 10 15

Glu Lys Ile Lys Leu Cys Leu Ser Lys Lys Pro Leu Pro Ser Pro Thr
20 25 30

Glu Arg Lys Lys Phe Asp His Asp Phe Ala Ile Ser Thr Ser Phe His
35 40 45

Gly Ile His Asn Ile Val Gln Asn Arg Ser Lys Ile Arg Arg Val Leu
50 55 60

Trp Leu Val Val Val Leu Gly Ser Val Ser Leu Val Thr Trp Gln Ile
65 70 75 80

Tyr Ile Arg Leu Leu Asn Tyr Phe Thr Trp Pro Thr Thr Thr Ser Ile
85 90 95

Glu Val Gln Tyr Val Glu Lys Met Glu Phe Pro Ala Val Thr Phe Cys
100 105 110

Asn Leu Asn Arg Phe Gln Thr Asp Ala Val Ala Lys Phe Gly Val Ile
115 120 125

Phe Phe Leu Trp His Ile Val Ser Lys Val Leu His Leu Gln Glu Ile
130 135 140

Thr Ala Asn Ser Thr Gly Ser Arg Glu Ala Thr Asp Phe Ala Ala Ser
145 150 155 160

His Gln Asn Phe Ser Ile Val Glu Phe Ile Arg Asn Lys Gly Phe Tyr
165 170 175

Leu Asn Asn Ser Thr Leu Leu Asp Cys Glu Phe Phe Gly Lys Pro Cys
180 185 190

Ser Pro Lys Asp Phe Ala His Val Phe Thr Glu Tyr Gly Asn Cys Phe
195 200 205

```
Thr Phe Asn His Gly Glu Thr Leu Gln Ala Lys Arg Lys Val Ser Val
    210                 215                 220

Ser Gly Arg Gly Leu Ser Leu Leu Phe Asn Val Asn Gln Glu Ala Phe
225                 230                 235                 240

Thr Asp Asn Pro Ala Leu Gly Phe Val Asp Ala Gly Ile Ile Phe Val
                245                 250                 255

Ile His Ser Pro Lys Lys Val Pro Gln Phe Asp Gly Leu Gly Leu Leu
            260                 265                 270

Ser Pro Val Gly Met His Ala Arg Val Thr Ile Arg Gln Val Lys Thr
        275                 280                 285

Val His Gln Glu Tyr Pro Trp Gly Glu Cys Asn Pro Asn Ile Lys Leu
    290                 295                 300

Gln Asn Phe Ser Ser Tyr Ser Thr Ser Gly Cys Leu Lys Glu Cys Lys
305                 310                 315                 320

Ala Gln His Ile Lys Lys Gln Cys Gly Cys Val Pro Phe Leu Leu Pro
                325                 330                 335

Gly Tyr Gly Ile Glu Cys Asp Leu Gln Lys Tyr Phe Ser Cys Val Ser
            340                 345                 350

Pro Val Leu Asp His Ile Glu Phe Lys Asp Leu Cys Thr Val Gly Thr
        355                 360                 365

His Asn Ser Ser Cys Pro Val Ser Cys Glu Glu Ile Glu Tyr Pro Ala
    370                 375                 380

Thr Ile Ser Tyr Ser Ser Phe Pro Ser Gln Lys Ala Leu Lys Tyr Leu
385                 390                 395                 400

Ser Lys Lys Leu Asn Gln Ser Arg Lys Tyr Ile Arg Glu Asn Leu Val
                405                 410                 415

Lys Ile Glu Ile Asn Tyr Ser Asp Leu Asn Tyr Lys Ile Thr Gln Gln
            420                 425                 430
```

```
Gln Lys Ala Val Ser Val Ser Glu Leu Leu Ala Asp Leu Gly Gly Gln
        435                 440                 445


Leu Gly Leu Phe Cys Gly Ala Ser Leu Ile Thr Ile Ile Glu Ile Ile
    450                 455                 460


Glu Tyr Leu Phe Thr Asn Phe Tyr Trp Ile Cys Ile Phe Phe Leu Leu
465                 470                 475                 480


Lys Ile Ser Glu Met Thr Gln Trp Thr Pro Pro Pro Gln Asn His Leu
                485                 490                 495


Gly Asn Lys Asn Arg Ile Glu Glu Cys
            500                 505


<210> 1368
<211> 411
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 406; "

<220>
<221> source
<223> /note="Gene Symbol: ASIC5; "

<220>
<221> source
<223> /note="Gene Name:
      Acid sensing ion channel
      subunit family
      member 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461559"

<400> 1368
Met Glu Gln Thr Glu Lys Ser Lys Val Tyr Ala Glu Asn Gly Leu Leu
1               5                   10                  15


Glu Lys Ile Lys Leu Cys Leu Ser Lys Lys Pro Leu Pro Ser Pro Thr
            20                  25                  30


Glu Arg Lys Lys Phe Asp His Asp Phe Ala Ile Ser Thr Ser Phe His
        35                  40                  45
```

```
Gly Ile His Asn Ile Val Gln Asn Arg Ser Lys Ile Arg Arg Val Leu
    50                  55                  60

Trp Leu Val Val Val Leu Gly Ser Val Ser Leu Val Thr Trp Gln Ile
65                  70                  75                  80

Tyr Ile Arg Leu Leu Asn Tyr Phe Thr Trp Pro Thr Thr Thr Ser Ile
                85                  90                  95

Glu Val Gln Tyr Val Glu Lys Met Glu Phe Pro Ala Val Thr Phe Cys
            100                 105                 110

Asn Leu Asn Arg Phe Gln Thr Asp Ala Val Ala Lys Phe Gly Val Ile
        115                 120                 125

Phe Phe Leu Trp His Ile Val Ser Lys Val Leu His Leu Gln Glu Ile
    130                 135                 140

Thr Ala Asn Ser Thr Gly Ser Arg Glu Ala Thr Asp Phe Ala Ala Ser
145                 150                 155                 160

His Gln Asn Phe Ser Ile Val Glu Phe Ile Arg Asn Lys Gly Phe Tyr
                165                 170                 175

Leu Asn Asn Ser Thr Leu Leu Asp Cys Glu Phe Phe Gly Lys Pro Cys
            180                 185                 190

Ser Pro Lys Asp Phe Ala His Val Phe Thr Glu Tyr Gly Asn Cys Phe
        195                 200                 205

Thr Phe Asn His Gly Glu Thr Leu Gln Ala Lys Arg Lys Val Ser Val
    210                 215                 220

Ser Gly Arg Gly Leu Ser Leu Leu Phe Asn Val Asn Gln Glu Ala Phe
225                 230                 235                 240

Thr Asp Asn Pro Ala Leu Gly Phe Val Asp Ala Gly Ile Ile Phe Val
                245                 250                 255

Ile His Ser Pro Lys Lys Val Pro Gln Phe Asp Gly Leu Gly Leu Leu
            260                 265                 270

Ser Pro Val Gly Met His Ala Arg Val Thr Ile Arg Gln Val Lys Thr
```

```
        275                 280                 285

Val His Gln Glu Tyr Pro Trp Gly Glu Cys Asn Pro Asn Ile Lys Leu
    290                 295                 300

Gln Asn Phe Ser Ser Tyr Ser Thr Ser Gly Cys Leu Lys Glu Cys Lys
305                 310                 315                 320

Ala Gln His Ile Lys Lys Gln Cys Gly Cys Val Pro Phe Leu Leu Pro
                325                 330                 335

Gly Tyr Gly Ile Glu Cys Asp Leu Gln Lys Tyr Phe Ser Cys Val Ser
            340                 345                 350

Pro Val Leu Asp His Ile Glu Phe Lys Asp Leu Cys Thr Val Gly Thr
        355                 360                 365

His Asn Ser Ser Cys Pro Val Ser Cys Glu Glu Ile Glu Tyr Pro Ala
    370                 375                 380

Thr Ile Ser Tyr Ser Ser Phe Pro Ser Gln Lys Ala Leu Lys Tyr Leu
385                 390                 395                 400

Ser Lys Lys Leu Asn Gln Ser Arg Lys Tyr Ile
                405                 410


<210> 1369
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 407; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32A; "

<220>
<221> source
<223> /note="Gene Name:
      acidic (leu-rich) nuclear phosphoprt 32 family,
      member A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000386496"
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<400> 1369
Met Glu Met Gly Arg Arg Ile His Leu Glu Leu Arg Asn Arg Thr Pro
1   5   10   15

Ser Asp Val Lys Glu Leu Val Leu Asp Asn Ser Arg Ser Asn Glu Gly
            20   25   30

Lys Leu Glu Gly Leu Thr Asp Glu Phe Glu Glu Leu Glu Phe Leu Ser
        35   40   45

Thr Ile Asn Val Gly Leu Thr Ser Ile Ala Asn Leu Pro Lys Leu Asn
    50   55   60

Lys Leu Lys Lys Tyr Trp Gln Lys Ser Val Arg Thr Ser Arg Ile
65   70   75

<210> 1370
<211> 249
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 407; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32A; "

<220>
<221> source
<223> /note="Gene Name:
      acidic (leu-rich) nuclear phosphoprt 32 family,
      member A; "

<220>
<221> source
<223> /note="Uniprot ID: P39687; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417864"

<400> 1370
Met Glu Met Gly Arg Arg Ile His Leu Glu Leu Arg Asn Arg Thr Pro
1   5   10   15

Ser Asp Val Lys Glu Leu Val Leu Asp Asn Ser Arg Ser Asn Glu Gly
            20   25   30

```
Lys Leu Glu Gly Leu Thr Asp Glu Phe Glu Glu Leu Glu Phe Leu Ser
        35                  40                  45

Thr Ile Asn Val Gly Leu Thr Ser Ile Ala Asn Leu Pro Lys Leu Asn
    50                  55                  60

Lys Leu Lys Lys Leu Glu Leu Ser Asp Asn Arg Val Ser Gly Gly Leu
65                  70                  75                  80

Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Thr His Leu Asn Leu Ser
                85                  90                  95

Gly Asn Lys Ile Lys Asp Leu Ser Thr Ile Glu Pro Leu Lys Lys Leu
            100                 105                 110

Glu Asn Leu Lys Ser Leu Asp Leu Phe Asn Cys Glu Val Thr Asn Leu
        115                 120                 125

Asn Asp Tyr Arg Glu Asn Val Phe Lys Leu Leu Pro Gln Leu Thr Tyr
    130                 135                 140

Leu Asp Gly Tyr Asp Arg Asp Asp Lys Glu Ala Pro Asp Ser Asp Ala
145                 150                 155                 160

Glu Gly Tyr Val Glu Gly Leu Asp Asp Glu Glu Glu Asp Glu Asp Glu
                165                 170                 175

Glu Glu Tyr Asp Glu Asp Ala Gln Val Val Glu Asp Glu Glu Asp Glu
            180                 185                 190

Asp Glu Glu Glu Glu Gly Glu Glu Glu Asp Val Ser Gly Glu Glu Glu
        195                 200                 205

Glu Asp Glu Glu Gly Tyr Asn Asp Gly Glu Val Asp Asp Glu Glu Asp
    210                 215                 220

Glu Glu Glu Leu Gly Glu Glu Glu Arg Gly Gln Lys Arg Lys Arg Glu
225                 230                 235                 240

Pro Glu Asp Glu Gly Glu Asp Asp Asp
                245
```

<210> 1371
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 407; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32A; "

<220>
<221> source
<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32 family,
member A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453838"

<400> 1371

```
Met Glu Met Gly Arg Arg Ile His Leu Glu Leu Arg Asn Arg Thr Pro
1               5                  10                  15

Ser Asp Val Lys Glu Leu Val Leu Asp Asn Ser Arg Ser Asn Glu Gly
            20                  25                  30

Lys Leu Glu Gly Leu Thr Asp Glu Phe Glu Glu Leu Glu Phe Leu Ser
        35                  40                  45

Thr Ile Asn Val Gly Leu Thr Ser Ile Ala Asn Leu Pro Lys Leu Asn
    50                  55                  60

Lys Leu Lys Lys Leu Glu Leu Ser Asp Asn Arg Val Ser Gly Gly Leu
65                  70                  75                  80

Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Thr His Leu Asn Leu Ser
                85                  90                  95

Gly Asn Lys Ile Lys Asp Leu Ser Thr Ile Glu Pro Leu Lys Lys Leu
            100                 105                 110

Glu Asn Leu Lys Ser Leu Asp Leu Phe Asn Cys Glu Val Thr Asn Leu
        115                 120                 125

Asn Asp Tyr Arg Glu Asn Val Phe Lys Leu Leu Pro Gln Leu Thr Tyr
```

```
    130                 135                 140

Leu Asp Gly Tyr Asp Arg Asp Asp Lys Glu Ala Pro Asp Ser Asp Ala
145                 150                 155                 160

Glu Gly Tyr Val Glu Gly Leu Asp Asp Glu Glu Glu Asp Glu Asp Gly
                165                 170                 175

Gly
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<210> 1372
<211> 251
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 408; "

<220>
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<223> /note="Gene Symbol: ANP32B; "

<220>
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<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member B; "

<220>
<221> source
<223> /note="Uniprot ID: Q92688; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000345848"

<400> 1372

```
Met Asp Met Lys Arg Arg Ile His Leu Glu Leu Arg Asn Arg Thr Pro
1               5                   10                  15

Ala Ala Val Arg Glu Leu Val Leu Asp Asn Cys Lys Ser Asn Asp Gly
            20                  25                  30

Lys Ile Glu Gly Leu Thr Ala Glu Phe Val Asn Leu Glu Phe Leu Ser
        35                  40                  45

Leu Ile Asn Val Gly Leu Ile Ser Val Ser Asn Leu Pro Lys Leu Pro
    50                  55                  60
```

```
Lys Leu Lys Lys Leu Glu Leu Ser Glu Asn Arg Ile Phe Gly Gly Leu
65                  70                  75                  80

Asp Met Leu Ala Glu Lys Leu Pro Asn Leu Thr His Leu Asn Leu Ser
                85                  90                  95

Gly Asn Lys Leu Lys Asp Ile Ser Thr Leu Glu Pro Leu Lys Lys Leu
            100                 105                 110

Glu Cys Leu Lys Ser Leu Asp Leu Phe Asn Cys Glu Val Thr Asn Leu
        115                 120                 125

Asn Asp Tyr Arg Glu Ser Val Phe Lys Leu Leu Pro Gln Leu Thr Tyr
    130                 135                 140

Leu Asp Gly Tyr Asp Arg Glu Asp Gln Glu Ala Pro Asp Ser Asp Ala
145                 150                 155                 160

Glu Val Asp Gly Val Asp Glu Glu Glu Glu Asp Glu Glu Gly Glu Asp
                165                 170                 175

Glu Glu Asp Glu Asp Asp Glu Asp Gly Glu Glu Glu Glu Phe Asp Glu
            180                 185                 190

Glu Asp Asp Glu Asp Glu Asp Val Glu Gly Asp Glu Asp Asp Asp Glu
        195                 200                 205

Val Ser Glu Glu Glu Glu Glu Phe Gly Leu Asp Glu Glu Asp Glu Asp
    210                 215                 220

Glu Asp Glu Asp Glu Glu Glu Glu Glu Gly Gly Lys Gly Glu Lys Arg
225                 230                 235                 240

Lys Arg Glu Thr Asp Asp Glu Gly Glu Asp Asp
                245                 250
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<210> 1373
<211> 131
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 409; "

<220>
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<223> /note="Gene Symbol: ANP32D; "

<220>
<221> source
<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member D; "

<220>
<221> source
<223> /note="Uniprot ID: O95626; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000266594"

<400> 1373

```
Met Glu Met Gly Lys Trp Ile His Leu Glu Leu Arg Asn Arg Thr Pro
1               5                  10                  15


Ser Asp Val Lys Glu Leu Phe Leu Asp Asn Ser Gln Ser Asn Glu Gly
            20                  25                  30


Lys Leu Glu Gly Leu Thr Asp Glu Phe Glu Glu Leu Glu Leu Leu Asn
        35                  40                  45


Thr Ile Asn Ile Gly Leu Thr Ser Ile Ala Asn Leu Pro Lys Leu Asn
    50                  55                  60


Lys Leu Lys Lys Leu Glu Leu Ser Ser Asn Arg Ala Ser Val Gly Leu
65                  70                  75                  80


Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Ile His Leu Asn Leu Ser
                85                  90                  95


Gly Asn Lys Ile Lys Asp Leu Ser Thr Ile Glu Pro Leu Lys Lys Leu
            100                 105                 110


Glu Asn Leu Glu Ser Leu Asp Leu Phe Thr Cys Glu Val Thr Asn Leu
        115                 120                 125


Asn Asn Tyr
    130
```

<210> 1374
<211> 149
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358110"

<400> 1374

```
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1               5                  10                  15

Glu Glu Val Thr Glu Leu Val Leu Asp Asn Cys Leu Cys Val Asn Gly
            20                  25                  30

Glu Ile Glu Gly Leu Asn Asp Thr Phe Lys Glu Leu Glu Phe Leu Ser
        35                  40                  45

Met Ala Asn Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn
    50                  55                  60

Lys Leu Arg Lys Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu
65                  70                  75                  80

Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser
                85                  90                  95

Gly Asn Lys Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Asp Glu Glu
            100                 105                 110

Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu Glu Glu
        115                 120                 125

Gly Gly Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu Asp Asp Gly
```

130 135 140

Glu Glu Glu Asp Asp
145

<210> 1375
<211> 136
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358111"

<400> 1375
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1 5 10 15

Glu Glu Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu Glu Asp Asp Glu
20 25 30

Asp Gly Asp Glu Asp Asp Glu Glu Glu Glu Glu Asn Glu Ala Gly Pro
35 40 45

Pro Glu Gly Tyr Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu
50 55 60

Asp Glu Asp Glu Asp Glu Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly
65 70 75 80

Glu Glu Glu Val Gly Leu Ser Tyr Leu Met Lys Glu Glu Ile Gln Asp
85 90 95

Glu Glu Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu
100 105 110

Glu Glu Glu Gly Gly Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu
        115   120   125

Asp Asp Gly Glu Glu Glu Asp Asp
    130   135

<210> 1376
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
      acidic (leu-rich) nuclear phosphoprt 32
      family, member E; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BTT0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393718"

<400> 1376
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1   5   10   15

Glu Glu Val Thr Glu Leu Val Leu Asp Asn Cys Leu Cys Val Asn Gly
            20   25   30

Glu Ile Glu Gly Leu Asn Asp Thr Phe Lys Glu Leu Glu Phe Leu Ser
        35   40   45

Met Ala Asn Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn
    50   55   60

Lys Leu Arg Lys Gln Asn Leu Lys Asn Leu Lys Ser Leu Asp Leu Phe
65   70   75   80

```
Asn Cys Glu Ile Thr Asn Leu Glu Asp Tyr Arg Glu Ser Ile Phe Glu
                85                  90                  95

Leu Leu Gln Gln Ile Thr Tyr Leu Asp Gly Phe Asp Gln Glu Asp Asn
            100                 105                 110

Glu Ala Pro Asp Ser Glu Glu Glu Asp Asp Glu Asp Gly Asp Glu Asp
        115                 120                 125

Asp Glu Glu Glu Glu Glu Asn Glu Ala Gly Pro Pro Glu Gly Tyr Glu
    130                 135                 140

Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp Glu Asp
145                 150                 155                 160

Glu Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly Glu Glu Glu Val Gly
                165                 170                 175

Leu Ser Tyr Leu Met Lys Glu Glu Ile Gln Asp Glu Glu Asp Asp Asp
            180                 185                 190

Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu Glu Glu Glu Gly Gly
        195                 200                 205

Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu Asp Asp Gly Glu Glu
    210                 215                 220

Glu Asp Asp
225
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<210> 1377
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:

acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431434"

<400> 1377
Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp Glu Asp Glu
1   5   10   15

Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly Glu Glu Glu Val Gly Leu
            20   25   30

Ser Tyr Leu Met Lys Glu Glu Ile Gln Ser Glu Lys Ser Tyr Gly Phe
        35   40   45

Phe Asn Leu Gln Thr Glu Tyr Leu Asn Phe Lys Asp Glu Glu Asp Asp
    50   55   60

Asp Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu Glu Glu Glu Gly
65   70   75   80

Gly Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu Asp Asp Gly Glu
                85   90   95

Glu Glu Asp Asp
            100

<210> 1378
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000432684"

<400> 1378
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1   5   10   15

Glu Glu Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu Glu Val
            20   25   30

Leu Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser Gly Asn
        35   40   45

Lys Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Gln Asn Leu Lys Asn
    50   55   60

Leu Lys Ser Leu Asp Leu Phe Asn Cys Glu Ile Thr Asn Leu Glu Asp
65   70   75   80

Tyr Arg Glu Ser Ile Phe Glu Leu Leu Gln Gln Ile Thr Tyr Leu Asp
                85   90   95

Gly Phe Asp Gln Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu Glu Asp
            100   105   110

Asp Glu

<210> 1379
<211> 165
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
      acidic (leu-rich) nuclear phosphoprt 32
      family, member E; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435215"

<400> 1379
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1   5   10   15

Glu Glu Val Thr Glu Leu Val Leu Asp Asn Cys Leu Cys Val Asn Gly
            20   25   30

Glu Ile Glu Gly Leu Asn Asp Thr Phe Lys Glu Leu Glu Phe Leu Ser
        35   40   45

Met Ala Asn Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn
    50   55   60

Lys Leu Arg Lys Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu
65   70   75   80

Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser
                85   90   95

Gly Asn Lys Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Met Ala Met
            100   105   110

Lys Met Met Lys Arg Lys Arg Lys Met Lys Leu Val His Arg Lys Asp
        115   120   125

Met Arg Lys Arg Arg Arg Lys Arg Lys Arg Arg Met Arg Met Arg Met
    130   135   140

Lys Met Lys Met Lys Gln Val Gln Ser Trp Glu Arg Glu Lys Arg Lys
145   150   155   160

Trp Ala Ser His Thr
                165

<210> 1380
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 410; "

<220>
<221> source

<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436529"

<400> 1380
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1 5 10 15

Glu Glu Gln Ile Thr Tyr Leu Asp Gly Phe Asp Gln Glu Asp Asn Glu
            20 25 30

Ala Pro Asp Ser Glu Glu Glu Asp Asp Glu Asp Gly Asp Glu Asp Asp
        35 40 45

Glu Glu Glu Glu Glu Asn Glu Ala Gly Pro Pro Glu Gly Tyr Glu Glu
    50 55 60

Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp Glu Asp Glu
65 70 75 80

Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly Glu Glu Glu Val Gly Leu
                85 90 95

Ser Tyr Leu Met Lys Glu Glu Ile Gln
            100 105

<210> 1381
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:

acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BTT0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463154"

<400> 1381
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1   5   10   15

Glu Glu Val Thr Glu Leu Val Leu Asp Asn Cys Leu Cys Val Asn Gly
            20   25   30

Glu Ile Glu Gly Leu Asn Asp Thr Phe Lys Glu Leu Glu Phe Leu Ser
        35   40   45

Met Ala Asn Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn
    50   55   60

Lys Leu Arg Lys Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu
65   70   75   80

Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser
                85   90   95

Gly Asn Lys Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Gln Asn Leu
            100   105   110

Lys Asn Leu Lys Ser Leu Asp Leu Phe Asn Cys Glu Ile Thr Asn Leu
        115   120   125

Glu Asp Tyr Arg Glu Ser Ile Phe Glu Leu Leu Gln Gln Ile Thr Tyr
    130   135   140

Leu Asp Gly Phe Asp Gln Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu
145   150   155   160

Glu Asp Asp Glu Asp Gly Asp Glu Asp Asp Glu Glu Glu Glu Glu Asn
                165   170   175

Glu Ala Gly Pro Pro Glu Gly Tyr Glu Glu Glu Glu Glu Glu Glu Glu

```
            180                 185                 190

Glu Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Ala Gly Ser Glu
        195                 200                 205

Leu Gly Glu Gly Glu Glu Glu Val Gly Leu Ser Tyr Leu Met Lys Glu
    210                 215                 220

Glu Ile Gln Asp Glu Glu Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu
225                 230                 235                 240

Glu Glu Glu Glu Glu Glu Glu Gly Gly Leu Arg Gly Glu Lys Arg Lys
                245                 250                 255

Arg Asp Ala Glu Asp Asp Gly Glu Glu Glu Asp Asp
            260                 265


<210> 1382
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
<221> source
<223> /note="Gene Name:
      acidic (leu-rich) nuclear phosphoprt 32
      family, member E;  "

<220>
<221> source
<223> /note="Uniprot ID:  Q9BTT0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481415"

<400> 1382
Met Ala Asn Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn
1               5                   10                  15

Lys Leu Arg Lys Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu
            20                  25                  30
```

```
Glu Val Leu Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser
        35                  40                  45

Gly Asn Lys Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Gln Asn Leu
    50                  55                  60

Lys Asn Leu Lys Ser Leu Asp Leu Phe Asn Cys Glu Ile Thr Asn Leu
65                  70                  75                  80

Glu Asp Tyr Arg Glu Ser Ile Phe Glu Leu Leu Gln Gln Ile Thr Tyr
                85                  90                  95

Leu Asp Gly Phe Asp Gln Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu
            100                 105                 110

Glu Asp Asp Glu Asp Gly Asp Glu Asp Asp Glu Glu Glu Glu Glu Asn
        115                 120                 125

Glu Ala Gly Pro Pro Glu Gly Tyr Glu Glu Glu Glu Glu Glu Glu Glu
    130                 135                 140

Glu Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Ala Gly Ser Glu
145                 150                 155                 160

Leu Gly Glu Gly Glu Glu Glu Val Gly Leu Ser Tyr Leu Met Lys Glu
                165                 170                 175

Glu Ile Gln Asp Glu Glu Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu
            180                 185                 190

Glu Glu Glu Glu Glu Glu Glu Gly Gly Leu Arg Gly Glu Lys Arg Lys
        195                 200                 205

Arg Asp Ala Glu Asp Asp Gly Glu Glu Glu Asp Asp
    210                 215                 220
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<210> 1383
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 410; "

<220>
<221> source
<223> /note="Gene Symbol: ANP32E; "

<220>
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<223> /note="Gene Name:
acidic (leu-rich) nuclear phosphoprt 32
family, member E; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487027"

<400> 1383
Met Glu Met Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro
1 5 10 15

Glu Glu Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu Glu Asp Asp Glu
            20 25 30

Asp Gly Asp Glu Asp Asp Glu Glu Glu Glu Glu Asn Glu Ala Gly Pro
        35 40 45

Pro Glu Gly Tyr Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu
    50 55 60

Asp Glu Asp Glu Asp Glu Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly
65 70 75 80

Glu Glu Glu Val Gly Leu Ser Tyr Leu Met Lys Glu Glu Ile Gln Asp
                85 90 95

Glu Glu Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu
            100 105 110

Glu Glu Glu Gly Gly Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu
        115 120 125

Asp Asp Gly Glu Glu Glu Asp Asp
    130 135

<210> 1384
<211> 691
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 411; "

<220>
<221> source
<223> /note="Gene Symbol: ACRC; "

<220>
<221> source
<223> /note="Gene Name:
acidic repeat containing; "

<220>
<221> source
<223> /note="Uniprot ID: Q96QF7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000362799"

<400> 1384
Met Asp Gly Cys Lys Lys Glu Leu Pro Arg Leu Gln Glu Pro Glu Glu
1   5   10   15

Asp Glu Asp Cys Tyr Ile Leu Asn Val Gln Ser Ser Ser Asp Asp Thr
            20   25   30

Ser Gly Ser Ser Val Ala Arg Arg Ala Pro Lys Arg Gln Ala Ser Cys
        35   40   45

Ile Leu Asn Val Gln Ser Arg Ser Gly Asp Thr Ser Gly Ser Ser Val
    50   55   60

Ala Arg Arg Ala Pro Lys Arg Gln Ala Ser Ser Val Val Val Ile Asp
65   70   75   80

Ser Asp Ser Asp Glu Glu Cys His Thr His Glu Glu Lys Lys Ala Lys
                85   90   95

Leu Leu Glu Ile Asn Ser Asp Asp Glu Ser Pro Glu Cys Cys His Val
            100   105   110

Lys Pro Ala Ile Gln Glu Pro Pro Ile Val Ile Ser Asp Asp Asp Asn
        115   120   125

Asp Asp Asp Asn Gly Asn Asp Leu Glu Val Pro Asp Asp Asn Ser Asp
    130   135   140

```
Asp Ser Glu Ala Pro Asp Asp Asn Ser Asp Asp Ser Glu Ala Pro Asp
145                 150                 155                 160

Asp Asn Ser Asp Asp Ser Glu Ala Pro Asp Asp Asn Ser Asp Asp Ser
                165                 170                 175

Glu Ala Pro Asp Asp Asn Ser Asp Asp Ser Asp Val Pro Asp Asp Asn
            180                 185                 190

Ser Asp Asp Ser Ser Asp Asp Asn Ser Asp Asp Ser Ser Asp Asp Asn
        195                 200                 205

Ser Asp Asp Ser Asp Val Pro Asp Asp Lys Ser Asp Asp Ser Asp Val
    210                 215                 220

Pro Asp Asp Ser Ser Asp Asp Ser Asp Val Pro Asp Asp Ser Ser Asp
225                 230                 235                 240

Asp Ser Glu Ala Pro Asp Asp Ser Ser Asp Asp Ser Glu Ala Pro Asp
                245                 250                 255

Asp Ser Ser Asp Asp Ser Glu Ala Pro Asp Asp Ser Ser Asp Asp Ser
            260                 265                 270

Glu Ala Pro Asp Asp Ser Ser Asp Asp Ser Glu Ala Ser Asp Asp Ser
        275                 280                 285

Ser Asp Asp Ser Glu Ala Ser Asp Asp Ser Ser Asp Asp Ser Glu Ala
    290                 295                 300

Pro Asp Asp Lys Ser Asp Asp Ser Asp Val Pro Glu Asp Lys Ser Asp
305                 310                 315                 320

Asp Ser Asp Val Pro Asp Asp Asn Ser Asp Asp Leu Glu Val Pro Val
                325                 330                 335

Pro Ala Glu Asp Leu Cys Asn Glu Gly Gln Ile Ala Ser Asp Glu Glu
            340                 345                 350

Glu Leu Val Glu Ala Ala Ala Ala Val Ser Gln His Asp Ser Ser Asp
        355                 360                 365
```

```
Asp Ala Gly Glu Gln Asp Leu Gly Glu Asn Leu Ser Lys Pro Pro Ser
    370                 375                 380

Asp Pro Glu Ala Asn Pro Glu Val Ser Glu Arg Lys Leu Pro Thr Glu
385                 390                 395                 400

Glu Glu Pro Ala Pro Val Val Glu Gln Ser Gly Lys Arg Lys Ser Lys
                405                 410                 415

Thr Lys Thr Ile Val Glu Pro Pro Arg Lys Arg Gln Thr Lys Thr Lys
            420                 425                 430

Asn Ile Val Glu Pro Pro Arg Lys Arg Gln Thr Lys Thr Lys Asn Ile
        435                 440                 445

Val Glu Pro Leu Arg Lys Arg Lys Ala Lys Thr Lys Asn Val Ser Val
    450                 455                 460

Thr Pro Gly His Lys Lys Arg Gly Pro Ser Lys Lys Lys Pro Gly Ala
465                 470                 475                 480

Ala Lys Val Glu Lys Arg Lys Thr Arg Thr Pro Lys Cys Lys Val Pro
                485                 490                 495

Gly Cys Phe Leu Gln Asp Leu Glu Lys Ser Lys Lys Tyr Ser Gly Lys
            500                 505                 510

Asn Leu Lys Arg Asn Lys Asp Glu Leu Val Gln Arg Ile Tyr Asp Leu
        515                 520                 525

Phe Asn Arg Ser Val Cys Asp Lys Lys Leu Pro Glu Lys Leu Arg Ile
    530                 535                 540

Gly Trp Asn Asn Lys Met Val Lys Thr Ala Gly Leu Cys Ser Thr Gly
545                 550                 555                 560

Glu Met Trp Tyr Pro Lys Trp Arg Arg Phe Ala Lys Ile Gln Ile Gly
                565                 570                 575

Leu Lys Val Cys Asp Ser Ala Asp Arg Ile Arg Asp Thr Leu Ile His
            580                 585                 590
```

```
Glu Met Cys His Ala Ala Ser Trp Leu Ile Asp Gly Ile His Asp Ser
        595                 600                 605

His Gly Asp Ala Trp Lys Tyr Tyr Ala Arg Lys Ser Asn Arg Ile His
    610                 615                 620

Pro Glu Leu Pro Arg Val Thr Arg Cys His Asn Tyr Lys Ile Asn Tyr
625                 630                 635                 640

Lys Val His Tyr Glu Cys Thr Gly Cys Lys Thr Arg Ile Gly Cys Tyr
                645                 650                 655

Thr Lys Ser Leu Asp Thr Ser Arg Phe Ile Cys Ala Lys Cys Lys Gly
            660                 665                 670

Ser Leu Val Met Val Pro Leu Thr Gln Lys Asp Gly Thr Arg Ile Val
        675                 680                 685

Pro His Val
    690
```

<210> 1385
<211> 691
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 411; "

<220>
<221> source
<223> /note="Gene Symbol: ACRC; "

<220>
<221> source
<223> /note="Gene Name:
acidic repeat containing; "

<220>
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<223> /note="Uniprot ID: Q96QF7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000362800"

<400> 1385

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Met Asp Gly Cys Lys Lys Glu Leu Pro Arg Leu Gln Glu Pro Glu Glu
1               5                  10                  15
```

```
Asp Glu Asp Cys Tyr Ile Leu Asn Val Gln Ser Ser Ser Asp Asp Thr
            20                  25                  30

Ser Gly Ser Ser Val Ala Arg Arg Ala Pro Lys Arg Gln Ala Ser Cys
        35                  40                  45

Ile Leu Asn Val Gln Ser Arg Ser Gly Asp Thr Ser Gly Ser Ser Val
    50                  55                  60

Ala Arg Arg Ala Pro Lys Arg Gln Ala Ser Ser Val Val Val Ile Asp
65                  70                  75                  80

Ser Asp Ser Asp Glu Glu Cys His Thr His Glu Glu Lys Lys Ala Lys
                85                  90                  95

Leu Leu Glu Ile Asn Ser Asp Asp Glu Ser Pro Glu Cys Cys His Val
            100                 105                 110

Lys Pro Ala Ile Gln Glu Pro Pro Ile Val Ile Ser Asp Asp Asp Asn
        115                 120                 125

Asp Asp Asp Asn Gly Asn Asp Leu Glu Val Pro Asp Asp Asn Ser Asp
    130                 135                 140

Asp Ser Glu Ala Pro Asp Asp Asn Ser Asp Asp Ser Glu Ala Pro Asp
145                 150                 155                 160

Asp Asn Ser Asp Asp Ser Glu Ala Pro Asp Asp Asn Ser Asp Asp Ser
                165                 170                 175

Glu Ala Pro Asp Asp Asn Ser Asp Asp Ser Asp Val Pro Asp Asp Asn
            180                 185                 190

Ser Asp Asp Ser Ser Asp Asp Asn Ser Asp Asp Ser Ser Asp Asp Asn
        195                 200                 205

Ser Asp Asp Ser Asp Val Pro Asp Asp Lys Ser Asp Asp Ser Asp Val
    210                 215                 220

Pro Asp Asp Ser Ser Asp Asp Ser Asp Val Pro Asp Asp Ser Ser Asp
225                 230                 235                 240
```

```
Asp Ser Glu Ala Pro Asp Asp Ser Ser Asp Asp Ser Glu Ala Pro Asp
                245                 250                 255

Asp Ser Ser Asp Asp Ser Glu Ala Pro Asp Asp Ser Ser Asp Asp Ser
            260                 265                 270

Glu Ala Pro Asp Asp Ser Ser Asp Asp Ser Glu Ala Ser Asp Asp Ser
        275                 280                 285

Ser Asp Asp Ser Glu Ala Ser Asp Asp Ser Ser Asp Asp Ser Glu Ala
    290                 295                 300

Pro Asp Asp Lys Ser Asp Asp Ser Asp Val Pro Glu Asp Lys Ser Asp
305                 310                 315                 320

Asp Ser Asp Val Pro Asp Asp Asn Ser Asp Asp Leu Glu Val Pro Val
                325                 330                 335

Pro Ala Glu Asp Leu Cys Asn Glu Gly Gln Ile Ala Ser Asp Glu Glu
            340                 345                 350

Glu Leu Val Glu Ala Ala Ala Ala Val Ser Gln His Asp Ser Ser Asp
        355                 360                 365

Asp Ala Gly Glu Gln Asp Leu Gly Glu Asn Leu Ser Lys Pro Pro Ser
    370                 375                 380

Asp Pro Glu Ala Asn Pro Glu Val Ser Glu Arg Lys Leu Pro Thr Glu
385                 390                 395                 400

Glu Glu Pro Ala Pro Val Val Glu Gln Ser Gly Lys Arg Lys Ser Lys
                405                 410                 415

Thr Lys Thr Ile Val Glu Pro Pro Arg Lys Arg Gln Thr Lys Thr Lys
            420                 425                 430

Asn Ile Val Glu Pro Pro Arg Lys Arg Gln Thr Lys Thr Lys Asn Ile
        435                 440                 445

Val Glu Pro Leu Arg Lys Arg Lys Ala Lys Thr Lys Asn Val Ser Val
    450                 455                 460
```

```
Thr Pro Gly His Lys Lys Arg Gly Pro Ser Lys Lys Lys Pro Gly Ala
465                 470                 475                 480

Ala Lys Val Glu Lys Arg Lys Thr Arg Thr Pro Lys Cys Lys Val Pro
                485                 490                 495

Gly Cys Phe Leu Gln Asp Leu Glu Lys Ser Lys Lys Tyr Ser Gly Lys
            500                 505                 510

Asn Leu Lys Arg Asn Lys Asp Glu Leu Val Gln Arg Ile Tyr Asp Leu
        515                 520                 525

Phe Asn Arg Ser Val Cys Asp Lys Lys Leu Pro Glu Lys Leu Arg Ile
    530                 535                 540

Gly Trp Asn Asn Lys Met Val Lys Thr Ala Gly Leu Cys Ser Thr Gly
545                 550                 555                 560

Glu Met Trp Tyr Pro Lys Trp Arg Arg Phe Ala Lys Ile Gln Ile Gly
                565                 570                 575

Leu Lys Val Cys Asp Ser Ala Asp Arg Ile Arg Asp Thr Leu Ile His
            580                 585                 590

Glu Met Cys His Ala Ala Ser Trp Leu Ile Asp Gly Ile His Asp Ser
        595                 600                 605

His Gly Asp Ala Trp Lys Tyr Tyr Ala Arg Lys Ser Asn Arg Ile His
    610                 615                 620

Pro Glu Leu Pro Arg Val Thr Arg Cys His Asn Tyr Lys Ile Asn Tyr
625                 630                 635                 640

Lys Val His Tyr Glu Cys Thr Gly Cys Lys Thr Arg Ile Gly Cys Tyr
                645                 650                 655

Thr Lys Ser Leu Asp Thr Ser Arg Phe Ile Cys Ala Lys Cys Lys Gly
            660                 665                 670

Ser Leu Val Met Val Pro Leu Thr Gln Lys Asp Gly Thr Arg Ile Val
        675                 680                 685

Pro His Val
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690

<210> 1386
<211> 441
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 412; "

<220>
<221> source
<223> /note="Gene Symbol: ARMT1; "

<220>
<221> source
<223> /note="Gene Name:
acidic residue methyltransferase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H993; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356263"

<400> 1386
Met Ala Val Val Pro Ala Ser Leu Ser Gly Gln Asp Val Gly Ser Phe
1 5 10 15

Ala Tyr Leu Thr Ile Lys Asp Arg Ile Pro Gln Ile Leu Thr Lys Val
20 25 30

Ile Asp Thr Leu His Arg His Lys Ser Glu Phe Phe Glu Lys His Gly
35 40 45

Glu Glu Gly Val Glu Ala Glu Lys Lys Ala Ile Ser Leu Leu Ser Lys
50 55 60

Leu Arg Asn Glu Leu Gln Thr Asp Lys Pro Phe Ile Pro Leu Val Glu
65 70 75 80

Lys Phe Val Asp Thr Asp Ile Trp Asn Gln Tyr Leu Glu Tyr Gln Gln
85 90 95

Ser Leu Leu Asn Glu Ser Asp Gly Lys Ser Arg Trp Phe Tyr Ser Pro
100 105 110

```
Trp Leu Leu Val Glu Cys Tyr Met Tyr Arg Arg Ile His Glu Ala Ile
        115                 120                 125

Ile Gln Ser Pro Pro Ile Asp Tyr Phe Asp Val Phe Lys Glu Ser Lys
    130                 135                 140

Glu Gln Asn Phe Tyr Gly Ser Gln Glu Ser Ile Ile Ala Leu Cys Thr
145                 150                 155                 160

His Leu Gln Gln Leu Ile Arg Thr Ile Glu Asp Leu Asp Glu Asn Gln
                165                 170                 175

Leu Lys Asp Glu Phe Phe Lys Leu Leu Gln Ile Ser Leu Trp Gly Asn
            180                 185                 190

Lys Cys Asp Leu Ser Leu Ser Gly Gly Glu Ser Ser Ser Gln Asn Thr
        195                 200                 205

Asn Val Leu Asn Ser Leu Glu Asp Leu Lys Pro Phe Ile Leu Leu Asn
    210                 215                 220

Asp Met Glu His Leu Trp Ser Leu Leu Ser Asn Cys Lys Lys Thr Arg
225                 230                 235                 240

Glu Lys Ala Ser Ala Thr Arg Val Tyr Ile Val Leu Asp Asn Ser Gly
                245                 250                 255

Phe Glu Leu Val Thr Asp Leu Ile Leu Ala Asp Phe Leu Leu Ser Ser
            260                 265                 270

Glu Leu Ala Thr Glu Val His Phe Tyr Gly Lys Thr Ile Pro Trp Phe
        275                 280                 285

Val Ser Asp Thr Thr Ile His Asp Phe Asn Trp Leu Ile Glu Gln Val
    290                 295                 300

Lys His Ser Asn His Lys Trp Met Ser Lys Cys Gly Ala Asp Trp Glu
305                 310                 315                 320

Glu Tyr Ile Lys Met Gly Lys Trp Val Tyr His Asn His Ile Phe Trp
                325                 330                 335
```

```
Thr Leu Pro His Glu Tyr Cys Ala Met Pro Gln Val Ala Pro Asp Leu
            340                 345                 350

Tyr Ala Glu Leu Gln Lys Ala His Leu Ile Leu Phe Lys Gly Asp Leu
        355                 360                 365

Asn Tyr Arg Lys Leu Thr Gly Asp Arg Lys Trp Glu Phe Ser Val Pro
    370                 375                 380

Phe His Gln Ala Leu Asn Gly Phe His Pro Ala Pro Leu Cys Thr Ile
385                 390                 395                 400

Arg Thr Leu Lys Ala Glu Ile Gln Val Gly Leu Gln Pro Gly Gln Gly
                405                 410                 415

Glu Gln Leu Leu Ala Ser Glu Pro Ser Trp Trp Thr Thr Gly Lys Tyr
            420                 425                 430

Gly Ile Phe Gln Tyr Asp Gly Pro Leu
        435                 440


<210> 1387
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 412; "

<220>
<221> source
<223> /note="Gene Symbol: ARMT1; "

<220>
<221> source
<223> /note="Gene Name:
      acidic residue methyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435882"

<400> 1387
Met Ala Val Val Pro Ala Ser Leu Ser Gly Gln Asp Val Gly Lys Ala
1               5                   10                  15

Trp Lys Leu Lys Arg Lys Leu Ser Leu Ser Phe Leu Asn Tyr Gly Met
            20                  25                  30
```

```
Asn Cys Lys Gln Ile Asn His Leu Ser Pro Trp Leu Arg Asn Leu Leu
        35                  40                  45

Ile Leu Ile Tyr Gly Ile Ser Thr
    50                  55
```

<210> 1388
<211> 322
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 412; "

<220>
<221> source
<223> /note="Gene Symbol: ARMT1; "

<220>
<221> source
<223> /note="Gene Name:
acidic residue methyltransferase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000444121"

<400> 1388

```
Met Tyr Arg Arg Ile His Glu Ala Ile Ile Gln Ser Pro Pro Ile Asp
1               5                  10                  15

Tyr Phe Asp Val Phe Lys Glu Ser Lys Glu Gln Asn Phe Tyr Gly Ser
            20                  25                  30

Gln Glu Ser Ile Ile Ala Leu Cys Thr His Leu Gln Gln Leu Ile Arg
        35                  40                  45

Thr Ile Glu Asp Leu Asp Glu Asn Gln Leu Lys Asp Glu Phe Phe Lys
    50                  55                  60

Leu Leu Gln Ile Ser Leu Trp Gly Asn Lys Cys Asp Leu Ser Leu Ser
65                  70                  75                  80

Gly Gly Glu Ser Ser Ser Gln Asn Thr Asn Val Leu Asn Ser Leu Glu
                85                  90                  95
```

```
Asp Leu Lys Pro Phe Ile Leu Leu Asn Asp Met Glu His Leu Trp Ser
            100                 105                 110

Leu Leu Ser Asn Cys Lys Lys Thr Arg Glu Lys Ala Ser Ala Thr Arg
        115                 120                 125

Val Tyr Ile Val Leu Asp Asn Ser Gly Phe Glu Leu Val Thr Asp Leu
    130                 135                 140

Ile Leu Ala Asp Phe Leu Leu Ser Ser Glu Leu Ala Thr Glu Val His
145                 150                 155                 160

Phe Tyr Gly Lys Thr Ile Pro Trp Phe Val Ser Asp Thr Thr Ile His
                165                 170                 175

Asp Phe Asn Trp Leu Ile Glu Gln Val Lys His Ser Asn His Lys Trp
            180                 185                 190

Met Ser Lys Cys Gly Ala Asp Trp Glu Glu Tyr Ile Lys Met Gly Lys
        195                 200                 205

Trp Val Tyr His Asn His Ile Phe Trp Thr Leu Pro His Glu Tyr Cys
    210                 215                 220

Ala Met Pro Gln Val Ala Pro Asp Leu Tyr Ala Glu Leu Gln Lys Ala
225                 230                 235                 240

His Leu Ile Leu Phe Lys Gly Asp Leu Asn Tyr Arg Lys Leu Thr Gly
                245                 250                 255

Asp Arg Lys Trp Glu Phe Ser Val Pro Phe His Gln Ala Leu Asn Gly
            260                 265                 270

Phe His Pro Ala Pro Leu Cys Thr Ile Arg Thr Leu Lys Ala Glu Ile
        275                 280                 285

Gln Val Gly Leu Gln Pro Gly Gln Gly Glu Gln Leu Leu Ala Ser Glu
    290                 295                 300

Pro Ser Trp Trp Thr Thr Gly Lys Tyr Gly Ile Phe Gln Tyr Asp Gly
305                 310                 315                 320

Pro Leu
```

<210> 1389
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 413; "

<220>
<221> source
<223> /note="Gene Symbol: ADI1; "

<220>
<221> source
<223> /note="Gene Name:
acireductone dioxygenase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BV57; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000333666"

<400> 1389
Met Val Gln Ala Trp Tyr Met Asp Asp Ala Pro Gly Asp Pro Arg Gln
1   5   10   15

Pro His Arg Pro Asp Pro Gly Arg Pro Val Gly Leu Glu Gln Leu Arg
            20   25   30

Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn
        35   40   45

Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met
    50   55   60

Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys
65   70   75   80

Ile Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg
                85   90   95

Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp
            100   105   110

```
Gln Trp Ile Arg Ile Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro
        115                 120                 125

Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys
    130                 135                 140

Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg
145                 150                 155                 160

Pro Ala Asp His Phe Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala
                165                 170                 175

Gln Thr Ala
```

<210> 1390
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 413; "

<220>
<221> source
<223> /note="Gene Symbol: ADI1; "

<220>
<221> source
<223> /note="Gene Name:
acireductone dioxygenase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BV57; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000371525"

<400> 1390

```
Met Ser Val Lys Ser Ser Lys Leu Met Phe Leu Cys His Gly Ser Ser
1               5                   10                  15

Arg Ser Leu His Ser Gly Ser Leu Thr Ser Cys Asn Thr Gly Val Cys
            20                  25                  30

Cys Ser Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys
```

```
        35                  40                  45

Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys
    50                  55                  60

Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu
65                  70                  75                  80

Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser
                85                  90                  95

Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe
            100                 105                 110

Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg
        115                 120                 125

Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val
    130                 135                 140

Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu
145                 150                 155                 160

Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
                165                 170


<210> 1391
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 413; "

<220>
<221> source
<223> /note="Gene Symbol: ADI1; "

<220>
<221> source
<223> /note="Gene Name:
      acireductone dioxygenase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410178"
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1391
Xaa Arg Trp Glu Cys Cys Ala Phe Ser Pro Gly Pro Ala Cys Val Val
1 5 10 15

Ala Leu Ala Val Ala Ser Leu Pro Leu Asn Cys Ala Ala Ser Ala Asp
20 25 30

Ser Lys Arg Gly Arg Trp Ala Arg Asp Ser Ser Thr Cys Ala Ser Arg
35 40 45

Arg Val Cys Gly Ala Ala Gly Asp Val Arg Gly Asp Ser Cys Pro Ser
50 55 60

Val Ala Ala Ser Val Ala Pro Ala Cys Asp Pro Gly Gly Gln Asn Tyr
65 70 75 80

Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Ala Tyr
85 90 95

Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln Tyr Val Lys Phe
100 105 110

Leu Ala Gln Thr Ala
115

<210> 1392
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 413; "

<220>
<221> source
<223> /note="Gene Symbol: ADI1; "

<220>
<221> source
<223> /note="Gene Name:
acireductone dioxygenase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486013"

<400> 1392
Ile Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg
1   5   10   15

Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp
            20   25   30

Gln Trp Ile Arg Ile Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro
        35   40   45

Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys
    50   55   60

Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg
65   70   75   80

Pro Ala Asp His Phe Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala
                85   90   95

Gln Thr Ala

<210> 1393
<211> 889
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 414; "

<220>
<221> source
<223> /note="Gene Symbol: ACO1; "

<220>
<221> source
<223> /note="Gene Name:
      aconitase 1, soluble; "

<220>
<221> source
<223> /note="Uniprot ID: P21399; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000309477"

<400> 1393

```
Met Ser Asn Pro Phe Ala His Leu Ala Glu Pro Leu Asp Pro Val Gln
1               5                  10                  15

Pro Gly Lys Lys Phe Phe Asn Leu Asn Lys Leu Glu Asp Ser Arg Tyr
            20                  25                  30

Gly Arg Leu Pro Phe Ser Ile Arg Val Leu Leu Glu Ala Ala Ile Arg
        35                  40                  45

Asn Cys Asp Glu Phe Leu Val Lys Lys Gln Asp Ile Glu Asn Ile Leu
    50                  55                  60

His Trp Asn Val Thr Gln His Lys Asn Ile Glu Val Pro Phe Lys Pro
65                  70                  75                  80

Ala Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro Ala Val Val Asp
                85                  90                  95

Phe Ala Ala Met Arg Asp Ala Val Lys Lys Leu Gly Gly Asp Pro Glu
            100                 105                 110

Lys Ile Asn Pro Val Cys Pro Ala Asp Leu Val Ile Asp His Ser Ile
        115                 120                 125

Gln Val Asp Phe Asn Arg Arg Ala Asp Ser Leu Gln Lys Asn Gln Asp
    130                 135                 140

Leu Glu Phe Glu Arg Asn Arg Glu Arg Phe Glu Phe Leu Lys Trp Gly
145                 150                 155                 160

Ser Gln Ala Phe His Asn Met Arg Ile Ile Pro Pro Gly Ser Gly Ile
                165                 170                 175

Ile His Gln Val Asn Leu Glu Tyr Leu Ala Arg Val Val Phe Asp Gln
            180                 185                 190

Asp Gly Tyr Tyr Tyr Pro Asp Ser Leu Val Gly Thr Asp Ser His Thr
        195                 200                 205

Thr Met Ile Asp Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220
```

```
Glu Ala Glu Ala Val Met Leu Gly Gln Pro Ile Ser Met Val Leu Pro
225                 230                 235                 240

Gln Val Ile Gly Tyr Arg Leu Met Gly Lys Pro His Pro Leu Val Thr
                245                 250                 255

Ser Thr Asp Ile Val Leu Thr Ile Thr Lys His Leu Arg Gln Val Gly
            260                 265                 270

Val Val Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Ala Gln Leu
        275                 280                 285

Ser Ile Ala Asp Arg Ala Thr Ile Ala Asn Met Cys Pro Glu Tyr Gly
    290                 295                 300

Ala Thr Ala Ala Phe Phe Pro Val Asp Glu Val Ser Ile Thr Tyr Leu
305                 310                 315                 320

Val Gln Thr Gly Arg Asp Glu Glu Lys Leu Lys Tyr Ile Lys Lys Tyr
                325                 330                 335

Leu Gln Ala Val Gly Met Phe Arg Asp Phe Asn Asp Pro Ser Gln Asp
            340                 345                 350

Pro Asp Phe Thr Gln Val Val Glu Leu Asp Leu Lys Thr Val Val Pro
        355                 360                 365

Cys Cys Ser Gly Pro Lys Arg Pro Gln Asp Lys Val Ala Val Ser Asp
    370                 375                 380

Met Lys Lys Asp Phe Glu Ser Cys Leu Gly Ala Lys Gln Gly Phe Lys
385                 390                 395                 400

Gly Phe Gln Val Ala Pro Glu His His Asn Asp His Lys Thr Phe Ile
                405                 410                 415

Tyr Asp Asn Thr Glu Phe Thr Leu Ala His Gly Ser Val Val Ile Ala
            420                 425                 430

Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Leu Gly
        435                 440                 445
```

```
Ala Gly Leu Leu Ala Lys Lys Ala Val Asp Ala Gly Leu Asn Val Met
    450                 455                 460

Pro Tyr Ile Lys Thr Ser Leu Ser Pro Gly Ser Gly Val Val Thr Tyr
465                 470                 475                 480

Tyr Leu Gln Glu Ser Gly Val Met Pro Tyr Leu Ser Gln Leu Gly Phe
                485                 490                 495

Asp Val Val Gly Tyr Gly Cys Met Thr Cys Ile Gly Asn Ser Gly Pro
            500                 505                 510

Leu Pro Glu Pro Val Val Glu Ala Ile Thr Gln Gly Asp Leu Val Ala
        515                 520                 525

Val Gly Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Val His Pro
    530                 535                 540

Asn Thr Arg Ala Asn Tyr Leu Ala Ser Pro Pro Leu Val Ile Ala Tyr
545                 550                 555                 560

Ala Ile Ala Gly Thr Ile Arg Ile Asp Phe Glu Lys Glu Pro Leu Gly
                565                 570                 575

Val Asn Ala Lys Gly Gln Gln Val Phe Leu Lys Asp Ile Trp Pro Thr
            580                 585                 590

Arg Asp Glu Ile Gln Ala Val Glu Arg Gln Tyr Val Ile Pro Gly Met
        595                 600                 605

Phe Lys Glu Val Tyr Gln Lys Ile Glu Thr Val Asn Glu Ser Trp Asn
    610                 615                 620

Ala Leu Ala Thr Pro Ser Asp Lys Leu Phe Phe Trp Asn Ser Lys Ser
625                 630                 635                 640

Thr Tyr Ile Lys Ser Pro Pro Phe Phe Glu Asn Leu Thr Leu Asp Leu
                645                 650                 655

Gln Pro Pro Lys Ser Ile Val Asp Ala Tyr Val Leu Leu Asn Leu Gly
            660                 665                 670
```

Asp Ser Val Thr Thr Asp His Ile Ser Pro Ala Gly Asn Ile Ala Arg
675 680 685

Asn Ser Pro Ala Ala Arg Tyr Leu Thr Asn Arg Gly Leu Thr Pro Arg
690 695 700

Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly Asn Asp Ala Val Met Ala
705 710 715 720

Arg Gly Thr Phe Ala Asn Ile Arg Leu Leu Asn Arg Phe Leu Asn Lys
725 730 735

Gln Ala Pro Gln Thr Ile His Leu Pro Ser Gly Glu Ile Leu Asp Val
740 745 750

Phe Asp Ala Ala Glu Arg Tyr Gln Gln Ala Gly Leu Pro Leu Ile Val
755 760 765

Leu Ala Gly Lys Glu Tyr Gly Ala Gly Ser Ser Arg Asp Trp Ala Ala
770 775 780

Lys Gly Pro Phe Leu Leu Gly Ile Lys Ala Val Leu Ala Glu Ser Tyr
785 790 795 800

Glu Arg Ile His Arg Ser Asn Leu Val Gly Met Gly Val Ile Pro Leu
805 810 815

Glu Tyr Leu Pro Gly Glu Asn Ala Asp Ala Leu Gly Leu Thr Gly Gln
820 825 830

Glu Arg Tyr Thr Ile Ile Ile Pro Glu Asn Leu Lys Pro Gln Met Lys
835 840 845

Val Gln Val Lys Leu Asp Thr Gly Lys Thr Phe Gln Ala Val Met Arg
850 855 860

Phe Asp Thr Asp Val Glu Leu Thr Tyr Phe Leu Asn Gly Gly Ile Leu
865 870 875 880

Asn Tyr Met Ile Arg Lys Met Ala Lys
885

<210> 1394

<211> 889
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 414; "

<220>
<221> source
<223> /note="Gene Symbol: ACO1; "

<220>
<221> source
<223> /note="Gene Name:
aconitase 1, soluble; "

<220>
<221> source
<223> /note="Uniprot ID: P21399; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369255"

<400> 1394

Met	Ser	Asn	Pro	Phe	Ala	His	Leu	Ala	Glu	Pro	Leu	Asp	Pro	Val	Gln
1				5				10					15		
Pro	Gly	Lys	Lys	Phe	Phe	Asn	Leu	Asn	Lys	Leu	Glu	Asp	Ser	Arg	Tyr
			20					25					30		
Gly	Arg	Leu	Pro	Phe	Ser	Ile	Arg	Val	Leu	Leu	Glu	Ala	Ala	Ile	Arg
		35					40					45			
Asn	Cys	Asp	Glu	Phe	Leu	Val	Lys	Lys	Gln	Asp	Ile	Glu	Asn	Ile	Leu
	50					55					60				
His	Trp	Asn	Val	Thr	Gln	His	Lys	Asn	Ile	Glu	Val	Pro	Phe	Lys	Pro
65					70					75					80
Ala	Arg	Val	Ile	Leu	Gln	Asp	Phe	Thr	Gly	Val	Pro	Ala	Val	Val	Asp
				85					90					95	
Phe	Ala	Ala	Met	Arg	Asp	Ala	Val	Lys	Lys	Leu	Gly	Gly	Asp	Pro	Glu
			100					105					110		
Lys	Ile	Asn	Pro	Val	Cys	Pro	Ala	Asp	Leu	Val	Ile	Asp	His	Ser	Ile
		115					120					125			

```
Gln Val Asp Phe Asn Arg Arg Ala Asp Ser Leu Gln Lys Asn Gln Asp
    130                 135                 140

Leu Glu Phe Glu Arg Asn Arg Glu Arg Phe Glu Phe Leu Lys Trp Gly
145                 150                 155                 160

Ser Gln Ala Phe His Asn Met Arg Ile Ile Pro Pro Gly Ser Gly Ile
                165                 170                 175

Ile His Gln Val Asn Leu Glu Tyr Leu Ala Arg Val Val Phe Asp Gln
            180                 185                 190

Asp Gly Tyr Tyr Tyr Pro Asp Ser Leu Val Gly Thr Asp Ser His Thr
        195                 200                 205

Thr Met Ile Asp Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220

Glu Ala Glu Ala Val Met Leu Gly Gln Pro Ile Ser Met Val Leu Pro
225                 230                 235                 240

Gln Val Ile Gly Tyr Arg Leu Met Gly Lys Pro His Pro Leu Val Thr
                245                 250                 255

Ser Thr Asp Ile Val Leu Thr Ile Thr Lys His Leu Arg Gln Val Gly
            260                 265                 270

Val Val Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Ala Gln Leu
        275                 280                 285

Ser Ile Ala Asp Arg Ala Thr Ile Ala Asn Met Cys Pro Glu Tyr Gly
    290                 295                 300

Ala Thr Ala Ala Phe Phe Pro Val Asp Glu Val Ser Ile Thr Tyr Leu
305                 310                 315                 320

Val Gln Thr Gly Arg Asp Glu Glu Lys Leu Lys Tyr Ile Lys Lys Tyr
                325                 330                 335

Leu Gln Ala Val Gly Met Phe Arg Asp Phe Asn Asp Pro Ser Gln Asp
            340                 345                 350
```

```
Pro Asp Phe Thr Gln Val Val Glu Leu Asp Leu Lys Thr Val Val Pro
        355                 360                 365

Cys Cys Ser Gly Pro Lys Arg Pro Gln Asp Lys Val Ala Val Ser Asp
    370                 375                 380

Met Lys Lys Asp Phe Glu Ser Cys Leu Gly Ala Lys Gln Gly Phe Lys
385                 390                 395                 400

Gly Phe Gln Val Ala Pro Glu His His Asn Asp His Lys Thr Phe Ile
                405                 410                 415

Tyr Asp Asn Thr Glu Phe Thr Leu Ala His Gly Ser Val Val Ile Ala
            420                 425                 430

Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Leu Gly
        435                 440                 445

Ala Gly Leu Leu Ala Lys Lys Ala Val Asp Ala Gly Leu Asn Val Met
    450                 455                 460

Pro Tyr Ile Lys Thr Ser Leu Ser Pro Gly Ser Gly Val Val Thr Tyr
465                 470                 475                 480

Tyr Leu Gln Glu Ser Gly Val Met Pro Tyr Leu Ser Gln Leu Gly Phe
                485                 490                 495

Asp Val Val Gly Tyr Gly Cys Met Thr Cys Ile Gly Asn Ser Gly Pro
            500                 505                 510

Leu Pro Glu Pro Val Val Glu Ala Ile Thr Gln Gly Asp Leu Val Ala
        515                 520                 525

Val Gly Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Val His Pro
    530                 535                 540

Asn Thr Arg Ala Asn Tyr Leu Ala Ser Pro Pro Leu Val Ile Ala Tyr
545                 550                 555                 560

Ala Ile Ala Gly Thr Ile Arg Ile Asp Phe Glu Lys Glu Pro Leu Gly
                565                 570                 575

Val Asn Ala Lys Gly Gln Gln Val Phe Leu Lys Asp Ile Trp Pro Thr
```

580 585 590

Arg Asp Glu Ile Gln Ala Val Glu Arg Gln Tyr Val Ile Pro Gly Met
595 600 605

Phe Lys Glu Val Tyr Gln Lys Ile Glu Thr Val Asn Glu Ser Trp Asn
610 615 620

Ala Leu Ala Thr Pro Ser Asp Lys Leu Phe Phe Trp Asn Ser Lys Ser
625 630 635 640

Thr Tyr Ile Lys Ser Pro Pro Phe Phe Glu Asn Leu Thr Leu Asp Leu
645 650 655

Gln Pro Pro Lys Ser Ile Val Asp Ala Tyr Val Leu Leu Asn Leu Gly
660 665 670

Asp Ser Val Thr Thr Asp His Ile Ser Pro Ala Gly Asn Ile Ala Arg
675 680 685

Asn Ser Pro Ala Ala Arg Tyr Leu Thr Asn Arg Gly Leu Thr Pro Arg
690 695 700

Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly Asn Asp Ala Val Met Ala
705 710 715 720

Arg Gly Thr Phe Ala Asn Ile Arg Leu Leu Asn Arg Phe Leu Asn Lys
725 730 735

Gln Ala Pro Gln Thr Ile His Leu Pro Ser Gly Glu Ile Leu Asp Val
740 745 750

Phe Asp Ala Ala Glu Arg Tyr Gln Gln Ala Gly Leu Pro Leu Ile Val
755 760 765

Leu Ala Gly Lys Glu Tyr Gly Ala Gly Ser Ser Arg Asp Trp Ala Ala
770 775 780

Lys Gly Pro Phe Leu Leu Gly Ile Lys Ala Val Leu Ala Glu Ser Tyr
785 790 795 800

Glu Arg Ile His Arg Ser Asn Leu Val Gly Met Gly Val Ile Pro Leu
805 810 815

```
Glu Tyr Leu Pro Gly Glu Asn Ala Asp Ala Leu Gly Leu Thr Gly Gln
            820                 825                 830

Glu Arg Tyr Thr Ile Ile Ile Pro Glu Asn Leu Lys Pro Gln Met Lys
        835                 840                 845

Val Gln Val Lys Leu Asp Thr Gly Lys Thr Phe Gln Ala Val Met Arg
    850                 855                 860

Phe Asp Thr Asp Val Glu Leu Thr Tyr Phe Leu Asn Gly Gly Ile Leu
865                 870                 875                 880

Asn Tyr Met Ile Arg Lys Met Ala Lys
                885
```

<210> 1395
<211> 889
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 414; "

<220>
<221> source
<223> /note="Gene Symbol: ACO1; "

<220>
<221> source
<223> /note="Gene Name:
aconitase 1, soluble; "

<220>
<221> source
<223> /note="Uniprot ID: P21399; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438733"

<400> 1395

```
Met Ser Asn Pro Phe Ala His Leu Ala Glu Pro Leu Asp Pro Val Gln
1               5                  10                  15

Pro Gly Lys Lys Phe Phe Asn Leu Asn Lys Leu Glu Asp Ser Arg Tyr
            20                  25                  30
```

```
Gly Arg Leu Pro Phe Ser Ile Arg Val Leu Leu Glu Ala Ala Ile Arg
        35                  40                  45

Asn Cys Asp Glu Phe Leu Val Lys Lys Gln Asp Ile Glu Asn Ile Leu
    50                  55                  60

His Trp Asn Val Thr Gln His Lys Asn Ile Glu Val Pro Phe Lys Pro
65                  70                  75                  80

Ala Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro Ala Val Val Asp
                85                  90                  95

Phe Ala Ala Met Arg Asp Ala Val Lys Lys Leu Gly Gly Asp Pro Glu
            100                 105                 110

Lys Ile Asn Pro Val Cys Pro Ala Asp Leu Val Ile Asp His Ser Ile
        115                 120                 125

Gln Val Asp Phe Asn Arg Arg Ala Asp Ser Leu Gln Lys Asn Gln Asp
    130                 135                 140

Leu Glu Phe Glu Arg Asn Arg Glu Arg Phe Glu Phe Leu Lys Trp Gly
145                 150                 155                 160

Ser Gln Ala Phe His Asn Met Arg Ile Ile Pro Pro Gly Ser Gly Ile
                165                 170                 175

Ile His Gln Val Asn Leu Glu Tyr Leu Ala Arg Val Val Phe Asp Gln
            180                 185                 190

Asp Gly Tyr Tyr Tyr Pro Asp Ser Leu Val Gly Thr Asp Ser His Thr
        195                 200                 205

Thr Met Ile Asp Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220

Glu Ala Glu Ala Val Met Leu Gly Gln Pro Ile Ser Met Val Leu Pro
225                 230                 235                 240

Gln Val Ile Gly Tyr Arg Leu Met Gly Lys Pro His Pro Leu Val Thr
                245                 250                 255

Ser Thr Asp Ile Val Leu Thr Ile Thr Lys His Leu Arg Gln Val Gly
```

260 265 270

Val Val Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Ala Gln Leu
275 280 285

Ser Ile Ala Asp Arg Ala Thr Ile Ala Asn Met Cys Pro Glu Tyr Gly
290 295 300

Ala Thr Ala Ala Phe Phe Pro Val Asp Glu Val Ser Ile Thr Tyr Leu
305 310 315 320

Val Gln Thr Gly Arg Asp Glu Glu Lys Leu Lys Tyr Ile Lys Lys Tyr
325 330 335

Leu Gln Ala Val Gly Met Phe Arg Asp Phe Asn Asp Pro Ser Gln Asp
340 345 350

Pro Asp Phe Thr Gln Val Val Glu Leu Asp Leu Lys Thr Val Val Pro
355 360 365

Cys Cys Ser Gly Pro Lys Arg Pro Gln Asp Lys Val Ala Val Ser Asp
370 375 380

Met Lys Lys Asp Phe Glu Ser Cys Leu Gly Ala Lys Gln Gly Phe Lys
385 390 395 400

Gly Phe Gln Val Ala Pro Glu His His Asn Asp His Lys Thr Phe Ile
405 410 415

Tyr Asp Asn Thr Glu Phe Thr Leu Ala His Gly Ser Val Val Ile Ala
420 425 430

Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Leu Gly
435 440 445

Ala Gly Leu Leu Ala Lys Lys Ala Val Asp Ala Gly Leu Asn Val Met
450 455 460

Pro Tyr Ile Lys Thr Ser Leu Ser Pro Gly Ser Gly Val Val Thr Tyr
465 470 475 480

Tyr Leu Gln Glu Ser Gly Val Met Pro Tyr Leu Ser Gln Leu Gly Phe
485 490 495

```
Asp Val Val Gly Tyr Gly Cys Met Thr Cys Ile Gly Asn Ser Gly Pro
            500                 505                 510

Leu Pro Glu Pro Val Val Glu Ala Ile Thr Gln Gly Asp Leu Val Ala
        515                 520                 525

Val Gly Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Val His Pro
    530                 535                 540

Asn Thr Arg Ala Asn Tyr Leu Ala Ser Pro Pro Leu Val Ile Ala Tyr
545                 550                 555                 560

Ala Ile Ala Gly Thr Ile Arg Ile Asp Phe Glu Lys Glu Pro Leu Gly
                565                 570                 575

Val Asn Ala Lys Gly Gln Gln Val Phe Leu Lys Asp Ile Trp Pro Thr
            580                 585                 590

Arg Asp Glu Ile Gln Ala Val Glu Arg Gln Tyr Val Ile Pro Gly Met
        595                 600                 605

Phe Lys Glu Val Tyr Gln Lys Ile Glu Thr Val Asn Glu Ser Trp Asn
    610                 615                 620

Ala Leu Ala Thr Pro Ser Asp Lys Leu Phe Phe Trp Asn Ser Lys Ser
625                 630                 635                 640

Thr Tyr Ile Lys Ser Pro Pro Phe Phe Glu Asn Leu Thr Leu Asp Leu
                645                 650                 655

Gln Pro Pro Lys Ser Ile Val Asp Ala Tyr Val Leu Leu Asn Leu Gly
            660                 665                 670

Asp Ser Val Thr Thr Asp His Ile Ser Pro Ala Gly Asn Ile Ala Arg
        675                 680                 685

Asn Ser Pro Ala Ala Arg Tyr Leu Thr Asn Arg Gly Leu Thr Pro Arg
    690                 695                 700

Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly Asn Asp Ala Val Met Ala
705                 710                 715                 720
```

```
Arg Gly Thr Phe Ala Asn Ile Arg Leu Leu Asn Arg Phe Leu Asn Lys
                725                 730                 735

Gln Ala Pro Gln Thr Ile His Leu Pro Ser Gly Glu Ile Leu Asp Val
            740                 745                 750

Phe Asp Ala Ala Glu Arg Tyr Gln Gln Ala Gly Leu Pro Leu Ile Val
        755                 760                 765

Leu Ala Gly Lys Glu Tyr Gly Ala Gly Ser Ser Arg Asp Trp Ala Ala
    770                 775                 780

Lys Gly Pro Phe Leu Leu Gly Ile Lys Ala Val Leu Ala Glu Ser Tyr
785                 790                 795                 800

Glu Arg Ile His Arg Ser Asn Leu Val Gly Met Gly Val Ile Pro Leu
                805                 810                 815

Glu Tyr Leu Pro Gly Glu Asn Ala Asp Ala Leu Gly Leu Thr Gly Gln
            820                 825                 830

Glu Arg Tyr Thr Ile Ile Ile Pro Glu Asn Leu Lys Pro Gln Met Lys
        835                 840                 845

Val Gln Val Lys Leu Asp Thr Gly Lys Thr Phe Gln Ala Val Met Arg
    850                 855                 860

Phe Asp Thr Asp Val Glu Leu Thr Tyr Phe Leu Asn Gly Gly Ile Leu
865                 870                 875                 880

Asn Tyr Met Ile Arg Lys Met Ala Lys
                885


<210> 1396
<211> 780
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 415; "

<220>
<221> source
<223> /note="Gene Symbol: ACO2; "
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<220>
<221> source
<223> /note="Gene Name:
aconitase 2,
mitochondrial; "

<220>
<221> source
<223> /note="Uniprot ID: Q99798; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000216254"

<400> 1396

```
Met Ala Pro Tyr Ser Leu Leu Val Thr Arg Leu Gln Lys Ala Leu Gly
1               5                  10                  15

Val Arg Gln Tyr His Val Ala Ser Val Leu Cys Gln Arg Ala Lys Val
            20                  25                  30

Ala Met Ser His Phe Glu Pro Asn Glu Tyr Ile His Tyr Asp Leu Leu
        35                  40                  45

Glu Lys Asn Ile Asn Ile Val Arg Lys Arg Leu Asn Arg Pro Leu Thr
    50                  55                  60

Leu Ser Glu Lys Ile Val Tyr Gly His Leu Asp Asp Pro Ala Ser Gln
65                  70                  75                  80

Glu Ile Glu Arg Gly Lys Ser Tyr Leu Arg Leu Arg Pro Asp Arg Val
                85                  90                  95

Ala Met Gln Asp Ala Thr Ala Gln Met Ala Met Leu Gln Phe Ile Ser
            100                 105                 110

Ser Gly Leu Ser Lys Val Ala Val Pro Ser Thr Ile His Cys Asp His
        115                 120                 125

Leu Ile Glu Ala Gln Val Gly Gly Glu Lys Asp Leu Arg Arg Ala Lys
    130                 135                 140

Asp Ile Asn Gln Glu Val Tyr Asn Phe Leu Ala Thr Ala Gly Ala Lys
145                 150                 155                 160

Tyr Gly Val Gly Phe Trp Lys Pro Gly Ser Gly Ile Ile His Gln Ile
```

```
                165                 170                 175

Ile Leu Glu Asn Tyr Ala Tyr Pro Gly Val Leu Leu Ile Gly Thr Asp
            180                 185                 190

Ser His Thr Pro Asn Gly Gly Gly Leu Gly Gly Ile Cys Ile Gly Val
        195                 200                 205

Gly Gly Ala Asp Ala Val Asp Val Met Ala Gly Ile Pro Trp Glu Leu
    210                 215                 220

Lys Cys Pro Lys Val Ile Gly Val Lys Leu Thr Gly Ser Leu Ser Gly
225                 230                 235                 240

Trp Ser Ser Pro Lys Asp Val Ile Leu Lys Val Ala Gly Ile Leu Thr
                245                 250                 255

Val Lys Gly Gly Thr Gly Ala Ile Val Glu Tyr His Gly Pro Gly Val
            260                 265                 270

Asp Ser Ile Ser Cys Thr Gly Met Ala Thr Ile Cys Asn Met Gly Ala
        275                 280                 285

Glu Ile Gly Ala Thr Thr Ser Val Phe Pro Tyr Asn His Arg Met Lys
    290                 295                 300

Lys Tyr Leu Ser Lys Thr Gly Arg Glu Asp Ile Ala Asn Leu Ala Asp
305                 310                 315                 320

Glu Phe Lys Asp His Leu Val Pro Asp Pro Gly Cys His Tyr Asp Gln
                325                 330                 335

Leu Ile Glu Ile Asn Leu Ser Glu Leu Lys Pro His Ile Asn Gly Pro
            340                 345                 350

Phe Thr Pro Asp Leu Ala His Pro Val Ala Glu Val Gly Lys Val Ala
        355                 360                 365

Glu Lys Glu Gly Trp Pro Leu Asp Ile Arg Val Gly Leu Ile Gly Ser
    370                 375                 380

Cys Thr Asn Ser Ser Tyr Glu Asp Met Gly Arg Ser Ala Ala Val Ala
385                 390                 395                 400
```

```
Lys Gln Ala Leu Ala His Gly Leu Lys Cys Lys Ser Gln Phe Thr Ile
                405                 410                 415

Thr Pro Gly Ser Glu Gln Ile Arg Ala Thr Ile Glu Arg Asp Gly Tyr
            420                 425                 430

Ala Gln Ile Leu Arg Asp Leu Gly Gly Ile Val Leu Ala Asn Ala Cys
        435                 440                 445

Gly Pro Cys Ile Gly Gln Trp Asp Arg Lys Asp Ile Lys Lys Gly Glu
    450                 455                 460

Lys Asn Thr Ile Val Thr Ser Tyr Asn Arg Asn Phe Thr Gly Arg Asn
465                 470                 475                 480

Asp Ala Asn Pro Glu Thr His Ala Phe Val Thr Ser Pro Glu Ile Val
                485                 490                 495

Thr Ala Leu Ala Ile Ala Gly Thr Leu Lys Phe Asn Pro Glu Thr Asp
            500                 505                 510

Tyr Leu Thr Gly Thr Asp Gly Lys Lys Phe Arg Leu Glu Ala Pro Asp
        515                 520                 525

Ala Asp Glu Leu Pro Lys Gly Glu Phe Asp Pro Gly Gln Asp Thr Tyr
    530                 535                 540

Gln His Pro Pro Lys Asp Ser Ser Gly Gln His Val Asp Val Ser Pro
545                 550                 555                 560

Thr Ser Gln Arg Leu Gln Leu Leu Glu Pro Phe Asp Lys Trp Asp Gly
                565                 570                 575

Lys Asp Leu Glu Asp Leu Gln Ile Leu Ile Lys Val Lys Gly Lys Cys
            580                 585                 590

Thr Thr Asp His Ile Ser Ala Ala Gly Pro Trp Leu Lys Phe Arg Gly
        595                 600                 605

His Leu Asp Asn Ile Ser Asn Asn Leu Leu Ile Gly Ala Ile Asn Ile
    610                 615                 620
```

```
Glu Asn Gly Lys Ala Asn Ser Val Arg Asn Ala Val Thr Gln Glu Phe
625                 630                 635                 640

Gly Pro Val Pro Asp Thr Ala Arg Tyr Tyr Lys Lys His Gly Ile Arg
                645                 650                 655

Trp Val Val Ile Gly Asp Glu Asn Tyr Gly Glu Gly Ser Ser Arg Glu
            660                 665                 670

His Ala Ala Leu Glu Pro Arg His Leu Gly Gly Arg Ala Ile Ile Thr
        675                 680                 685

Lys Ser Phe Ala Arg Ile His Glu Thr Asn Leu Lys Lys Gln Gly Leu
    690                 695                 700

Leu Pro Leu Thr Phe Ala Asp Pro Ala Asp Tyr Asn Lys Ile His Pro
705                 710                 715                 720

Val Asp Lys Leu Thr Ile Gln Gly Leu Lys Asp Phe Thr Pro Gly Lys
                725                 730                 735

Pro Leu Lys Cys Ile Ile Lys His Pro Asn Gly Thr Gln Glu Thr Ile
            740                 745                 750

Leu Leu Asn His Thr Phe Asn Glu Thr Gln Ile Glu Trp Phe Arg Ala
        755                 760                 765

Gly Ser Ala Leu Asn Arg Met Lys Glu Leu Gln Gln
    770                 775                 780


<210> 1397
<211> 805
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 415; "

<220>
<221> source
<223> /note="Gene Symbol: ACO2; "

<220>
<221> source
<223> /note="Gene Name:
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aconitase 2,
mitochondrial; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000379769"

<400> 1397
Met Ala Pro Tyr Ser Leu Leu Val Thr Arg Leu Gln Lys Ala Leu Gly
1 5 10 15

Val Arg Gln Tyr His Val Ala Ser Val Leu Cys Gln Arg Ala Lys Val
20 25 30

Ala Met Ser His Phe Glu Pro Asn Glu Tyr Ile His Tyr Asp Leu Leu
35 40 45

Glu Lys Asn Ile Asn Ile Val Arg Lys Arg Leu Asn Arg Pro Leu Thr
50 55 60

Leu Ser Glu Lys Ile Val Tyr Gly His Leu Asp Asp Pro Ala Ser Gln
65 70 75 80

Glu Ile Glu Arg Gly Lys Ser Tyr Leu Arg Leu Arg Pro Asp Arg Val
85 90 95

Ala Met Gln Asp Ala Thr Ala Gln Met Ala Met Leu Gln Phe Ile Ser
100 105 110

Ser Gly Leu Ser Lys Val Ala Val Pro Ser Thr Ile His Cys Asp His
115 120 125

Leu Ile Glu Ala Gln Val Gly Gly Glu Lys Asp Leu Arg Arg Ala Lys
130 135 140

Asp Ile Asn Gln Glu Val Tyr Asn Phe Leu Ala Thr Ala Gly Ala Lys
145 150 155 160

Tyr Gly Val Gly Phe Trp Lys Pro Gly Ser Gly Ile Ile His Gln Ile
165 170 175

Ile Leu Glu Asn Tyr Ala Tyr Pro Gly Val Leu Leu Ile Gly Thr Asp
180 185 190

Ser His Thr Pro Asn Gly Gly Gly Leu Gly Gly Ile Cys Ile Gly Val

195 200 205

Gly Gly Ala Asp Ala Val Asp Val Met Ala Gly Ile Pro Trp Glu Leu
210 215 220

Lys Cys Pro Lys Val Ile Gly Val Lys Leu Thr Gly Ser Leu Ser Gly
225 230 235 240

Trp Ser Ser Pro Lys Asp Val Ile Leu Lys Val Ala Gly Ile Leu Thr
245 250 255

Val Lys Gly Gly Thr Gly Ala Ile Val Glu Tyr His Gly Pro Gly Val
260 265 270

Asp Ser Ile Ser Cys Thr Gly Glu Glu Gly Gly Gln Ala Thr Trp Pro
275 280 285

Leu Pro Cys Ala Gly Pro Asp Gly Ser Pro Val Gly Ser Arg Ser Gly
290 295 300

Met Ala Thr Ile Cys Asn Met Gly Ala Glu Ile Gly Ala Thr Thr Ser
305 310 315 320

Val Phe Pro Tyr Asn His Arg Met Lys Lys Tyr Leu Ser Lys Thr Gly
325 330 335

Arg Glu Asp Ile Ala Asn Leu Ala Asp Glu Phe Lys Asp His Leu Val
340 345 350

Pro Asp Pro Gly Cys His Tyr Asp Gln Leu Ile Glu Ile Asn Leu Ser
355 360 365

Glu Leu Lys Pro His Ile Asn Gly Pro Phe Thr Pro Asp Leu Ala His
370 375 380

Pro Val Ala Glu Val Gly Lys Val Ala Glu Lys Glu Gly Trp Pro Leu
385 390 395 400

Asp Ile Arg Val Gly Leu Ile Gly Ser Cys Thr Asn Ser Ser Tyr Glu
405 410 415

Asp Met Gly Arg Ser Ala Ala Val Ala Lys Gln Ala Leu Ala His Gly
420 425 430

```
Leu Lys Cys Lys Ser Gln Phe Thr Ile Thr Pro Gly Ser Glu Gln Ile
        435                 440                 445

Arg Ala Thr Ile Glu Arg Asp Gly Tyr Ala Gln Ile Leu Arg Asp Leu
    450                 455                 460

Gly Gly Ile Val Leu Ala Asn Ala Cys Gly Pro Cys Ile Gly Gln Trp
465                 470                 475                 480

Asp Arg Lys Asp Ile Lys Lys Gly Glu Lys Asn Thr Ile Val Thr Ser
                485                 490                 495

Tyr Asn Arg Asn Phe Thr Gly Arg Asn Asp Ala Asn Pro Glu Thr His
            500                 505                 510

Ala Phe Val Thr Ser Pro Glu Ile Val Thr Ala Leu Ala Ile Ala Gly
        515                 520                 525

Thr Leu Lys Phe Asn Pro Glu Thr Asp Tyr Leu Thr Gly Thr Asp Gly
    530                 535                 540

Lys Lys Phe Arg Leu Glu Ala Pro Asp Ala Asp Glu Leu Pro Lys Gly
545                 550                 555                 560

Glu Phe Asp Pro Gly Gln Asp Thr Tyr Gln His Pro Pro Lys Asp Ser
                565                 570                 575

Ser Gly Gln His Val Asp Val Ser Pro Thr Ser Gln Arg Leu Gln Leu
            580                 585                 590

Leu Glu Pro Phe Asp Lys Trp Asp Gly Lys Asp Leu Glu Asp Leu Gln
        595                 600                 605

Ile Leu Ile Lys Val Lys Gly Lys Cys Thr Thr Asp His Ile Ser Ala
    610                 615                 620

Ala Gly Pro Trp Leu Lys Phe Arg Gly His Leu Asp Asn Ile Ser Asn
625                 630                 635                 640

Asn Leu Leu Ile Gly Ala Ile Asn Ile Glu Asn Gly Lys Ala Asn Ser
                645                 650                 655
```

```
Val Arg Asn Ala Val Thr Gln Glu Phe Gly Pro Val Pro Asp Thr Ala
            660                 665                 670

Arg Tyr Tyr Lys Lys His Gly Ile Arg Trp Val Val Ile Gly Asp Glu
        675                 680                 685

Asn Tyr Gly Glu Gly Ser Ser Arg Glu His Ala Ala Leu Glu Pro Arg
    690                 695                 700

His Leu Gly Gly Arg Ala Ile Ile Thr Lys Ser Phe Ala Arg Ile His
705                 710                 715                 720

Glu Thr Asn Leu Lys Lys Gln Gly Leu Leu Pro Leu Thr Phe Ala Asp
                725                 730                 735

Pro Ala Asp Tyr Asn Lys Ile His Pro Val Asp Lys Leu Thr Ile Gln
            740                 745                 750

Gly Leu Lys Asp Phe Thr Pro Gly Lys Pro Leu Lys Cys Ile Ile Lys
        755                 760                 765

His Pro Asn Gly Thr Gln Glu Thr Ile Leu Leu Asn His Thr Phe Asn
    770                 775                 780

Glu Thr Gln Ile Glu Trp Phe Arg Ala Gly Ser Ala Leu Asn Arg Met
785                 790                 795                 800

Lys Glu Leu Gln Gln
                805


<210> 1398
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 416; "

<220>
<221> source
<223> /note="Gene Symbol: ACR; "

<220>
<221> source
<223> /note="Gene Name:
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acrosin; "

<220>
<221> source
<223> /note="Uniprot ID: P10323; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000216139"

<400> 1398
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 Leu 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 Phe 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

<210> 1399
<211> 212
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 416; "

<220>
<221> source
<223> /note="Gene Symbol: ACR; "

<220>
<221> source
<223> /note="Gene Name:
acrosin; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435120"

<400> 1399
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 Leu 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 Phe 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 Gly Phe Leu Glu
            180                 185                 190

Cys Pro Ala Gly Thr Ser Pro Phe Lys Thr Gly Val Ala Val Ala Leu
        195                 200                 205

Glu Leu Cys Pro
    210


<210> 1400
<211> 543
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 417; "

<220>
<221> source
<223> /note="Gene Symbol: ACRBP; "

<220>
<221> source
<223> /note="Gene Name:
      acrosin binding prt; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8NEB7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000229243"

<400> 1400
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
1               5                   10                  15
```

```
Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
            20                  25                  30

Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala
        35                  40                  45

Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
    50                  55                  60

Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
65                  70                  75                  80

Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
                85                  90                  95

Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
            100                 105                 110

Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
        115                 120                 125

Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val
    130                 135                 140

Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Val Thr
145                 150                 155                 160

Glu Arg Gln Thr Phe Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val
                165                 170                 175

Glu Glu Leu Leu Gln Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala
            180                 185                 190

Pro Glu His Lys Gln Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr
        195                 200                 205

Gln Glu His Lys Gln Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu
    210                 215                 220

Glu Gln Glu Glu Glu Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu
225                 230                 235                 240
```

```
Gly Arg Glu Ala Val Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe
                245                 250                 255

His Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val
            260                 265                 270

Arg Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu
        275                 280                 285

Ile Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu
    290                 295                 300

Asn Ser Tyr Trp Arg Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro
305                 310                 315                 320

His Thr Glu Ala Leu Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr
                325                 330                 335

Cys Ile Ile Thr Pro Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu
            340                 345                 350

Ile Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His
        355                 360                 365

Met Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln
    370                 375                 380

Cys His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His
385                 390                 395                 400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile
                405                 410                 415

Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp
            420                 425                 430

Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr
        435                 440                 445

Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe
    450                 455                 460

Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp
```

```
465                 470                 475                 480

Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu
                485                 490                 495

Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn
            500                 505                 510

Glu Thr Tyr Ser Ala Leu Ser Pro Gly Lys Ser Glu Asp Val Val Leu
        515                 520                 525

Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly
    530                 535                 540


<210> 1401
<211> 510
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 417; "

<220>
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<223> /note="Gene Symbol: ACRBP; "

<220>
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<223> /note="Gene Name:
      acrosin binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402725"

<400> 1401
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
1               5                   10                  15

Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
            20                  25                  30

Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala
        35                  40                  45

Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
    50                  55                  60
```

```
Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
65                  70                  75                  80

Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
                85                  90                  95

Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
            100                 105                 110

Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
        115                 120                 125

Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val
    130                 135                 140

Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Ala Pro
145                 150                 155                 160

Glu His Lys Gln Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr Gln
                165                 170                 175

Glu His Lys Gln Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu Glu
            180                 185                 190

Gln Glu Glu Glu Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu Gly
        195                 200                 205

Arg Glu Ala Val Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe His
    210                 215                 220

Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val Arg
225                 230                 235                 240

Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu Ile
                245                 250                 255

Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu Asn
            260                 265                 270

Ser Tyr Trp Arg Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro His
        275                 280                 285
```

Thr Glu Ala Leu Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr Cys
290 295 300

Ile Ile Thr Pro Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu Ile
305 310 315 320

Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His Met
325 330 335

Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln Cys
340 345 350

His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His Lys
355 360 365

Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile Gly
370 375 380

Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp Leu
385 390 395 400

Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr Lys
405 410 415

Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe Leu
420 425 430

Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp Tyr
435 440 445

Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu Met
450 455 460

Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn Glu
465 470 475 480

Thr Tyr Ser Ala Leu Ser Pro Gly Lys Ser Glu Asp Val Val Leu Arg
485 490 495

Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly
500 505 510

<210> 1402

<211> 173
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acrosin binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438656"

<400> 1402

```
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
1               5                   10                  15


Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
            20                  25                  30


Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala
        35                  40                  45


Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
    50                  55                  60


Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
65                  70                  75                  80


Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
                85                  90                  95


Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
            100                 105                 110


Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
        115                 120                 125


Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val
    130                 135                 140
```

```
Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Glu Arg
145                 150                 155                 160


Gln Thr Phe Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn
                165                 170


<210> 1403
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 417; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
      acrosin binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443153"

<400> 1403
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
1               5                   10                  15


Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
            20                  25                  30


Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala
        35                  40                  45


Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
    50                  55                  60


Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
65                  70                  75                  80


Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
                85                  90                  95


Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
```

100 105 110

Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
115 120 125

Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val
130 135 140

Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Val Thr
145 150 155 160

Glu Arg Gln Thr Phe Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val
165 170 175

Glu Glu Leu Leu Gln Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala
180 185 190

Pro Glu His Lys Gln Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr
195 200 205

Gln Glu His Lys Gln Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu
210 215 220

Glu Gln Glu Glu Glu Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu
225 230 235 240

Gly Arg Glu Ala Val Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe
245 250 255

His Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val
260 265 270

Arg Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu
275 280 285

Ile Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu
290 295 300

Asn Ser Tyr Trp Arg Asn Gln Asn Pro Gly Arg Tyr Arg Lys Phe
305 310 315

<210> 1404
<211> 100

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 417; "

<220>
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<223> /note="Gene Symbol: ACRBP; "

<220>
<221> source
<223> /note="Gene Name:
acrosin binding prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445262"

<400> 1404
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
1 5 10 15

Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
20 25 30

Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala
35 40 45

Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
50 55 60

Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
65 70 75 80

Asn His Gly Leu Val Pro Asp Glu Ser Pro Val Phe Pro Ala Ser Leu
85 90 95

Tyr Ser Leu Thr
100

<210> 1405
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 418; "

<220>
<221> source
<223> /note="Gene Symbol: ACRV1; "

<220>
<221> source
<223> /note="Gene Name:
acrosomal vesicle prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: P26436; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000317684"

<400> 1405

Met	Asn	Arg	Phe	Leu	Leu	Leu	Met	Ser	Leu	Tyr	Leu	Leu	Gly	Ser	Ala
1				5					10						15

Arg	Gly	Thr	Ser	Ser	Gln	Pro	Asn	Glu	Leu	Ser	Gly	Ser	Ile	Asp	His
			20					25					30		

Gln	Thr	Ser	Val	Gln	Gln	Leu	Pro	Gly	Glu	Phe	Phe	Ser	Leu	Glu	Asn
		35					40					45			

Pro	Ser	Asp	Ala	Glu	Ala	Leu	Tyr	Glu	Thr	Ser	Ser	Gly	Leu	Asn	Thr
	50					55					60				

Leu	Ser	Glu	His	Gly	Ser	Ser	Glu	His	Gly	Ser	Ser	Lys	His	Thr	Val
65					70					75					80

Ala	Glu	His	Thr	Ser	Gly	Glu	His	Ala	Glu	Ser	Glu	His	Ala	Ser	Gly
				85					90					95	

Glu	Pro	Ala	Ala	Thr	Glu	His	Ala	Glu	Gly	Glu	His	Thr	Val	Gly	Glu
			100					105					110		

Gln	Pro	Ser	Gly	Glu	Gln	Pro	Ser	Gly	Glu	His	Leu	Ser	Gly	Glu	Gln
		115					120					125			

Pro	Leu	Ser	Glu	Leu	Glu	Ser	Gly	Glu	Gln	Pro	Ser	Asp	Glu	Gln	Pro
	130					135					140				

Ser	Gly	Glu	His	Gly	Ser	Gly	Glu	Gln	Pro	Ser	Gly	Glu	Gln	Ala	Ser
145					150					155					160

```
Gly Glu Gln Pro Ser Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala Tyr
                165                 170                 175

Met Asn Asp Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr Cys Ile Thr
            180                 185                 190

Gln Asn Ser Gln Gln Cys Met Leu Lys Lys Ile Phe Glu Gly Gly Lys
        195                 200                 205

Leu Gln Phe Met Val Gln Gly Cys Glu Asn Met Cys Pro Ser Met Asn
    210                 215                 220

Leu Phe Ser His Gly Thr Arg Met Gln Ile Ile Cys Cys Arg Asn Gln
225                 230                 235                 240

Ser Phe Cys Asn Lys Ile
                245
```

<210> 1406
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 418; "

<220>
<221> source
<223> /note="Gene Symbol: ACRV1; "

<220>
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<223> /note="Gene Name:
acrosomal vesicle prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: P26436; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432816"

<400> 1406

```
Met Asn Arg Phe Leu Leu Leu Met Ser Leu Tyr Leu Leu Gly Ser Ala
1               5                   10                  15
```

```
Arg Gly Thr Ser Ser Gln Pro Asn Glu Leu Ser Gly Ser Ile Asp His
            20                  25                  30

Gln Thr Ser Val Gln Gln Leu Pro Gly Glu Phe Phe Ser Leu Glu Asn
        35                  40                  45

Pro Ser Asp Ala Glu Ala Leu Tyr Glu Thr Ser Ser Gly Leu Asn Thr
    50                  55                  60

Leu Ser Glu His Gly Ser Ser Glu His Gly Ser Ser Lys His Thr Val
65                  70                  75                  80

Ala Glu His Thr Ser Gly Glu His Ala Glu Ser Glu His Ala Ser Gly
                85                  90                  95

Glu Pro Ala Ala Thr Glu His Ala Glu Gly Glu His Thr Val Gly Glu
            100                 105                 110

Gln Pro Ser Gly Glu Gln Pro Ser Gly Glu His Leu Ser Gly Glu Gln
        115                 120                 125

Pro Leu Ser Glu Leu Glu Ser Gly Glu Gln Pro Ser Asp Glu Gln Pro
    130                 135                 140

Ser Gly Glu His Gly Ser Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser
145                 150                 155                 160

Gly Glu Gln Pro Ser Gly Glu His Ala Ser Gly Glu Gln Ala Ser Gly
                165                 170                 175

Ala Pro Ile Ser Ser Thr Ser Thr Gly Thr Ile Leu Asn Cys Tyr Thr
            180                 185                 190

Cys Ala Tyr Met Asn Asp Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr
        195                 200                 205

Cys Ile Thr Gln Asn Ser Gln Gln Cys Met Leu Lys Lys Ile Phe Glu
    210                 215                 220

Gly Gly Lys Leu Gln Phe Met Val Gln Gly Cys Glu Asn Met Cys Pro
225                 230                 235                 240

Ser Met Asn Leu Phe Ser His Gly Thr Arg Met Gln Ile Ile Cys Cys
```

```
                245                 250                 255

Arg Asn Gln Ser Phe Cys Asn Lys Ile
            260                 265


<210> 1407
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 418; "

<220>
<221> source
<223> /note="Gene Symbol: ACRV1; "

<220>
<221> source
<223> /note="Gene Name:
      acrosomal vesicle prt 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P26436; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433720"

<400> 1407
Met Asn Arg Phe Leu Leu Leu Met Ser Leu Tyr Leu Leu Gly Ser Ala
1               5                   10                  15


Arg Gly Thr Ser Ser Gln Pro Asn Glu Leu Ser Gly Ser Ile Asp His
            20                  25                  30


Gln Thr Ser Val Gln Gln Leu Pro Gly Glu Pro Ala Ala Thr Glu His
        35                  40                  45


Ala Glu Gly Glu His Thr Val Gly Glu Gln Pro Ser Gly Glu Gln Pro
    50                  55                  60


Ser Gly Glu His Leu Ser Gly Glu Gln Pro Leu Ser Glu Leu Glu Ser
65                  70                  75                  80


Gly Glu Gln Pro Ser Asp Glu Gln Pro Ser Gly Glu His Gly Ser Gly
                85                  90                  95
```

```
Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro Ser Gly Glu
            100                 105                 110

His Ala Ser Gly Glu Gln Ala Ser Gly Ala Pro Ile Ser Ser Thr Ser
        115                 120                 125

Thr Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala Tyr Met Asn Asp Gln
    130                 135                 140

Gly Lys Cys Leu Arg Gly Glu Gly Thr Cys Ile Thr Gln Asn Ser Gln
145                 150                 155                 160

Gln Cys Met Leu Lys Lys Ile Phe Glu Gly Gly Lys Leu Gln Phe Met
                165                 170                 175

Val Gln Gly Cys Glu Asn Met Cys Pro Ser Met Asn Leu Phe Ser His
            180                 185                 190

Gly Thr Arg Met Gln Ile Ile Cys Cys Arg Asn Gln Ser Phe Cys Asn
        195                 200                 205

Lys Ile
    210


<210> 1408
<211> 195
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 418; "

<220>
<221> source
<223> /note="Gene Symbol: ACRV1; "

<220>
<221> source
<223> /note="Gene Name:
      acrosomal vesicle prt 1; "

<220>
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<223> /note="Uniprot ID:  P26436; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000436819"

<400> 1408

```
Met Asn Arg Phe Leu Leu Leu Met Ser Leu Tyr Leu Leu Gly Ser Ala
1               5                  10                  15

Arg Gly Thr Ser Ser Gln Pro Asn Glu Leu Ser Gly Ser Ile Asp His
            20                  25                  30

Gln Thr Ser Val Gln Gln Leu Pro Gly Glu Gln Pro Ser Gly Glu Gln
        35                  40                  45

Pro Ser Gly Glu His Leu Ser Gly Glu Gln Pro Leu Ser Glu Leu Glu
    50                  55                  60

Ser Gly Glu Gln Pro Ser Asp Glu Gln Pro Ser Gly Glu His Gly Ser
65                  70                  75                  80

Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro Ser Gly
                85                  90                  95

Glu His Ala Ser Gly Glu Gln Ala Ser Gly Ala Pro Ile Ser Ser Thr
            100                 105                 110

Ser Thr Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala Tyr Met Asn Asp
        115                 120                 125

Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr Cys Ile Thr Gln Asn Ser
    130                 135                 140

Gln Gln Cys Met Leu Lys Lys Ile Phe Glu Gly Gly Lys Leu Gln Phe
145                 150                 155                 160

Met Val Gln Gly Cys Glu Asn Met Cys Pro Ser Met Asn Leu Phe Ser
                165                 170                 175

His Gly Thr Arg Met Gln Ile Ile Cys Cys Arg Asn Gln Ser Phe Cys
            180                 185                 190

Asn Lys Ile
        195
```

<210> 1409
<211> 778

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 419; "

<220>
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<223> /note="Gene Symbol: ABLIM1; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: O14639; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000277895"

<400> 1409
Met Pro Ala Phe Leu Gly Leu Lys Cys Leu Gly Lys Leu Cys Ser Ser
1   5   10   15

Glu Lys Ser Lys Val Thr Ser Ser Glu Arg Thr Ser Ala Arg Gly Ser
            20   25   30

Asn Arg Lys Arg Leu Ile Val Glu Asp Arg Arg Val Ser Gly Thr Ser
        35   40   45

Phe Thr Ala His Arg Arg Ala Thr Ile Thr His Leu Leu Tyr Leu Cys
    50   55   60

Pro Lys Asp Tyr Cys Pro Arg Gly Arg Val Cys Asn Ser Val Asp Pro
65   70   75   80

Phe Val Ala His Pro Gln Asp Pro His His Pro Ser Glu Lys Pro Val
                85   90   95

Ile His Cys His Lys Cys Gly Glu Pro Cys Lys Gly Glu Val Leu Arg
            100   105   110

Val Gln Thr Lys His Phe His Ile Lys Cys Phe Thr Cys Lys Val Cys
        115   120   125

```
Gly Cys Asp Leu Ala Gln Gly Gly Phe Phe Ile Lys Asn Gly Glu Tyr
    130                 135                 140

Leu Cys Thr Leu Asp Tyr Gln Arg Met Tyr Gly Thr Arg Cys His Gly
145                 150                 155                 160

Cys Gly Glu Phe Val Glu Gly Glu Val Val Thr Ala Leu Gly Lys Thr
                165                 170                 175

Tyr His Pro Asn Cys Phe Ala Cys Thr Ile Cys Lys Arg Pro Phe Pro
            180                 185                 190

Pro Gly Asp Arg Val Thr Phe Asn Gly Arg Asp Cys Leu Cys Gln Leu
        195                 200                 205

Cys Ala Gln Pro Met Ser Ser Ser Pro Lys Glu Thr Thr Phe Ser Ser
    210                 215                 220

Asn Cys Ala Gly Cys Gly Arg Asp Ile Lys Asn Gly Gln Ala Leu Leu
225                 230                 235                 240

Ala Leu Asp Lys Gln Trp His Leu Gly Cys Phe Lys Cys Lys Ser Cys
                245                 250                 255

Gly Lys Val Leu Thr Gly Glu Tyr Ile Ser Lys Asp Gly Ala Pro Tyr
            260                 265                 270

Cys Glu Lys Asp Tyr Gln Gly Leu Phe Gly Val Lys Cys Glu Ala Cys
        275                 280                 285

His Gln Phe Ile Thr Gly Lys Val Leu Glu Ala Gly Asp Lys His Tyr
    290                 295                 300

His Pro Ser Cys Ala Arg Cys Ser Arg Cys Asn Gln Met Phe Thr Glu
305                 310                 315                 320

Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp His Pro Asp Cys
                325                 330                 335

Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Pro Thr Arg Thr Ser
            340                 345                 350

Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile Pro Gly Ser Pro
```

```
        355                 360                 365

Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile Leu Asp Tyr Lys
    370                 375                 380

Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr Asp Ile Glu Arg
385                 390                 395                 400

Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser Gly Tyr Asp Asp
                405                 410                 415

Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg Thr Leu Ser Pro
            420                 425                 430

Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp Arg Met Ile His
        435                 440                 445

Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val Tyr Ser Arg His
    450                 455                 460

Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His Phe His Arg Pro
465                 470                 475                 480

Gly Asn Glu Pro Ser Ser Gly Arg Asn Ser Pro Leu Pro Tyr Arg Pro
                485                 490                 495

Asp Ser Arg Pro Leu Thr Pro Thr Tyr Ala Gln Ala Pro Lys His Phe
            500                 505                 510

His Val Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys Pro Pro Ile Tyr
        515                 520                 525

Lys Gln His Ala Ala Leu Ala Ala Gln Ser Lys Ser Ser Glu Asp Ile
    530                 535                 540

Ile Lys Phe Ser Lys Phe Pro Ala Ala Gln Ala Pro Asp Pro Ser Glu
545                 550                 555                 560

Thr Pro Lys Ile Glu Thr Asp His Trp Pro Gly Pro Pro Ser Phe Ala
                565                 570                 575

Val Val Gly Pro Asp Met Lys Arg Arg Ser Ser Gly Arg Glu Glu Asp
            580                 585                 590
```

```
Asp Glu Glu Leu Leu Arg Arg Arg Gln Leu Gln Glu Glu Gln Leu Met
        595                 600                 605

Lys Leu Asn Ser Gly Leu Gly Gln Leu Ile Leu Lys Glu Glu Met Glu
    610                 615                 620

Lys Glu Ser Arg Glu Arg Ser Ser Leu Leu Ala Ser Arg Tyr Asp Ser
625                 630                 635                 640

Pro Ile Asn Ser Ala Ser His Ile Pro Ser Ser Lys Thr Ala Ser Leu
                645                 650                 655

Pro Gly Tyr Gly Arg Asn Gly Leu His Arg Pro Val Ser Thr Asp Phe
            660                 665                 670

Ala Gln Tyr Asn Ser Tyr Gly Asp Val Ser Gly Gly Val Arg Asp Tyr
        675                 680                 685

Gln Thr Leu Pro Asp Gly His Met Pro Ala Met Arg Met Asp Arg Gly
    690                 695                 700

Val Ser Met Pro Asn Met Leu Glu Pro Lys Ile Phe Pro Tyr Glu Met
705                 710                 715                 720

Leu Met Val Thr Asn Arg Gly Arg Asn Lys Ile Leu Arg Glu Val Asp
                725                 730                 735

Arg Thr Arg Leu Glu Arg His Leu Ala Pro Glu Val Phe Arg Glu Ile
            740                 745                 750

Phe Gly Met Ser Ile Gln Glu Phe Asp Arg Leu Pro Leu Trp Arg Arg
        755                 760                 765

Asn Asp Met Lys Lys Lys Ala Lys Leu Phe
    770                 775
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<210> 1410
<211> 746
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 419; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM1; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358256"

<400> 1410

```
Met Leu Met Thr Leu Glu Met Thr Glu Leu Thr Asp Pro His His Thr
1               5                  10                  15

Met Gly Asp Tyr Lys Val Ala His Pro Gln Asp Pro His His Pro Ser
            20                  25                  30

Glu Lys Pro Val Ile His Cys His Lys Cys Gly Glu Pro Cys Lys Gly
        35                  40                  45

Glu Val Leu Arg Val Gln Thr Lys His Phe His Ile Lys Cys Phe Thr
    50                  55                  60

Cys Lys Val Cys Gly Cys Asp Leu Ala Gln Gly Gly Phe Phe Ile Lys
65                  70                  75                  80

Asn Gly Glu Tyr Leu Cys Thr Leu Asp Tyr Gln Arg Met Tyr Gly Thr
                85                  90                  95

Arg Cys His Gly Cys Gly Glu Phe Val Glu Gly Glu Val Val Thr Ala
            100                 105                 110

Leu Gly Lys Thr Tyr His Pro Asn Cys Phe Ala Cys Thr Ile Cys Lys
        115                 120                 125

Arg Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Arg Asp Cys
    130                 135                 140

Leu Cys Gln Leu Cys Ala Gln Pro Met Ser Ser Ser Pro Lys Glu Thr
145                 150                 155                 160

Thr Phe Ser Ser Asn Cys Ala Gly Cys Gly Arg Asp Ile Lys Asn Gly
```

```
                165                 170                 175

Gln Ala Leu Leu Ala Leu Asp Lys Gln Trp His Leu Gly Cys Phe Lys
            180                 185                 190

Cys Lys Ser Cys Gly Lys Val Leu Thr Gly Glu Tyr Ile Ser Lys Asp
        195                 200                 205

Gly Ala Pro Tyr Cys Glu Lys Asp Tyr Gln Gly Leu Phe Gly Val Lys
    210                 215                 220

Cys Glu Ala Cys His Gln Phe Ile Thr Gly Lys Val Leu Glu Ala Gly
225                 230                 235                 240

Asp Lys His Tyr His Pro Ser Cys Ala Arg Cys Ser Arg Cys Asn Gln
                245                 250                 255

Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
            260                 265                 270

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Leu
        275                 280                 285

Pro Asn Ile Arg Arg Ser Ser Ser Asp Phe Phe Tyr Ser Lys Ser Leu
    290                 295                 300

Ile Arg Arg Thr Gly Arg Ser Pro Ser Leu Gln Pro Thr Arg Thr Ser
305                 310                 315                 320

Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile Pro Gly Ser Pro
                325                 330                 335

Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile Leu Asp Tyr Lys
            340                 345                 350

Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr Asp Ile Glu Arg
        355                 360                 365

Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser Gly Tyr Asp Asp
    370                 375                 380

Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg Thr Leu Ser Pro
385                 390                 395                 400
```

```
Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp Arg Met Ile His
                405                 410                 415

Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val Tyr Ser Arg His
            420                 425                 430

Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His Phe His Arg Pro
        435                 440                 445

Gly Asn Glu Pro Ser Ser Gly Arg Asn Ser Pro Leu Pro Tyr Arg Pro
    450                 455                 460

Asp Ser Arg Pro Leu Thr Pro Thr Tyr Ala Gln Ala Pro Lys His Phe
465                 470                 475                 480

His Val Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys Pro Pro Ile Tyr
                485                 490                 495

Lys Gln His Ala Ala Leu Ala Ala Gln Ser Lys Ser Ser Glu Asp Ile
            500                 505                 510

Ile Lys Phe Ser Lys Phe Pro Ala Ala Gln Ala Pro Asp Pro Ser Glu
        515                 520                 525

Thr Pro Lys Ile Glu Thr Asp His Trp Pro Gly Pro Pro Ser Phe Ala
    530                 535                 540

Val Val Gly Pro Asp Met Lys Arg Arg Ser Ser Gly Arg Glu Glu Asp
545                 550                 555                 560

Asp Glu Glu Leu Leu Arg Arg Arg Gln Leu Gln Glu Glu Gln Leu Met
                565                 570                 575

Lys Leu Asn Ser Gly Leu Gly Gln Leu Ile Leu Lys Glu Glu Met Glu
            580                 585                 590

Lys Glu Ser Arg Glu Arg Ser Ser Leu Leu Ala Ser Arg Tyr Asp Ser
        595                 600                 605

Pro Ile Asn Ser Ala Ser His Ile Pro Ser Ser Lys Thr Ala Ser Leu
    610                 615                 620
```

```
Pro Gly Tyr Gly Arg Asn Gly Leu His Arg Pro Val Ser Thr Asp Phe
625                 630                 635                 640

Ala Gln Tyr Asn Ser Tyr Gly Asp Val Ser Gly Gly Val Arg Asp Phe
                645                 650                 655

Gln Thr Leu Pro Asp Gly His Met Pro Ala Met Arg Met Asp Arg Gly
            660                 665                 670

Val Ser Met Pro Asn Met Leu Glu Pro Lys Ile Phe Pro Tyr Glu Met
        675                 680                 685

Leu Met Val Thr Asn Arg Gly Arg Asn Lys Ile Leu Arg Glu Val Asp
    690                 695                 700

Arg Thr Arg Leu Glu Arg His Leu Ala Pro Glu Val Phe Arg Glu Ile
705                 710                 715                 720

Phe Gly Met Ser Ile Gln Glu Phe Asp Arg Leu Pro Leu Trp Arg Arg
                725                 730                 735

Asn Asp Met Lys Lys Lys Ala Lys Leu Phe
            740                 745


<210> 1411
<211> 401
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 419; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM1; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt 1; "

<220>
<221> source
<223> /note="Uniprot ID:  O14639; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000358257"

<400> 1411

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Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
1               5                  10                  15

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Ala
            20                  25                  30

Lys Val Asp Asn Glu Ile Leu Asp Tyr Lys Asp Leu Ala Ala Ile Pro
        35                  40                  45

Lys Val Lys Ala Ile Tyr Asp Ile Glu Arg Pro Asp Leu Ile Thr Tyr
    50                  55                  60

Glu Pro Phe Tyr Thr Ser Gly Tyr Asp Asp Lys Gln Glu Arg Gln Ser
65                  70                  75                  80

Leu Gly Glu Ser Pro Arg Thr Leu Ser Pro Thr Pro Ser Ala Glu Gly
                85                  90                  95

Tyr Gln Asp Val Arg Asp Arg Met Ile His Arg Ser Thr Ser Gln Gly
            100                 105                 110

Ser Ile Asn Ser Pro Val Tyr Ser Arg His Ser Tyr Thr Pro Thr Thr
        115                 120                 125

Ser Arg Ser Pro Gln His Phe His Arg Pro Asp Gln Gly Ile Asn Ile
    130                 135                 140

Tyr Arg Lys Pro Pro Ile Tyr Lys Gln His Ala Ala Leu Ala Ala Gln
145                 150                 155                 160

Ser Lys Ser Ser Glu Asp Ile Ile Lys Phe Ser Lys Phe Pro Ala Ala
                165                 170                 175

Gln Ala Pro Asp Pro Ser Glu Thr Pro Lys Ile Glu Thr Asp His Trp
            180                 185                 190

Pro Gly Pro Pro Ser Phe Ala Val Val Gly Pro Asp Met Lys Arg Arg
        195                 200                 205

Ser Ser Gly Arg Glu Glu Asp Asp Glu Glu Leu Leu Arg Arg Arg Gln
    210                 215                 220
```

Leu Gln Glu Glu Gln Leu Met Lys Leu Asn Ser Gly Leu Gly Gln Leu
225 230 235 240

Ile Leu Lys Glu Glu Met Glu Lys Glu Ser Arg Glu Arg Ser Ser Leu
245 250 255

Leu Ala Ser Arg Tyr Asp Ser Pro Ile Asn Ser Ala Ser His Ile Pro
260 265 270

Ser Ser Lys Thr Ala Ser Leu Pro Gly Tyr Gly Arg Asn Gly Leu His
275 280 285

Arg Pro Val Ser Thr Asp Phe Ala Gln Tyr Asn Ser Tyr Gly Asp Val
290 295 300

Ser Gly Gly Val Arg Asp Tyr Gln Thr Leu Pro Asp Gly His Met Pro
305 310 315 320

Ala Met Arg Met Asp Arg Gly Val Ser Met Pro Asn Met Leu Glu Pro
325 330 335

Lys Ile Phe Pro Tyr Glu Met Leu Met Val Thr Asn Arg Gly Arg Asn
340 345 350

Lys Ile Leu Arg Glu Val Asp Arg Thr Arg Leu Glu Arg His Leu Ala
355 360 365

Pro Glu Val Phe Arg Glu Ile Phe Gly Met Ser Ile Gln Glu Phe Asp
370 375 380

Arg Leu Pro Leu Trp Arg Arg Asn Asp Met Lys Lys Lys Ala Lys Leu
385 390 395 400

Phe

<210> 1412
<211> 748
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 419; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM1; "

<220>
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<223> /note="Gene Name:
actin binding LIM prt 1; "

<220>
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<223> /note="Uniprot ID: O14639; "

<220>
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<223> /note="ENSP ID: ENSP00000358260"

<400> 1412
Met Leu Met Thr Leu Glu Met Thr Glu Leu Thr Asp Pro His His Thr
1   5   10   15

Met Gly Asp Tyr Lys Val Ala His Pro Gln Asp Pro His His Pro Ser
            20   25   30

Glu Lys Pro Val Ile His Cys His Lys Cys Gly Glu Pro Cys Lys Gly
        35   40   45

Glu Val Leu Arg Val Gln Thr Lys His Phe His Ile Lys Cys Phe Thr
    50   55   60

Cys Lys Val Cys Gly Cys Asp Leu Ala Gln Gly Gly Phe Phe Ile Lys
65   70   75   80

Asn Gly Glu Tyr Leu Cys Thr Leu Asp Tyr Gln Arg Met Tyr Gly Thr
                85   90   95

Arg Cys His Gly Cys Gly Glu Phe Val Glu Gly Glu Val Val Thr Ala
            100   105   110

Leu Gly Lys Thr Tyr His Pro Asn Cys Phe Ala Cys Thr Ile Cys Lys
        115   120   125

Arg Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Arg Asp Cys
    130   135   140

Leu Cys Gln Leu Cys Ala Gln Pro Met Ser Ser Ser Pro Lys Glu Thr

145 150 155 160

Thr Phe Ser Ser Asn Cys Ala Gly Cys Gly Arg Asp Ile Lys Asn Gly
165 170 175

Gln Ala Leu Leu Ala Leu Asp Lys Gln Trp His Leu Gly Cys Phe Lys
180 185 190

Cys Lys Ser Cys Gly Lys Val Leu Thr Gly Glu Tyr Ile Ser Lys Asp
195 200 205

Gly Ala Pro Tyr Cys Glu Lys Asp Tyr Gln Gly Leu Phe Gly Val Lys
210 215 220

Cys Glu Ala Cys His Gln Phe Ile Thr Gly Lys Val Leu Glu Ala Gly
225 230 235 240

Asp Lys His Tyr His Pro Ser Cys Ala Arg Cys Ser Arg Cys Asn Gln
245 250 255

Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
260 265 270

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Leu
275 280 285

Pro Asn Ile Arg Arg Ser Ser Ser Asp Phe Phe Tyr Ser Lys Ser Leu
290 295 300

Ile Arg Arg Thr Gly Arg Ser Pro Ser Leu Gln Pro Thr Arg Thr Ser
305 310 315 320

Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile Pro Gly Ser Pro
325 330 335

Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile Leu Asp Tyr Lys
340 345 350

Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr Asp Ile Glu Arg
355 360 365

Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser Gly Tyr Asp Asp
370 375 380

```
Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg Thr Leu Ser Pro
385                 390                 395                 400

Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp Arg Met Ile His
                405                 410                 415

Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val Tyr Ser Arg His
            420                 425                 430

Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His Phe His Arg Pro
        435                 440                 445

Gly Asn Glu Pro Ser Ser Gly Arg Asn Ser Pro Leu Pro Tyr Arg Pro
    450                 455                 460

Asp Ser Arg Pro Leu Thr Pro Thr Tyr Ala Gln Ala Pro Lys His Phe
465                 470                 475                 480

His Val Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys Pro Pro Ile Tyr
                485                 490                 495

Lys Gln His Asp Ala Ala Ala Leu Ala Ala Gln Ser Lys Ser Ser Glu
            500                 505                 510

Asp Ile Ile Lys Phe Ser Lys Phe Pro Ala Ala Gln Ala Pro Asp Pro
        515                 520                 525

Ser Glu Thr Pro Lys Ile Glu Thr Asp His Trp Pro Gly Pro Pro Ser
    530                 535                 540

Phe Ala Val Val Gly Pro Asp Met Lys Arg Arg Ser Ser Gly Arg Glu
545                 550                 555                 560

Glu Asp Asp Glu Glu Leu Leu Arg Arg Arg Gln Leu Gln Glu Glu Gln
                565                 570                 575

Leu Met Lys Leu Asn Ser Gly Leu Gly Gln Leu Ile Leu Lys Glu Glu
            580                 585                 590

Met Glu Lys Glu Ser Arg Glu Arg Ser Ser Leu Leu Ala Ser Arg Tyr
        595                 600                 605
```

```
Asp Ser Pro Ile Asn Ser Ala Ser His Ile Pro Ser Ser Lys Thr Ala
    610                 615                 620

Ser Leu Pro Gly Tyr Gly Arg Asn Gly Leu His Arg Pro Val Ser Thr
625                 630                 635                 640

Asp Phe Ala Gln Tyr Asn Ser Tyr Gly Asp Val Ser Gly Gly Val Arg
                645                 650                 655

Asp Tyr Gln Thr Leu Pro Asp Gly His Met Pro Ala Met Arg Met Asp
            660                 665                 670

Arg Gly Val Ser Met Pro Asn Met Leu Glu Pro Lys Ile Phe Pro Tyr
        675                 680                 685

Glu Met Leu Met Val Thr Asn Arg Gly Arg Asn Lys Ile Leu Arg Glu
    690                 695                 700

Val Asp Arg Thr Arg Leu Glu Arg His Leu Ala Pro Glu Val Phe Arg
705                 710                 715                 720

Glu Ile Phe Gly Met Ser Ile Gln Glu Phe Asp Arg Leu Pro Leu Trp
                725                 730                 735

Arg Arg Asn Asp Met Lys Lys Lys Ala Lys Leu Phe
            740                 745
```

<210> 1413
<211> 401
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 419; "

<220>
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<220>
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<223> /note="Gene Name:
actin binding LIM prt 1; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000358270"

<400> 1413

```
Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
1               5                  10                  15

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Ala
            20                  25                  30

Lys Val Asp Asn Glu Ile Leu Asp Tyr Lys Asp Leu Ala Ala Ile Pro
        35                  40                  45

Lys Val Lys Ala Ile Tyr Asp Ile Glu Arg Pro Asp Leu Ile Thr Tyr
    50                  55                  60

Glu Pro Phe Tyr Thr Ser Gly Tyr Asp Asp Lys Gln Glu Arg Gln Ser
65                  70                  75                  80

Leu Gly Glu Ser Pro Arg Thr Leu Ser Pro Thr Pro Ser Ala Glu Gly
                85                  90                  95

Tyr Gln Asp Val Arg Asp Arg Met Ile His Arg Ser Thr Ser Gln Gly
            100                 105                 110

Ser Ile Asn Ser Pro Val Tyr Ser Arg His Ser Tyr Thr Pro Thr Thr
        115                 120                 125

Ser Arg Ser Pro Gln His Phe His Arg Pro Asp Gln Gly Ile Asn Ile
    130                 135                 140

Tyr Arg Lys Pro Pro Ile Tyr Lys Gln His Ala Ala Leu Ala Ala Gln
145                 150                 155                 160

Ser Lys Ser Ser Glu Asp Ile Ile Lys Phe Ser Lys Phe Pro Ala Ala
                165                 170                 175

Gln Ala Pro Asp Pro Ser Glu Thr Pro Lys Ile Glu Thr Asp His Trp
            180                 185                 190

Pro Gly Pro Pro Ser Phe Ala Val Val Gly Pro Asp Met Lys Arg Arg
        195                 200                 205

Ser Ser Gly Arg Glu Glu Asp Asp Glu Glu Leu Leu Arg Arg Arg Gln
    210                 215                 220
```

Leu Gln Glu Glu Gln Leu Met Lys Leu Asn Ser Gly Leu Gly Gln Leu
225 230 235 240

Ile Leu Lys Glu Glu Met Glu Lys Glu Ser Arg Glu Arg Ser Ser Leu
245 250 255

Leu Ala Ser Arg Tyr Asp Ser Pro Ile Asn Ser Ala Ser His Ile Pro
260 265 270

Ser Ser Lys Thr Ala Ser Leu Pro Gly Tyr Gly Arg Asn Gly Leu His
275 280 285

Arg Pro Val Ser Thr Asp Phe Ala Gln Tyr Asn Ser Tyr Gly Asp Val
290 295 300

Ser Gly Gly Val Arg Asp Phe Gln Thr Leu Pro Asp Gly His Met Pro
305 310 315 320

Ala Met Arg Met Asp Arg Gly Val Ser Met Pro Asn Met Leu Glu Pro
325 330 335

Lys Ile Phe Pro Tyr Glu Met Leu Met Val Thr Asn Arg Gly Arg Asn
340 345 350

Lys Ile Leu Arg Glu Val Asp Arg Thr Arg Leu Glu Arg His Leu Ala
355 360 365

Pro Glu Val Phe Arg Glu Ile Phe Gly Met Ser Ile Gln Glu Phe Asp
370 375 380

Arg Leu Pro Leu Trp Arg Arg Asn Asp Met Lys Lys Lys Ala Lys Leu
385 390 395 400

Phe

<210> 1414
<211> 455
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000376679"

<400> 1414
Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
1   5   10   15

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Leu
            20   25   30

Pro Asn Ile Arg Arg Ser Ser Ser Asp Phe Phe Tyr Ser Lys Ser Leu
        35   40   45

Ile Arg Arg Thr Gly Arg Ser Pro Ser Leu Gln Pro Thr Arg Thr Ser
    50   55   60

Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile Pro Gly Ser Pro
65   70   75   80

Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile Leu Asp Tyr Lys
                85   90   95

Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr Asp Ile Glu Arg
            100   105   110

Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser Gly Tyr Asp Asp
        115   120   125

Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg Thr Leu Ser Pro
    130   135   140

Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp Arg Met Ile His

145 150 155 160

Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val Tyr Ser Arg His
165 170 175

Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His Phe His Arg Pro
180 185 190

Asp Gln Gly Ile Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Lys Gln His
195 200 205

Ala Ala Leu Ala Ala Gln Ser Lys Ser Ser Glu Asp Ile Ile Lys Phe
210 215 220

Ser Lys Phe Pro Ala Ala Gln Ala Pro Asp Pro Ser Glu Thr Pro Lys
225 230 235 240

Ile Glu Thr Asp His Trp Pro Gly Pro Pro Ser Phe Ala Val Val Gly
245 250 255

Pro Asp Met Lys Arg Arg Ser Ser Gly Arg Glu Glu Asp Asp Glu Glu
260 265 270

Leu Leu Arg Arg Arg Gln Leu Gln Glu Glu Gln Leu Met Lys Leu Asn
275 280 285

Ser Gly Leu Gly Gln Leu Ile Leu Lys Glu Glu Met Glu Lys Glu Ser
290 295 300

Arg Glu Arg Ser Ser Leu Leu Ala Ser Arg Tyr Asp Ser Pro Ile Asn
305 310 315 320

Ser Ala Ser His Ile Pro Ser Ser Lys Thr Ala Ser Leu Pro Gly Tyr
325 330 335

Gly Arg Asn Gly Leu His Arg Pro Val Ser Thr Asp Phe Ala Gln Tyr
340 345 350

Asn Ser Tyr Gly Asp Val Ser Gly Gly Val Arg Asp Tyr Gln Thr Leu
355 360 365

Pro Asp Gly His Met Pro Ala Met Arg Met Asp Arg Gly Val Ser Met
370 375 380

```
Pro Asn Met Leu Glu Pro Lys Ile Phe Pro Tyr Glu Met Leu Met Val
385                 390                 395                 400


Thr Asn Arg Gly Arg Asn Lys Ile Leu Arg Glu Val Asp Arg Thr Arg
                405                 410                 415


Leu Glu Arg His Leu Ala Pro Glu Val Phe Arg Glu Ile Phe Gly Met
            420                 425                 430


Ser Ile Gln Glu Phe Asp Arg Leu Pro Leu Trp Arg Arg Asn Asp Met
        435                 440                 445


Lys Lys Lys Ala Lys Leu Phe
    450                 455


<210> 1415
<211> 718
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Name:
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<223> /note="Uniprot ID:  O14639; "

<220>
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<223> /note="ENSP ID: ENSP00000376682"

<400> 1415
Met Leu Met Thr Leu Glu Met Thr Glu Leu Thr Asp Pro His His Thr
1               5                   10                  15


Met Gly Asp Tyr Lys Val Ala His Pro Gln Asp Pro His His Pro Ser
            20                  25                  30
```

```
Glu Lys Pro Val Ile His Cys His Lys Cys Gly Glu Pro Cys Lys Gly
        35                  40                  45

Glu Val Leu Arg Val Gln Thr Lys His Phe His Ile Lys Cys Phe Thr
    50                  55                  60

Cys Lys Val Cys Gly Cys Asp Leu Ala Gln Gly Gly Phe Phe Ile Lys
65                  70                  75                  80

Asn Gly Glu Tyr Leu Cys Thr Leu Asp Tyr Gln Arg Met Tyr Gly Thr
                85                  90                  95

Arg Cys His Gly Cys Gly Glu Phe Val Glu Gly Glu Val Val Thr Ala
            100                 105                 110

Leu Gly Lys Thr Tyr His Pro Asn Cys Phe Ala Cys Thr Ile Cys Lys
        115                 120                 125

Arg Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Arg Asp Cys
    130                 135                 140

Leu Cys Gln Leu Cys Ala Gln Pro Met Ser Ser Ser Pro Lys Glu Thr
145                 150                 155                 160

Thr Phe Ser Ser Asn Cys Ala Gly Cys Gly Arg Asp Ile Lys Asn Gly
                165                 170                 175

Gln Ala Leu Leu Ala Leu Asp Lys Gln Trp His Leu Gly Cys Phe Lys
            180                 185                 190

Cys Lys Ser Cys Gly Lys Val Leu Thr Gly Glu Tyr Ile Ser Lys Asp
        195                 200                 205

Gly Ala Pro Tyr Cys Glu Lys Asp Tyr Gln Gly Leu Phe Gly Val Lys
    210                 215                 220

Cys Glu Ala Cys His Gln Phe Ile Thr Gly Lys Val Leu Glu Ala Gly
225                 230                 235                 240

Asp Lys His Tyr His Pro Ser Cys Ala Arg Cys Ser Arg Cys Asn Gln
                245                 250                 255

Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
```

```
            260                 265                 270

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Pro
        275                 280                 285

Thr Arg Thr Ser Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile
    290                 295                 300

Pro Gly Ser Pro Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile
305                 310                 315                 320

Leu Asp Tyr Lys Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr
                325                 330                 335

Asp Ile Glu Arg Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser
            340                 345                 350

Gly Tyr Asp Asp Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg
        355                 360                 365

Thr Leu Ser Pro Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp
    370                 375                 380

Arg Met Ile His Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val
385                 390                 395                 400

Tyr Ser Arg His Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His
                405                 410                 415

Phe His Arg Pro Gly Asn Glu Pro Ser Ser Gly Arg Asn Ser Pro Leu
            420                 425                 430

Pro Tyr Arg Pro Asp Ser Arg Pro Leu Thr Pro Thr Tyr Ala Gln Ala
        435                 440                 445

Pro Lys His Phe His Val Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys
    450                 455                 460

Pro Pro Ile Tyr Lys Gln His Ala Ala Leu Ala Ala Gln Ser Lys Ser
465                 470                 475                 480

Ser Glu Asp Ile Ile Lys Phe Ser Lys Phe Pro Ala Ala Gln Ala Pro
                485                 490                 495
```

```
Asp Pro Ser Glu Thr Pro Lys Ile Glu Thr Asp His Trp Pro Gly Pro
            500                 505                 510

Pro Ser Phe Ala Val Val Gly Pro Asp Met Lys Arg Arg Ser Ser Gly
        515                 520                 525

Arg Glu Glu Asp Asp Glu Glu Leu Leu Arg Arg Arg Gln Leu Gln Glu
    530                 535                 540

Glu Gln Leu Met Lys Leu Asn Ser Gly Leu Gly Gln Leu Ile Leu Lys
545                 550                 555                 560

Glu Glu Met Glu Lys Glu Ser Arg Glu Arg Ser Ser Leu Leu Ala Ser
                565                 570                 575

Arg Tyr Asp Ser Pro Ile Asn Ser Ala Ser His Ile Pro Ser Ser Lys
            580                 585                 590

Thr Ala Ser Leu Pro Gly Tyr Gly Arg Asn Gly Leu His Arg Pro Val
        595                 600                 605

Ser Thr Asp Phe Ala Gln Tyr Asn Ser Tyr Gly Asp Val Ser Gly Gly
    610                 615                 620

Val Arg Asp Tyr Gln Thr Leu Pro Asp Gly His Met Pro Ala Met Arg
625                 630                 635                 640

Met Asp Arg Gly Val Ser Met Pro Asn Met Leu Glu Pro Lys Ile Phe
                645                 650                 655

Pro Tyr Glu Met Leu Met Val Thr Asn Arg Gly Arg Asn Lys Ile Leu
            660                 665                 670

Arg Glu Val Asp Arg Thr Arg Leu Glu Arg His Leu Ala Pro Glu Val
        675                 680                 685

Phe Arg Glu Ile Phe Gly Met Ser Ile Gln Glu Phe Asp Arg Leu Pro
    690                 695                 700

Leu Trp Arg Arg Asn Asp Met Lys Lys Lys Ala Lys Leu Phe
705                 710                 715
```

<210> 1416
<211> 173
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 419; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM1; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000400934"

<400> 1416
Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
1 5 10 15

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Pro
20 25 30

Thr Arg Thr Ser Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile
35 40 45

Pro Gly Ser Pro Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile
50 55 60

Leu Asp Tyr Lys Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr
65 70 75 80

Asp Ile Glu Arg Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser
85 90 95

Gly Tyr Asp Asp Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg
100 105 110

Thr Leu Ser Pro Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp
115 120 125

Arg Met Ile His Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val

130 135 140

Tyr Ser Arg His Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His
145 150 155 160

Phe His Arg Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys
165 170

<210> 1417
<211> 172
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<221> source
<223> /note="Gene Name:
actin binding LIM prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414154"

<400> 1417
Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Pro Thr Arg Thr
1 5 10 15

Ser Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile Pro Gly Ser
20 25 30

Pro Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile Leu Asp Tyr
35 40 45

Lys Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr Asp Ile Glu
50 55 60

Arg Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser Gly Tyr Asp
65 70 75 80

Asp Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg Thr Leu Ser
85 90 95

```
Pro Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp Arg Met Ile
            100                 105                 110

His Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val Tyr Ser Arg
        115                 120                 125

His Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His Phe His Arg
    130                 135                 140

Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Lys Gln
145                 150                 155                 160

His Val Leu Phe Glu Val Ile Leu Leu Leu Leu Ile
                165                 170


<210> 1418
<211> 718
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<221> source
<223> /note="Gene Name:
      actin binding LIM prt 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000433629"

<400> 1418
Met Leu Met Thr Leu Glu Met Thr Glu Leu Thr Asp Pro His His Thr
1               5                   10                  15

Met Gly Asp Tyr Lys Val Ala His Pro Gln Asp Pro His His Pro Ser
            20                  25                  30

Glu Lys Pro Val Ile His Cys His Lys Cys Gly Glu Pro Cys Lys Gly
        35                  40                  45

Glu Val Leu Arg Val Gln Thr Lys His Phe His Ile Lys Cys Phe Thr
```

```
    50                  55                  60

Cys Lys Val Cys Gly Cys Asp Leu Ala Gln Gly Gly Phe Phe Ile Lys
65                  70                  75                  80

Asn Gly Glu Tyr Leu Cys Thr Leu Asp Tyr Gln Arg Met Tyr Gly Thr
                85                  90                  95

Arg Cys His Gly Cys Gly Glu Phe Val Glu Gly Glu Val Val Thr Ala
            100                 105                 110

Leu Gly Lys Thr Tyr His Pro Asn Cys Phe Ala Cys Thr Ile Cys Lys
        115                 120                 125

Arg Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Arg Asp Cys
    130                 135                 140

Leu Cys Gln Leu Cys Ala Gln Pro Met Ser Ser Ser Pro Lys Glu Thr
145                 150                 155                 160

Thr Phe Ser Ser Asn Cys Ala Gly Cys Gly Arg Asp Ile Lys Asn Gly
                165                 170                 175

Gln Ala Leu Leu Ala Leu Asp Lys Gln Trp His Leu Gly Cys Phe Lys
            180                 185                 190

Cys Lys Ser Cys Gly Lys Val Leu Thr Gly Glu Tyr Ile Ser Lys Asp
        195                 200                 205

Gly Ala Pro Tyr Cys Glu Lys Asp Tyr Gln Gly Leu Phe Gly Val Lys
    210                 215                 220

Cys Glu Ala Cys His Gln Phe Ile Thr Gly Lys Val Leu Glu Ala Gly
225                 230                 235                 240

Asp Lys His Tyr His Pro Ser Cys Ala Arg Cys Ser Arg Cys Asn Gln
                245                 250                 255

Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Thr Val Trp
            260                 265                 270

His Pro Asp Cys Lys Gln Ser Thr Lys Thr Glu Glu Lys Leu Arg Pro
        275                 280                 285
```

```
Thr Arg Thr Ser Ser Glu Ser Ile Tyr Ser Arg Pro Gly Ser Ser Ile
    290                 295                 300

Pro Gly Ser Pro Gly His Thr Ile Tyr Ala Lys Val Asp Asn Glu Ile
305                 310                 315                 320

Leu Asp Tyr Lys Asp Leu Ala Ala Ile Pro Lys Val Lys Ala Ile Tyr
                325                 330                 335

Asp Ile Glu Arg Pro Asp Leu Ile Thr Tyr Glu Pro Phe Tyr Thr Ser
            340                 345                 350

Gly Tyr Asp Asp Lys Gln Glu Arg Gln Ser Leu Gly Glu Ser Pro Arg
        355                 360                 365

Thr Leu Ser Pro Thr Pro Ser Ala Glu Gly Tyr Gln Asp Val Arg Asp
    370                 375                 380

Arg Met Ile His Arg Ser Thr Ser Gln Gly Ser Ile Asn Ser Pro Val
385                 390                 395                 400

Tyr Ser Arg His Ser Tyr Thr Pro Thr Thr Ser Arg Ser Pro Gln His
                405                 410                 415

Phe His Arg Pro Gly Asn Glu Pro Ser Ser Gly Arg Asn Ser Pro Leu
            420                 425                 430

Pro Tyr Arg Pro Asp Ser Arg Pro Leu Thr Pro Thr Tyr Ala Gln Ala
        435                 440                 445

Pro Lys His Phe His Val Pro Asp Gln Gly Ile Asn Ile Tyr Arg Lys
    450                 455                 460

Pro Pro Ile Tyr Lys Gln His Ala Ala Leu Ala Ala Gln Ser Lys Ser
465                 470                 475                 480

Ser Glu Asp Ile Ile Lys Phe Ser Lys Phe Pro Ala Ala Gln Ala Pro
                485                 490                 495

Asp Pro Ser Glu Thr Pro Lys Ile Glu Thr Asp His Trp Pro Gly Pro
            500                 505                 510
```

```
Pro Ser Phe Ala Val Val Gly Pro Asp Met Lys Arg Arg Ser Ser Gly
        515                 520                 525

Arg Glu Glu Asp Asp Glu Glu Leu Leu Arg Arg Arg Gln Leu Gln Glu
    530                 535                 540

Glu Gln Leu Met Lys Leu Asn Ser Gly Leu Gly Gln Leu Ile Leu Lys
545                 550                 555                 560

Glu Glu Met Glu Lys Glu Ser Arg Glu Arg Ser Ser Leu Leu Ala Ser
                565                 570                 575

Arg Tyr Asp Ser Pro Ile Asn Ser Ala Ser His Ile Pro Ser Ser Lys
            580                 585                 590

Thr Ala Ser Leu Pro Gly Tyr Gly Arg Asn Gly Leu His Arg Pro Val
        595                 600                 605

Ser Thr Asp Phe Ala Gln Tyr Asn Ser Tyr Gly Asp Val Ser Gly Gly
    610                 615                 620

Val Arg Asp Phe Gln Thr Leu Pro Asp Gly His Met Pro Ala Met Arg
625                 630                 635                 640

Met Asp Arg Gly Val Ser Met Pro Asn Met Leu Glu Pro Lys Ile Phe
                645                 650                 655

Pro Tyr Glu Met Leu Met Val Thr Asn Arg Gly Arg Asn Lys Ile Leu
            660                 665                 670

Arg Glu Val Asp Arg Thr Arg Leu Glu Arg His Leu Ala Pro Glu Val
        675                 680                 685

Phe Arg Glu Ile Phe Gly Met Ser Ile Gln Glu Phe Asp Arg Leu Pro
    690                 695                 700

Leu Trp Arg Arg Asn Asp Met Lys Lys Lys Ala Lys Leu Phe
705                 710                 715
```

<210> 1419
<211> 644
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000317020"

<400> 1419
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1 5 10 15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
20 25 30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
35 40 45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
50 55 60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65 70 75 80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
85 90 95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
100 105 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
115 120 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
130 135 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile

145 150 155 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
165 170 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
180 185 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
195 200 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
210 215 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225 230 235 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
245 250 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
260 265 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
275 280 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
290 295 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305 310 315 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
325 330 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
340 345 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
355 360 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
370 375 380

```
His Tyr Ser Arg Pro Ala Gly Thr Val Ser Val Gly Thr Ser Ser Cys
385                 390                 395                 400

Leu Ser Leu Ser Gln His Pro Ser Pro Thr Ser Val Phe Arg His His
                405                 410                 415

Tyr Ile Pro Tyr Phe Arg Gly Ser Glu Ser Gly Arg Ser Thr Pro Ser
            420                 425                 430

Leu Ser Val Leu Ser Asp Ser Lys Pro Pro Pro Pro Pro Thr Ser Arg
        435                 440                 445

His Leu Ala Thr His Val Pro Asp Thr Gly Val Lys Asp Asn Ile Tyr
    450                 455                 460

Arg Lys Pro Pro Ile Tyr Arg Gln His Ala Ala Arg Arg Ser Asp Gly
465                 470                 475                 480

Glu Asp Gly Ser Leu Asp Gln Asp Asn Arg Lys Gln Lys Ser Ser Trp
                485                 490                 495

Leu Met Leu Lys Gly Asp Ala Asp Thr Arg Thr Asn Ser Pro Asp Leu
            500                 505                 510

Asp Thr Gln Ser Leu Ser His Ser Ser Gly Thr Asp Arg Asp Pro Leu
        515                 520                 525

Gln Arg Met Ala Gly Asp Ser Phe His Ser Arg Phe Pro Tyr Ser Lys
    530                 535                 540

Ser Asp Pro Leu Pro Gly His Gly Lys Asn Gly Leu Asp Gln Arg Asn
545                 550                 555                 560

Ala Asn Leu Ala Pro Cys Gly Ala Asp Pro Asp Ala Ser Trp Gly Met
                565                 570                 575

Arg Glu Tyr Lys Ile Tyr Pro Tyr Asp Ser Leu Ile Val Thr Asn Arg
            580                 585                 590

Ile Arg Val Lys Leu Pro Lys Asp Val Asp Arg Thr Arg Leu Glu Arg
        595                 600                 605
```

```
His Leu Ser Pro Glu Glu Phe Gln Glu Val Phe Gly Met Ser Ile Glu
    610                 615                 620

Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn Asp Leu Lys Lys Lys
625                 630                 635                 640

Ala Leu Leu Phe
```

<210> 1420
<211> 611
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000342813"

<400> 1420

```
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1               5                   10                  15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
            20                  25                  30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
        35                  40                  45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
    50                  55                  60
```

```
Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65                  70                  75                  80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
                85                  90                  95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
```

290 295 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305 310 315 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
325 330 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
340 345 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
355 360 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
370 375 380

His Tyr Ser Arg Pro Gly Ser Glu Ser Gly Arg Ser Thr Pro Ser Leu
385 390 395 400

Ser Val Leu Ser Asp Ser Lys Pro Pro Pro Ser Thr Tyr Gln Gln Ala
405 410 415

Pro Arg His Phe His Val Pro Asp Thr Gly Val Lys Asp Asn Ile Tyr
420 425 430

Arg Lys Pro Pro Ile Tyr Arg Gln His Ala Ala Arg Arg Ser Asp Gly
435 440 445

Glu Asp Gly Ser Leu Asp Gln Asp Asn Arg Lys Lys Ser Ser Trp Leu
450 455 460

Met Leu Lys Gly Asp Ala Asp Thr Arg Thr Asn Ser Pro Asp Leu Asp
465 470 475 480

Thr Gln Ser Leu Ser His Ser Ser Gly Thr Asp Arg Asp Pro Leu Gln
485 490 495

Arg Met Ala Gly Asp Ser Phe His Ser Arg Phe Pro Tyr Ser Lys Ser
500 505 510

Asp Pro Leu Pro Gly His Gly Lys Asn Gly Leu Asp Gln Arg Asn Ala
515 520 525

```
Asn Leu Ala Pro Cys Gly Ala Asp Pro Asp Ala Ser Trp Gly Met Arg
    530                 535                 540

Glu Tyr Lys Ile Tyr Pro Tyr Asp Ser Leu Ile Val Thr Asn Arg Ile
545                 550                 555                 560

Arg Val Lys Leu Pro Lys Asp Val Asp Arg Thr Arg Leu Glu Arg His
                565                 570                 575

Leu Ser Pro Glu Glu Phe Gln Glu Val Phe Gly Met Ser Ile Glu Glu
            580                 585                 590

Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn Asp Leu Lys Lys Lys Ala
        595                 600                 605

Leu Leu Phe
    610
```

<210> 1421
<211> 531
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000354887"

<400> 1421

```
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1               5                   10                  15
```

```
Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
            20                  25                  30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
        35                  40                  45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
    50                  55                  60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65                  70                  75                  80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
                85                  90                  95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240
```

```
Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
    290                 295                 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305                 310                 315                 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
                325                 330                 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Ser Pro Gln
            340                 345                 350

Leu Leu Ser Pro Thr Pro Thr Glu Gly Asp Gln Asp Asp Arg Ser Tyr
        355                 360                 365

Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr Gly Ser Val Ser Leu
    370                 375                 380

Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln His Tyr Ser Arg Pro
385                 390                 395                 400

Ala Ala Arg Arg Ser Asp Gly Glu Asp Gly Ser Leu Asp Gln Asp Asn
                405                 410                 415

Arg Lys Lys Ser Ser Trp Leu Met Leu Lys Gly Asp Ala Asp Thr Arg
            420                 425                 430

Thr Asn Ser Pro Asp Leu Asp Thr Gln Ser Leu Ser His Ser Ser Gly
        435                 440                 445

Thr Asp Arg Asp Pro Leu Gln Arg Met Ala Gly Asp Ser Phe His Ser
    450                 455                 460

Gln Tyr Lys Ile Tyr Pro Tyr Asp Ser Leu Ile Val Thr Asn Arg Ile
```

```
465                 470                 475                 480

Arg Val Lys Leu Pro Lys Asp Val Asp Arg Thr Arg Leu Glu Arg His
                485                 490                 495

Leu Ser Pro Glu Glu Phe Gln Glu Val Phe Gly Met Ser Ile Glu Glu
            500                 505                 510

Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn Asp Leu Lys Lys Lys Ala
        515                 520                 525

Leu Leu Phe
    530


<210> 1422
<211> 572
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt
      family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355003"

<400> 1422
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1               5                   10                  15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
            20                  25                  30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
        35                  40                  45
```

```
Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
    50                  55                  60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65                  70                  75                  80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
                85                  90                  95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270
```

```
Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
    290                 295                 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305                 310                 315                 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
                325                 330                 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
            340                 345                 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
        355                 360                 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
    370                 375                 380

His Tyr Ser Arg Pro Gly Ser Glu Ser Gly Arg Ser Thr Pro Ser Leu
385                 390                 395                 400

Ser Val Leu Ser Asp Ser Lys Pro Pro Pro Ser Thr Tyr Gln Gln Ala
                405                 410                 415

Pro Arg His Phe His Val Pro Asp Thr Gly Val Lys Asp Asn Ile Tyr
            420                 425                 430

Arg Lys Pro Pro Ile Tyr Arg Gln His Ala Ala Arg Arg Ser Asp Gly
        435                 440                 445

Glu Asp Gly Ser Leu Asp Gln Asp Asn Arg Lys Lys Ser Ser Trp Leu
    450                 455                 460

Met Leu Lys Gly Asp Ala Asp Thr Arg Thr Asn Ser Pro Asp Leu Asp
465                 470                 475                 480

Thr Gln Ser Leu Ser His Ser Ser Gly Thr Asp Arg Asp Pro Leu Gln
                485                 490                 495
```

```
Arg Met Ala Gly Asp Ser Phe His Ser Gln Tyr Lys Ile Tyr Pro Tyr
            500                 505                 510

Asp Ser Leu Ile Val Thr Asn Arg Ile Arg Val Lys Leu Pro Lys Asp
        515                 520                 525

Val Asp Arg Thr Arg Leu Glu Arg His Leu Ser Pro Glu Glu Phe Gln
    530                 535                 540

Glu Val Phe Gly Met Ser Ile Glu Glu Phe Asp Arg Leu Ala Leu Trp
545                 550                 555                 560

Lys Arg Asn Asp Leu Lys Lys Lys Ala Leu Leu Phe
                565                 570


<210> 1423
<211> 521
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<220>
<221> source
<223> /note="Uniprot ID:  Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384658"

<400> 1423
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1               5                   10                  15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
            20                  25                  30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
```

```
        35                  40                  45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
    50                  55                  60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65                  70                  75                  80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
                85                  90                  95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270
```

```
Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
    290                 295                 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305                 310                 315                 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
                325                 330                 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
            340                 345                 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
        355                 360                 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
    370                 375                 380

His Tyr Ser Arg Pro Ala Ala Arg Arg Ser Asp Gly Glu Asp Gly Ser
385                 390                 395                 400

Leu Asp Gln Asp Asn Arg Lys Gln Lys Ser Ser Trp Leu Met Leu Lys
                405                 410                 415

Gly Asp Ala Asp Thr Arg Thr Asn Ser Pro Asp Leu Asp Thr Gln Ser
            420                 425                 430

Leu Ser His Ser Ser Gly Thr Asp Arg Asp Pro Leu Gln Arg Met Ala
        435                 440                 445

Gly Asp Ser Phe His Ser Gln Tyr Lys Ile Tyr Pro Tyr Asp Ser Leu
    450                 455                 460

Ile Val Thr Asn Arg Ile Arg Val Lys Leu Pro Lys Asp Val Asp Arg
465                 470                 475                 480

Thr Arg Leu Glu Arg His Leu Ser Pro Glu Glu Phe Gln Glu Val Phe
                485                 490                 495
```

```
Gly Met Ser Ile Glu Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn
            500                 505                 510

Asp Leu Lys Lys Lys Ala Leu Leu Phe
        515                 520


<210> 1424
<211> 470
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
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<223> /note="Gene Name:
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      family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389410"

<400> 1424
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1               5                   10                  15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
            20                  25                  30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
        35                  40                  45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
    50                  55                  60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65                  70                  75                  80
```

```
Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
                85                  90                  95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
    290                 295                 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
```

```
305                 310                 315                 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
                325                 330                 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Ser Pro Gln
            340                 345                 350

Leu Leu Ser Pro Thr Pro Thr Glu Gly Asp Gln Asp Asp Arg Ser Tyr
        355                 360                 365

Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr Gly Ser Val Ser Leu
    370                 375                 380

Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln His Tyr Ser Arg Pro
385                 390                 395                 400

Ala Ala Arg Arg Ser Asp Gly Glu Asp Gly Ser Leu Asp Gln Asp Asn
                405                 410                 415

Arg Lys Gln Lys Ser Ser Trp Leu Met Leu Lys Gly Asp Ala Asp Thr
            420                 425                 430

Arg Thr Asn Ser Pro Asp Leu Asp Thr Gln Ser Leu Ser His Ser Ser
        435                 440                 445

Gly Thr Asp Arg Asp Pro Leu Gln Arg Met Ala Gly Asp Ser Phe His
    450                 455                 460

Ser Arg Glu Trp Phe Phe
465                 470


<210> 1425
<211> 645
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
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<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393511"

<400> 1425

```
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1               5                  10                  15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
            20                  25                  30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
        35                  40                  45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
    50                  55                  60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65                  70                  75                  80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
                85                  90                  95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175
```

```
Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
    290                 295                 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305                 310                 315                 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
                325                 330                 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
            340                 345                 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
        355                 360                 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
    370                 375                 380

His Tyr Ser Arg Pro Ala Gly Thr Val Ser Val Gly Thr Ser Ser Cys
385                 390                 395                 400
```

```
Leu Ser Leu Ser Gln His Pro Ser Pro Thr Ser Val Phe Arg His His
                405                 410                 415

Tyr Ile Pro Tyr Phe Arg Gly Ser Glu Ser Gly Arg Ser Thr Pro Ser
            420                 425                 430

Leu Ser Val Leu Ser Asp Ser Lys Pro Pro Pro Ser Thr Tyr Gln Gln
        435                 440                 445

Ala Pro Arg His Phe His Val Pro Asp Thr Gly Val Lys Asp Asn Ile
    450                 455                 460

Tyr Arg Lys Pro Pro Ile Tyr Arg Gln His Ala Ala Arg Arg Ser Asp
465                 470                 475                 480

Gly Glu Asp Gly Ser Leu Asp Gln Asp Asn Arg Lys Gln Lys Ser Ser
                485                 490                 495

Trp Leu Met Leu Lys Gly Asp Ala Asp Thr Arg Thr Asn Ser Pro Asp
            500                 505                 510

Leu Asp Thr Gln Ser Leu Ser His Ser Ser Gly Thr Asp Arg Asp Pro
        515                 520                 525

Leu Gln Arg Met Ala Gly Asp Ser Phe His Ser Arg Phe Pro Tyr Ser
    530                 535                 540

Lys Ser Asp Pro Leu Pro Gly His Gly Lys Asn Gly Leu Asp Gln Arg
545                 550                 555                 560

Asn Ala Asn Leu Ala Pro Cys Gly Ala Asp Pro Asp Ala Ser Trp Gly
                565                 570                 575

Met Arg Glu Tyr Lys Ile Tyr Pro Tyr Asp Ser Leu Ile Val Thr Asn
            580                 585                 590

Arg Ile Arg Val Lys Leu Pro Lys Asp Val Asp Arg Thr Arg Leu Glu
        595                 600                 605

Arg His Leu Ser Pro Glu Glu Phe Gln Glu Val Phe Gly Met Ser Ile
    610                 615                 620

Glu Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn Asp Leu Lys Lys
```

625 630 635 640

Lys Ala Leu Leu Phe
645

<210> 1426
<211> 559
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421283"

<400> 1426
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1 5 10 15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
20 25 30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
35 40 45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
50 55 60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65 70 75 80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
85 90 95

```
Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
            100                 105                 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
        115                 120                 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
    130                 135                 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile
145                 150                 155                 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
                165                 170                 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
            180                 185                 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
        195                 200                 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
    210                 215                 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225                 230                 235                 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
                245                 250                 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
            260                 265                 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
        275                 280                 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
    290                 295                 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305                 310                 315                 320
```

```
Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
                325                 330                 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
            340                 345                 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
        355                 360                 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
    370                 375                 380

His Tyr Ser Arg Pro Ala Ala Arg Arg Ser Asp Gly Glu Asp Gly Ser
385                 390                 395                 400

Leu Asp Gln Asp Asn Arg Lys Lys Ser Ser Trp Leu Met Leu Lys Gly
                405                 410                 415

Asp Ala Asp Thr Arg Thr Asn Ser Pro Asp Leu Asp Thr Gln Ser Leu
            420                 425                 430

Ser His Ser Ser Gly Thr Asp Arg Asp Pro Leu Gln Arg Met Ala Gly
        435                 440                 445

Asp Ser Phe His Ser Arg Phe Pro Tyr Ser Lys Ser Asp Pro Leu Pro
    450                 455                 460

Gly His Gly Lys Asn Gly Leu Asp Gln Arg Asn Ala Asn Leu Ala Pro
465                 470                 475                 480

Cys Gly Ala Asp Pro Asp Ala Ser Trp Gly Met Arg Glu Tyr Lys Ile
                485                 490                 495

Tyr Pro Tyr Asp Ser Leu Ile Val Thr Asn Arg Ile Arg Val Lys Leu
            500                 505                 510

Pro Lys Asp Val Asp Arg Thr Arg Leu Glu Arg His Leu Ser Pro Glu
        515                 520                 525

Glu Phe Gln Glu Val Phe Gly Met Ser Ile Glu Glu Phe Asp Arg Leu
    530                 535                 540
```

```
Ala Leu Trp Lys Arg Asn Asp Leu Lys Lys Lys Ala Leu Leu Phe
545                 550                 555


<210> 1427
<211> 305
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt
      family, member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421718"

<400> 1427
Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser Ser Ile Trp
1               5                   10                  15


His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg Asn Lys Glu
            20                  25                  30


Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala Ser Ser Thr
        35                  40                  45


Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly Gly Glu Ile
    50                  55                  60


Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys Ala Ile Tyr
65                  70                  75                  80


Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr Ile Ser His
                85                  90                  95


Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Ser Pro Gln Leu Leu Ser
            100                 105                 110


Pro Thr Pro Thr Glu Gly Asp Gln Asp Asp Arg Ser Tyr Lys Gln Cys
```

```
        115                 120                 125

Arg Thr Ser Ser Pro Ser Ser Thr Gly Ser Val Ser Leu Gly Arg Tyr
    130                 135                 140

Thr Pro Thr Ser Arg Ser Pro Gln His Tyr Ser Arg Pro Ala Gly Thr
145                 150                 155                 160

Val Ser Val Gly Thr Ser Ser Cys Leu Ser Leu Ser Gln His Pro Ser
                165                 170                 175

Pro Thr Ser Val Phe Arg His His Tyr Ile Pro Tyr Phe Arg Gly Ser
            180                 185                 190

Glu Ser Gly Arg Ser Thr Pro Ser Leu Ser Val Leu Ser Asp Ser Lys
        195                 200                 205

Pro Pro Pro Ser Thr Tyr Gln Gln Ala Pro Arg His Phe His Val Pro
    210                 215                 220

Asp Thr Gly Val Lys Asp Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Arg
225                 230                 235                 240

Gln His Ala Ala Arg Arg Ser Asp Gly Glu Asp Gly Ser Leu Asp Gln
                245                 250                 255

Asp Asn Arg Lys Lys Ser Ser Trp Leu Met Leu Lys Gly Asp Ala Asp
            260                 265                 270

Thr Arg Thr Asn Ser Pro Asp Leu Asp Thr Gln Ser Leu Ser His Ser
        275                 280                 285

Ser Gly Thr Asp Arg Asp Pro Leu Gln Arg Met Ala Gly Asp Ser Phe
    290                 295                 300

His
305
```

<210> 1428
<211> 346
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q6H8Q1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423661"

<400> 1428

Met	Phe	Ala	Glu	Gly	Glu	Glu	Met	Tyr	Leu	Gln	Gly	Ser	Ser	Ile	Trp
1				5				10						15	

His	Pro	Ala	Cys	Arg	Gln	Ala	Ala	Arg	Thr	Glu	Asp	Arg	Asn	Lys	Glu
			20					25					30		

Thr	Arg	Thr	Ser	Ser	Glu	Ser	Ile	Ile	Ser	Val	Pro	Ala	Ser	Ser	Thr
		35					40					45			

Ser	Gly	Ser	Pro	Ser	Arg	Val	Ile	Tyr	Ala	Lys	Leu	Gly	Gly	Glu	Ile
	50					55					60				

Leu	Asp	Tyr	Arg	Asp	Leu	Ala	Ala	Leu	Pro	Lys	Ser	Lys	Ala	Ile	Tyr
65				70					75					80	

Asp	Ile	Asp	Arg	Pro	Asp	Met	Ile	Ser	Tyr	Ser	Pro	Tyr	Ile	Ser	His
				85					90					95	

Ser	Ala	Gly	Asp	Arg	Gln	Ser	Tyr	Gly	Glu	Ser	Pro	Gln	Leu	Leu	Ser
			100					105					110		

Pro	Thr	Pro	Thr	Glu	Gly	Asp	Gln	Asp	Asp	Arg	Ser	Tyr	Lys	Gln	Cys
		115					120					125			

Arg	Thr	Ser	Ser	Pro	Ser	Ser	Thr	Gly	Ser	Val	Ser	Leu	Gly	Arg	Tyr
	130					135					140				

```
Thr Pro Thr Ser Arg Ser Pro Gln His Tyr Ser Arg Pro Asp Thr Gly
145                 150                 155                 160

Val Lys Asp Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Arg Gln His Ala
                165                 170                 175

Ala Arg Arg Ser Asp Gly Glu Asp Gly Ser Leu Asp Gln Asp Asn Arg
            180                 185                 190

Lys Gln Lys Ser Ser Trp Leu Met Leu Lys Gly Asp Ala Asp Thr Arg
        195                 200                 205

Thr Asn Ser Pro Asp Leu Asp Thr Gln Ser Leu Ser His Ser Ser Gly
    210                 215                 220

Thr Asp Arg Asp Pro Leu Gln Arg Met Ala Gly Asp Ser Phe His Ser
225                 230                 235                 240

Arg Phe Pro Tyr Ser Lys Ser Asp Pro Leu Pro Gly His Gly Lys Asn
                245                 250                 255

Gly Leu Asp Gln Arg Asn Ala Asn Leu Ala Pro Cys Gly Ala Asp Pro
            260                 265                 270

Asp Ala Ser Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr Asp Ser
        275                 280                 285

Leu Ile Val Thr Asn Arg Ile Arg Val Lys Leu Pro Lys Asp Val Asp
    290                 295                 300

Arg Thr Arg Leu Glu Arg His Leu Ser Pro Glu Glu Phe Gln Glu Val
305                 310                 315                 320

Phe Gly Met Ser Ile Glu Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg
                325                 330                 335

Asn Asp Leu Lys Lys Lys Ala Leu Leu Phe
            340                 345
```

<210> 1429
<211> 646
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 420; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM2; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000441255"

<400> 1429
Met Ser Ala Val Ser Gln Pro Gln Ala Ala Pro Ser Pro Leu Glu Lys
1 5 10 15

Ser Pro Ser Thr Ala Ile Leu Cys Asn Thr Cys Gly Asn Val Cys Lys
20 25 30

Gly Glu Val Leu Arg Val Gln Asp Lys Tyr Phe His Ile Lys Cys Phe
35 40 45

Val Cys Lys Ala Cys Gly Cys Asp Leu Ala Glu Gly Gly Phe Phe Val
50 55 60

Arg Gln Gly Glu Tyr Ile Cys Thr Leu Asp Tyr Gln Arg Leu Tyr Gly
65 70 75 80

Thr Arg Cys Phe Ser Cys Asp Gln Phe Ile Glu Gly Glu Val Val Ser
85 90 95

Ala Leu Gly Lys Thr Tyr His Pro Asp Cys Phe Val Cys Ala Val Cys
100 105 110

Arg Leu Pro Phe Pro Pro Gly Asp Arg Val Thr Phe Asn Gly Lys Glu
115 120 125

Cys Met Cys Gln Lys Cys Ser Leu Pro Val Ser Val Gly Ser Ser Ala
130 135 140

His Leu Ser Gln Gly Leu Arg Ser Cys Gly Gly Cys Gly Thr Glu Ile

145 150 155 160

Lys Asn Gly Gln Ala Leu Val Ala Leu Asp Lys His Trp His Leu Gly
165 170 175

Cys Phe Lys Cys Lys Ser Cys Gly Lys Leu Leu Asn Ala Glu Tyr Ile
180 185 190

Ser Lys Asp Gly Leu Pro Tyr Cys Glu Ala Asp Tyr His Ala Lys Phe
195 200 205

Gly Ile Arg Cys Asp Ser Cys Glu Lys Tyr Ile Thr Gly Arg Val Leu
210 215 220

Glu Ala Gly Glu Lys His Tyr His Pro Ser Cys Ala Leu Cys Val Arg
225 230 235 240

Cys Gly Gln Met Phe Ala Glu Gly Glu Glu Met Tyr Leu Gln Gly Ser
245 250 255

Ser Ile Trp His Pro Ala Cys Arg Gln Ala Ala Arg Thr Glu Asp Arg
260 265 270

Asn Lys Glu Thr Arg Thr Ser Ser Glu Ser Ile Ile Ser Val Pro Ala
275 280 285

Ser Ser Thr Ser Gly Ser Pro Ser Arg Val Ile Tyr Ala Lys Leu Gly
290 295 300

Gly Glu Ile Leu Asp Tyr Arg Asp Leu Ala Ala Leu Pro Lys Ser Lys
305 310 315 320

Ala Ile Tyr Asp Ile Asp Arg Pro Asp Met Ile Ser Tyr Ser Pro Tyr
325 330 335

Ile Ser His Ser Ala Gly Asp Arg Gln Ser Tyr Gly Glu Gly Asp Gln
340 345 350

Asp Asp Arg Ser Tyr Lys Gln Cys Arg Thr Ser Ser Pro Ser Ser Thr
355 360 365

Gly Ser Val Ser Leu Gly Arg Tyr Thr Pro Thr Ser Arg Ser Pro Gln
370 375 380

```
His Tyr Ser Arg Pro Ala Gly Thr Val Ser Val Gly Thr Ser Ser Cys
385                 390                 395                 400

Leu Ser Leu Ser Gln His Pro Ser Pro Thr Ser Val Phe Arg His His
                405                 410                 415

Tyr Ile Pro Tyr Phe Arg Gly Ser Glu Ser Gly Arg Ser Thr Pro Ser
            420                 425                 430

Leu Ser Val Leu Ser Asp Ser Lys Pro Pro Pro Pro Pro Thr Ser Arg
        435                 440                 445

His Leu Ala Thr Ser Thr Ser Gln Ala Pro Asp Thr Gly Val Lys Asp
    450                 455                 460

Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Arg Gln His Ala Ala Arg Arg
465                 470                 475                 480

Ser Asp Gly Glu Asp Gly Ser Leu Asp Gln Asp Asn Arg Lys Gln Lys
                485                 490                 495

Ser Ser Trp Leu Met Leu Lys Gly Asp Ala Asp Thr Arg Thr Asn Ser
            500                 505                 510

Pro Asp Leu Asp Thr Gln Ser Leu Ser His Ser Ser Gly Thr Asp Arg
        515                 520                 525

Asp Pro Leu Gln Arg Met Ala Gly Asp Ser Phe His Ser Arg Phe Pro
    530                 535                 540

Tyr Ser Lys Ser Asp Pro Leu Pro Gly His Gly Lys Asn Gly Leu Asp
545                 550                 555                 560

Gln Arg Asn Ala Asn Leu Ala Pro Cys Gly Ala Asp Pro Asp Ala Ser
                565                 570                 575

Trp Gly Met Arg Glu Gln Ile Tyr Pro Tyr Asp Ser Leu Ile Val Thr
            580                 585                 590

Asn Arg Ile Arg Val Lys Leu Pro Lys Asp Val Asp Arg Thr Arg Leu
        595                 600                 605
```

```
Glu Arg His Leu Ser Pro Glu Glu Phe Gln Glu Val Phe Gly Met Ser
    610                 615                 620

Ile Glu Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn Asp Leu Lys
625                 630                 635                 640

Lys Lys Ala Leu Leu Phe
                645

<210> 1430
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt
      family, member 3; "

<220>
<221> source
<223> /note="Uniprot ID:  O94929; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000310309"

<400> 1430
Met Asn Thr Ser Ile Pro Tyr Gln Gln Asn Pro Tyr Asn Pro Arg Gly
1               5                   10                  15

Ser Ser Asn Val Ile Gln Cys Tyr Arg Cys Gly Asp Thr Cys Lys Gly
            20                  25                  30

Glu Val Val Arg Val His Asn Asn His Phe His Ile Arg Cys Phe Thr
        35                  40                  45

Cys Gln Val Cys Gly Cys Gly Leu Ala Gln Ser Gly Phe Phe Phe Lys
    50                  55                  60
```

```
Asn Gln Glu Tyr Ile Cys Thr Gln Asp Tyr Gln Gln Leu Tyr Gly Thr
65                  70                  75                  80

Arg Cys Asp Ser Cys Arg Asp Phe Ile Thr Gly Glu Val Ile Ser Ala
                85                  90                  95

Leu Gly Arg Thr Tyr His Pro Lys Cys Phe Val Cys Ser Leu Cys Arg
            100                 105                 110

Lys Pro Phe Pro Ile Gly Asp Lys Val Thr Phe Ser Gly Lys Glu Cys
        115                 120                 125

Val Cys Gln Thr Cys Ser Gln Ser Met Ala Ser Ser Lys Pro Ile Lys
    130                 135                 140

Ile Arg Gly Pro Ser His Cys Ala Gly Cys Lys Glu Glu Ile Lys His
145                 150                 155                 160

Gly Gln Ser Leu Leu Ala Leu Asp Lys Gln Trp His Val Ser Cys Phe
                165                 170                 175

Lys Cys Gln Thr Cys Ser Val Ile Leu Thr Gly Glu Tyr Ile Ser Lys
            180                 185                 190

Asp Gly Val Pro Tyr Cys Glu Ser Asp Tyr His Ala Gln Phe Gly Ile
        195                 200                 205

Lys Cys Glu Thr Cys Asp Arg Tyr Ile Ser Gly Arg Val Leu Glu Ala
    210                 215                 220

Gly Gly Lys His Tyr His Pro Thr Cys Ala Arg Cys Val Arg Cys His
225                 230                 235                 240

Gln Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Thr Gly Ser Glu Val
                245                 250                 255

Trp His Pro Ile Cys Lys Gln Ala Ala Arg Ala Glu Lys Lys Leu Lys
            260                 265                 270

His Arg Arg Thr Ser Glu Thr Ser Ile Ser Pro Pro Gly Ser Ser Ile
        275                 280                 285

Gly Ser Pro Asn Arg Val Ile Cys Ala Lys Val Asp Asn Glu Ile Leu
```

290 295 300

Asn Tyr Lys Asp Leu Ala Ala Leu Pro Lys Val Lys Ser Ile Tyr Glu
305 310 315 320

Val Gln Arg Pro Asp Leu Ile Ser Tyr Glu Pro His Ser Arg Tyr Met
325 330 335

Ser Asp Glu Met Leu Glu Arg Cys Gly Tyr Gly Glu Ser Leu Gly Thr
340 345 350

Leu Ser Pro Tyr Ser Gln Asp Ile Tyr Glu Asn Leu Asp Leu Arg Gln
355 360 365

Arg Arg Ala Ser Ser Pro Gly Tyr Ile Asp Ser Pro Thr Tyr Ser Arg
370 375 380

Gln Gly Met Ser Pro Thr Phe Ser Arg Ser Pro His His Tyr Tyr Arg
385 390 395 400

Ser Gly Pro Glu Ser Gly Arg Ser Ser Pro Tyr His Ser Gln Leu Asp
405 410 415

Val Arg Ser Ser Thr Pro Thr Ser Tyr Gln Ala Pro Lys His Phe His
420 425 430

Ile Pro Ala Gly Asp Ser Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Lys
435 440 445

Arg His Gly Asp Leu Ser Thr Ala Thr Lys Ser Lys Thr Ser Glu Asp
450 455 460

Ile Ser Gln Thr Ser Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr
465 470 475 480

Tyr Ala Ser Glu Ser Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val
485 490 495

Pro Arg Ala Arg Arg Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp
500 505 510

Arg Ser Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys
515 520 525

```
Glu Glu Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr Pro
    530                 535                 540

Pro Arg Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly Tyr
545                 550                 555                 560

Glu Met Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp Ser
                565                 570                 575

Asp Pro Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg Asn
            580                 585                 590

Gly Leu His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser Met
        595                 600                 605

Asn Ala Val Asn Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr Glu
    610                 615                 620

Leu Leu Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp Val
625                 630                 635                 640

Asp Arg Thr Arg Leu Glu Arg His Leu Ser Gln Glu Glu Phe Tyr Gln
                645                 650                 655

Val Phe Gly Met Thr Ile Ser Glu Phe Asp Arg Leu Ala Leu Trp Lys
            660                 665                 670

Arg Asn Glu Leu Lys Lys Gln Ala Arg Leu Phe
        675                 680


<210> 1431
<211> 588
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
<221> source
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<223> /note="Gene Name:
actin binding LIM prt
family, member 3; "

<220>
<221> source
<223> /note="Uniprot ID: O94929; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000315841"

<400> 1431

```
Met Asn Thr Ser Ile Pro Tyr Gln Gln Asn Pro Tyr Asn Pro Arg Gly
1               5                  10                  15

Ser Ser Asn Val Ile Gln Cys Tyr Arg Cys Gly Asp Thr Cys Lys Gly
            20                  25                  30

Glu Val Val Arg Val His Asn Asn His Phe His Ile Arg Cys Phe Thr
        35                  40                  45

Cys Gln Val Cys Gly Cys Gly Leu Ala Gln Ser Gly Phe Phe Phe Lys
    50                  55                  60

Asn Gln Glu Tyr Ile Cys Thr Gln Asp Tyr Gln Gln Leu Tyr Gly Thr
65                  70                  75                  80

Arg Cys Asp Ser Cys Arg Asp Phe Ile Thr Gly Glu Val Ile Ser Ala
                85                  90                  95

Leu Gly Arg Thr Tyr His Pro Lys Cys Phe Val Cys Ser Leu Cys Arg
            100                 105                 110

Lys Pro Phe Pro Ile Gly Asp Lys Val Thr Phe Ser Gly Lys Glu Cys
        115                 120                 125

Val Cys Gln Thr Cys Ser Gln Ser Met Ala Ser Ser Lys Pro Ile Lys
    130                 135                 140

Ile Arg Gly Pro Ser His Cys Ala Gly Cys Lys Glu Glu Ile Lys His
145                 150                 155                 160

Gly Gln Ser Leu Leu Ala Leu Asp Lys Gln Trp His Val Ser Cys Phe
                165                 170                 175
```

```
Lys Cys Gln Thr Cys Ser Val Ile Leu Thr Gly Glu Tyr Ile Ser Lys
            180                 185                 190

Asp Gly Val Pro Tyr Cys Glu Ser Asp Tyr His Ala Gln Phe Gly Ile
        195                 200                 205

Lys Cys Glu Thr Cys Asp Arg Tyr Ile Ser Gly Arg Val Leu Glu Ala
    210                 215                 220

Gly Gly Lys His Tyr His Pro Thr Cys Ala Arg Cys Val Arg Cys His
225                 230                 235                 240

Gln Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Thr Gly Ser Glu Val
                245                 250                 255

Trp His Pro Ile Cys Lys Gln Ala Ala Arg Ala Glu Lys Lys Leu Lys
            260                 265                 270

His Arg Arg Thr Ser Glu Thr Ser Ile Ser Pro Pro Gly Ser Ser Ile
        275                 280                 285

Gly Ser Pro Asn Arg Val Ile Cys Asp Ile Tyr Glu Asn Leu Asp Leu
    290                 295                 300

Arg Gln Arg Arg Ala Ser Ser Pro Gly Tyr Ile Asp Ser Pro Thr Tyr
305                 310                 315                 320

Ser Arg Gln Gly Met Ser Pro Thr Phe Ser Arg Ser Pro His His Tyr
                325                 330                 335

Tyr Arg Ser Ala Gly Asp Ser Asn Ile Tyr Arg Lys Pro Pro Ile Tyr
            340                 345                 350

Lys Arg His Gly Asp Leu Ser Thr Ala Thr Lys Ser Lys Thr Ser Glu
        355                 360                 365

Asp Ile Ser Gln Thr Ser Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro
    370                 375                 380

Tyr Tyr Ala Ser Glu Ser Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys
385                 390                 395                 400

Val Pro Arg Ala Arg Arg Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe
```

```
                405                 410                 415

Asp Arg Ser Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu
            420                 425                 430

Lys Glu Glu Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr
        435                 440                 445

Pro Pro Arg Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly
    450                 455                 460

Tyr Glu Met Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp
465                 470                 475                 480

Ser Asp Pro Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg
                485                 490                 495

Asn Gly Leu His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser
            500                 505                 510

Met Asn Ala Val Asn Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr
        515                 520                 525

Glu Leu Leu Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp
    530                 535                 540

Val Asp Arg Thr Arg Leu Glu Arg His Leu Ser Gln Glu Glu Phe Tyr
545                 550                 555                 560

Gln Val Phe Gly Met Thr Ile Ser Glu Phe Asp Arg Leu Ala Leu Trp
                565                 570                 575

Lys Arg Asn Glu Leu Lys Lys Gln Ala Arg Leu Phe
            580                 585


<210> 1432
<211> 170
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

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<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
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<223> /note="Gene Name:
actin binding LIM prt
family, member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000348938"

<400> 1432

```
Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys Glu Glu
1               5                  10                  15

Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr Pro Pro Arg
            20                  25                  30

Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly Tyr Glu Met
        35                  40                  45

Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp Ser Asp Pro
    50                  55                  60

Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg Asn Gly Leu
65                  70                  75                  80

His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser Met Asn Ala
                85                  90                  95

Val Asn Trp Gly Met Arg Gly Glu Cys Lys Ile Tyr Pro Tyr Glu Leu
            100                 105                 110

Leu Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp Val Asp
        115                 120                 125

Arg Thr Arg Leu Glu Arg His Leu Ser Gln Glu Glu Phe Tyr Gln Val
    130                 135                 140

Phe Gly Met Thr Ile Ser Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg
145                 150                 155                 160

Asn Glu Leu Lys Lys Gln Ala Arg Leu Phe
                165                 170
```

<210> 1433
<211> 650
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ABLIM3; "

<220>
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<223> /note="Gene Name:
actin binding LIM prt
family, member 3; "

<220>
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<223> /note="ENSP ID: ENSP00000420855"

<400> 1433

Met	Asn	Thr	Ser	Ile	Pro	Tyr	Gln	Gln	Asn	Pro	Tyr	Asn	Pro	Arg	Gly
1					5				10					15	
Ser	Ser	Asn	Val	Ile	Gln	Cys	Tyr	Arg	Cys	Gly	Asp	Thr	Cys	Lys	Gly
			20					25					30		
Glu	Val	Val	Arg	Val	His	Asn	Asn	His	Phe	His	Ile	Arg	Cys	Phe	Thr
		35					40					45			
Cys	Gln	Val	Cys	Gly	Cys	Gly	Leu	Ala	Gln	Ser	Gly	Phe	Phe	Phe	Lys
	50					55					60				
Asn	Gln	Glu	Tyr	Ile	Cys	Thr	Gln	Asp	Tyr	Gln	Gln	Leu	Tyr	Gly	Thr
65					70					75					80
Arg	Cys	Asp	Ser	Cys	Arg	Asp	Phe	Ile	Thr	Gly	Glu	Val	Ile	Ser	Ala
				85					90					95	
Leu	Gly	Arg	Thr	Tyr	His	Pro	Lys	Cys	Phe	Val	Cys	Ser	Leu	Cys	Arg
			100					105					110		
Lys	Pro	Phe	Pro	Ile	Gly	Asp	Lys	Val	Thr	Phe	Ser	Gly	Lys	Glu	Cys
		115					120					125			

```
Val Cys Gln Thr Cys Ser Gln Ser Met Ala Ser Ser Lys Pro Ile Lys
    130                 135                 140

Ile Arg Gly Pro Ser His Cys Ala Gly Cys Lys Glu Glu Ile Lys His
145                 150                 155                 160

Gly Gln Ser Leu Leu Ala Leu Asp Lys Gln Trp His Val Ser Cys Phe
                165                 170                 175

Lys Cys Gln Thr Cys Ser Val Ile Leu Thr Gly Glu Tyr Ile Ser Lys
            180                 185                 190

Asp Gly Val Pro Tyr Cys Glu Ser Asp Tyr His Ala Gln Phe Gly Ile
        195                 200                 205

Lys Cys Glu Thr Cys Asp Arg Tyr Ile Ser Gly Arg Val Leu Glu Ala
    210                 215                 220

Gly Gly Lys His Tyr His Pro Thr Cys Ala Arg Cys Val Arg Cys His
225                 230                 235                 240

Gln Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Thr Gly Ser Glu Val
                245                 250                 255

Trp His Pro Ile Cys Lys Gln Ala Ala Arg Ala Glu Lys Lys Leu Lys
            260                 265                 270

His Arg Arg Thr Ser Glu Thr Ser Ile Ser Pro Pro Gly Ser Ser Ile
        275                 280                 285

Gly Ser Pro Asn Arg Val Ile Cys Ala Lys Val Asp Asn Glu Ile Leu
    290                 295                 300

Asn Tyr Lys Asp Leu Ala Ala Leu Pro Lys Val Lys Ser Ile Tyr Glu
305                 310                 315                 320

Val Gln Arg Pro Asp Leu Ile Ser Tyr Glu Pro His Ser Arg Tyr Met
                325                 330                 335

Ser Asp Glu Met Leu Glu Arg Cys Gly Tyr Gly Glu Ser Leu Gly Thr
            340                 345                 350

Leu Ser Pro Tyr Ser Gln Asp Ile Tyr Glu Asn Leu Asp Leu Arg Gln
```

```
        355                 360                 365

Arg Arg Ala Ser Ser Pro Gly Tyr Ile Asp Ser Pro Thr Tyr Ser Arg
    370                 375                 380

Gln Gly Met Ser Pro Thr Phe Ser Arg Ser Pro His His Tyr Tyr Arg
385                 390                 395                 400

Ser Ala Gly Asp Ser Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Lys Arg
                405                 410                 415

His Gly Asp Leu Ser Thr Ala Thr Lys Ser Lys Thr Ser Glu Asp Ile
            420                 425                 430

Ser Gln Thr Ser Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr Tyr
        435                 440                 445

Ala Ser Glu Ser Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val Pro
    450                 455                 460

Arg Ala Arg Arg Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp Arg
465                 470                 475                 480

Ser Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys Glu
                485                 490                 495

Glu Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr Pro Pro
            500                 505                 510

Arg Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly Tyr Glu
        515                 520                 525

Met Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp Ser Asp
    530                 535                 540

Pro Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg Asn Gly
545                 550                 555                 560

Leu His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser Met Asn
                565                 570                 575

Ala Val Asn Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr Glu Leu
            580                 585                 590
```

```
Leu Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp Val Asp
        595                 600                 605

Arg Thr Arg Leu Glu Arg His Leu Ser Gln Glu Glu Phe Tyr Gln Val
    610                 615                 620

Phe Gly Met Thr Ile Ser Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg
625                 630                 635                 640

Asn Glu Leu Lys Lys Gln Ala Arg Leu Phe
                645                 650


<210> 1434
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt
      family, member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421002"

<400> 1434
Met Asn Thr Ser Ile Pro Tyr Gln Gln Asn Pro Tyr Asn Pro Arg Gly
1               5                   10                  15

Ser Ser Asn Val Ile Gln Cys Tyr Arg Cys Gly Asp Thr Cys Lys Gly
            20                  25                  30

Glu Val Val Arg Val His Asn Asn His Phe His Ile Arg Cys Phe Thr
        35                  40                  45

Cys Gln Val Cys Gly Cys Gly Leu Ala Gln Ser Gly Phe Phe Phe Lys
    50                  55                  60
```

```
Asn Gln Glu Tyr Ile Cys Thr Gln Asp Tyr Gln Gln Leu Tyr Gly Thr
65                  70                  75                  80

Arg Cys Asp Ser Cys Arg Asp Phe Ile Thr Gly Glu Val Ile Ser Ala
                85                  90                  95

Leu Gly Arg Thr Tyr His Pro Lys Cys Phe Val Cys Ser Leu Cys Arg
            100                 105                 110

Thr Ser Pro Gly Met Glu Ser Ser Ser Leu Pro Pro Ala Leu Pro Ser
        115                 120                 125

Ala Ser Pro Ser Leu Val Asn Ser Ala Ser Glu Ala Phe Pro His Trp
    130                 135                 140

Arg Gln Gly Asp Leu Gln Arg
145                 150


<210> 1435
<211> 544
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt
      family, member 3; "

<220>
<221> source
<223> /note="Uniprot ID:  O94929; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421183"

<400> 1435
Met Asn Thr Ser Ile Pro Tyr Gln Gln Asn Pro Tyr Asn Pro Arg Gly
1               5                   10                  15
```

```
Ser Ser Asn Val Ile Gln Cys Tyr Arg Cys Gly Asp Thr Cys Lys Gly
            20                  25                  30

Glu Val Val Arg Val His Asn Asn His Phe His Ile Arg Cys Phe Thr
        35                  40                  45

Cys Gln Val Cys Gly Cys Gly Leu Ala Gln Ser Gly Phe Phe Phe Lys
    50                  55                  60

Asn Gln Glu Tyr Ile Cys Thr Gln Asp Tyr Gln Gln Leu Tyr Gly Thr
65                  70                  75                  80

Arg Cys Asp Ser Cys Arg Asp Phe Ile Thr Gly Glu Val Ile Ser Ala
                85                  90                  95

Leu Gly Arg Thr Tyr His Pro Lys Cys Phe Val Cys Ser Leu Cys Arg
            100                 105                 110

Lys Pro Phe Pro Ile Gly Asp Lys Val Thr Phe Ser Gly Lys Glu Cys
        115                 120                 125

Val Cys Gln Thr Cys Ser Gln Ser Met Ala Ser Ser Lys Pro Ile Lys
    130                 135                 140

Ile Arg Gly Pro Ser His Cys Ala Gly Cys Lys Glu Glu Ile Lys His
145                 150                 155                 160

Gly Gln Ser Leu Leu Ala Leu Asp Lys Gln Trp His Val Ser Cys Phe
                165                 170                 175

Lys Cys Gln Thr Cys Ser Val Ile Leu Thr Gly Glu Tyr Ile Ser Lys
            180                 185                 190

Asp Gly Val Pro Tyr Cys Glu Ser Asp Tyr His Ala Gln Phe Gly Ile
        195                 200                 205

Lys Cys Glu Thr Cys Asp Arg Tyr Ile Ser Gly Arg Val Leu Glu Ala
    210                 215                 220

Gly Gly Lys His Tyr His Pro Thr Cys Ala Arg Cys Val Arg Cys His
225                 230                 235                 240

Gln Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Thr Gly Ser Glu Val
```

```
                245                 250                 255

Trp His Pro Ile Cys Lys Gln Ala Ala Arg Ala Glu Lys Lys Leu Lys
            260                 265                 270

His Arg Arg Thr Ser Glu Thr Ser Ile Ser Pro Pro Gly Ser Ser Ile
        275                 280                 285

Gly Ser Pro Asn Arg Val Ile Cys Asp Ile Tyr Glu Asn Leu Asp Leu
    290                 295                 300

Arg Gln Arg Arg Ala Ser Ser Pro Gly Tyr Ile Asp Ser Pro Thr Tyr
305                 310                 315                 320

Ser Arg Gln Gly Met Ser Pro Thr Phe Ser Arg Ser Pro His His Tyr
                325                 330                 335

Tyr Arg Ser Gly Asp Leu Ser Thr Ala Thr Lys Ser Lys Thr Ser Glu
            340                 345                 350

Asp Ile Ser Gln Thr Ser Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro
        355                 360                 365

Tyr Tyr Ala Ser Glu Ser Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys
    370                 375                 380

Val Pro Arg Ala Arg Arg Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe
385                 390                 395                 400

Asp Arg Ser Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu
                405                 410                 415

Lys Glu Glu Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr
            420                 425                 430

Pro Pro Arg Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly
        435                 440                 445

Tyr Glu Met Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp
    450                 455                 460

Ser Asp Pro Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg
465                 470                 475                 480
```

```
Asn Gly Leu His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser
                485                 490                 495

Met Asn Ala Val Asn Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr
            500                 505                 510

Glu Leu Leu Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp
        515                 520                 525

Val Asp Arg Thr Arg Leu Glu Gly Asn Phe Trp Lys Ser Gly Cys Leu
    530                 535                 540


<210> 1436
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

<220>
<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
<221> source
<223> /note="Gene Name:
      actin binding LIM prt
      family, member 3; "

<220>
<221> source
<223> /note="Uniprot ID:  O94929; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425394"

<400> 1436
Met Asn Thr Ser Ile Pro Tyr Gln Gln Asn Pro Tyr Asn Pro Arg Gly
1               5                   10                  15

Ser Ser Asn Val Ile Gln Cys Tyr Arg Cys Gly Asp Thr Cys Lys Gly
            20                  25                  30

Glu Val Val Arg Val His Asn Asn His Phe His Ile Arg Cys Phe Thr
        35                  40                  45
```

```
Cys Gln Val Cys Gly Cys Gly Leu Ala Gln Ser Gly Phe Phe Phe Lys
    50                  55                  60

Asn Gln Glu Tyr Ile Cys Thr Gln Asp Tyr Gln Gln Leu Tyr Gly Thr
65                  70                  75                  80

Arg Cys Asp Ser Cys Arg Asp Phe Ile Thr Gly Glu Val Ile Ser Ala
                85                  90                  95

Leu Gly Arg Thr Tyr His Pro Lys Cys Phe Val Cys Ser Leu Cys Arg
            100                 105                 110

Lys Pro Phe Pro Ile Gly Asp Lys Val Thr Phe Ser Gly Lys Glu Cys
        115                 120                 125

Val Cys Gln Thr Cys Ser Gln Ser Met Ala Ser Ser Lys Pro Ile Lys
    130                 135                 140

Ile Arg Gly Pro Ser His Cys Ala Gly Cys Lys Glu Glu Ile Lys His
145                 150                 155                 160

Gly Gln Ser Leu Leu Ala Leu Asp Lys Gln Trp His Val Ser Cys Phe
                165                 170                 175

Lys Cys Gln Thr Cys Ser Val Ile Leu Thr Gly Glu Tyr Ile Ser Lys
            180                 185                 190

Asp Gly Val Pro Tyr Cys Glu Ser Asp Tyr His Ala Gln Phe Gly Ile
        195                 200                 205

Lys Cys Glu Thr Cys Asp Arg Tyr Ile Ser Gly Arg Val Leu Glu Ala
    210                 215                 220

Gly Gly Lys His Tyr His Pro Thr Cys Ala Arg Cys Val Arg Cys His
225                 230                 235                 240

Gln Met Phe Thr Glu Gly Glu Glu Met Tyr Leu Thr Gly Ser Glu Val
                245                 250                 255

Trp His Pro Ile Cys Lys Gln Ala Ala Arg Ala Glu Lys Lys Leu Lys
            260                 265                 270
```

```
His Arg Arg Thr Ser Glu Thr Ser Ile Ser Pro Pro Gly Ser Ser Ile
        275                 280                 285

Gly Ser Pro Asn Arg Val Ile Cys Ala Lys Val Asp Asn Glu Ile Leu
    290                 295                 300

Asn Tyr Lys Asp Leu Ala Ala Leu Pro Lys Val Lys Ser Ile Tyr Glu
305                 310                 315                 320

Val Gln Arg Pro Asp Leu Ile Ser Tyr Glu Pro His Ser Arg Tyr Met
                325                 330                 335

Ser Asp Glu Met Leu Glu Arg Cys Gly Tyr Gly Glu Ser Leu Gly Thr
            340                 345                 350

Leu Ser Pro Tyr Ser Gln Asp Ile Tyr Glu Asn Leu Asp Leu Arg Gln
        355                 360                 365

Arg Arg Ala Ser Ser Pro Gly Tyr Ile Asp Ser Pro Thr Tyr Ser Arg
    370                 375                 380

Gln Gly Met Ser Pro Thr Phe Ser Arg Ser Pro His His Tyr Tyr Arg
385                 390                 395                 400

Ser Gly Pro Glu Ser Gly Arg Ser Ser Pro Tyr His Ser Gln Leu Asp
                405                 410                 415

Val Arg Ser Ser Thr Pro Thr Ser Tyr Gln Ala Pro Lys His Phe His
            420                 425                 430

Ile Pro Ala Gly Asp Ser Asn Ile Tyr Arg Lys Pro Pro Ile Tyr Lys
        435                 440                 445

Arg His Gly Asp Leu Ser Thr Ala Thr Lys Ser Lys Thr Ser Glu Asp
    450                 455                 460

Ile Ser Gln Thr Ser Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr
465                 470                 475                 480

Tyr Ala Ser Glu Ser Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val
                485                 490                 495

Pro Arg Ala Arg Arg Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp
```

```
            500                 505                 510

Arg Ser Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys
        515                 520                 525

Glu Glu Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr Pro
    530                 535                 540

Pro Arg Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly Tyr
545                 550                 555                 560

Glu Met Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp Ser
                565                 570                 575

Asp Pro Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg Asn
            580                 585                 590

Gly Leu His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser Met
        595                 600                 605

Asn Ala Val Asn Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr Glu
    610                 615                 620

Leu Leu Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp Val
625                 630                 635                 640

Asp Arg Thr Arg Leu Glu Arg His Leu Ser Gln Glu Glu Phe Tyr Gln
                645                 650                 655

Val Phe Gly Met Thr Ile Ser Glu Phe Asp Arg Leu Ala Leu Trp Lys
            660                 665                 670

Arg Asn Glu Leu Lys Lys Gln Ala Arg Leu Phe
        675                 680


<210> 1437
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 421; "

<220>
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<221> source
<223> /note="Gene Symbol: ABLIM3; "

<220>
<221> source
<223> /note="Gene Name:
actin binding LIM prt
family, member 3; "

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<223> /note="Uniprot ID: O94929; "

<220>
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<223> /note="ENSP ID: ENSP00000430150"

<400> 1437

```
Met His Lys Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys Glu Glu
1               5                  10                  15

Met Lys Ala Arg Ser Ser Ser Tyr Ala Asp Pro Trp Thr Pro Pro Arg
            20                  25                  30

Ser Ser Thr Ser Ser Arg Glu Ala Leu His Thr Ala Gly Tyr Glu Met
        35                  40                  45

Ser Leu Asn Gly Ser Pro Arg Ser His Tyr Leu Ala Asp Ser Asp Pro
    50                  55                  60

Leu Ile Ser Lys Ser Ala Ser Leu Pro Ala Tyr Arg Arg Asn Gly Leu
65                  70                  75                  80

His Arg Thr Pro Ser Ala Asp Leu Phe His Tyr Asp Ser Met Asn Ala
                85                  90                  95

Val Asn Trp Gly Met Arg Glu Tyr Lys Ile Tyr Pro Tyr Glu Leu Leu
            100                 105                 110

Leu Val Thr Thr Arg Gly Arg Asn Arg Leu Pro Lys Asp Val Asp Arg
        115                 120                 125

Thr Arg Leu Glu Arg His Leu Ser Gln Glu Glu Phe Tyr Gln Val Phe
    130                 135                 140

Gly Met Thr Ile Ser Glu Phe Asp Arg Leu Ala Leu Trp Lys Arg Asn
145                 150                 155                 160
```

Glu Leu Lys Lys Gln Ala Arg Leu Phe
165

<210> 1438
<211> 381
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 422; "

<220>
<221> source
<223> /note="Gene Symbol: ABRA; "

<220>
<221> source
<223> /note="Gene Name:
actin binding Rho activating prt; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N0Z2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000311436"

<400> 1438
Met Ala Pro Gly Glu Lys Glu Ser Gly Glu Gly Pro Ala Lys Ser Ala
1 5 10 15

Leu Arg Lys Ile Arg Thr Ala Thr Leu Val Ile Ser Leu Ala Arg Gly
20 25 30

Trp Gln Gln Trp Ala Asn Glu Asn Ser Ile Arg Gln Ala Gln Glu Pro
35 40 45

Thr Gly Trp Leu Pro Gly Gly Thr Gln Asp Ser Pro Gln Ala Pro Lys
50 55 60

Pro Ile Thr Pro Pro Thr Ser His Gln Lys Ala Gln Ser Ala Pro Lys
65 70 75 80

Ser Pro Pro Arg Leu Pro Glu Gly His Gly Asp Gly Gln Ser Ser Glu
85 90 95

Lys Ala Pro Glu Val Ser His Ile Lys Lys Lys Glu Val Ser Lys Thr

```
            100                 105                 110

Val Val Ser Lys Thr Tyr Glu Arg Gly Gly Asp Val Ser His Leu Ser
        115                 120                 125

His Arg Tyr Glu Arg Asp Ala Gly Val Leu Glu Pro Gly Gln Pro Glu
    130                 135                 140

Asn Asp Ile Asp Arg Ile Leu His Ser His Gly Ser Pro Thr Arg Arg
145                 150                 155                 160

Arg Lys Cys Ala Asn Leu Val Ser Glu Leu Thr Lys Gly Trp Arg Val
                165                 170                 175

Met Glu Gln Glu Glu Pro Thr Trp Arg Ser Asp Ser Val Asp Thr Glu
            180                 185                 190

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Glu Arg Pro Glu Gln Asp Gly
        195                 200                 205

Val Gln Val Ala Val Val Arg Ile Lys Arg Pro Leu Pro Ser Gln Val
    210                 215                 220

Asn Arg Phe Thr Glu Lys Leu Asn Cys Lys Ala Gln Gln Lys Tyr Ser
225                 230                 235                 240

Pro Val Gly Asn Leu Lys Gly Arg Trp Gln Gln Trp Ala Asp Glu His
                245                 250                 255

Ile Gln Ser Gln Lys Leu Asn Pro Phe Ser Glu Glu Phe Asp Tyr Glu
            260                 265                 270

Leu Ala Met Ser Thr Arg Leu His Lys Gly Asp Glu Gly Tyr Gly Arg
        275                 280                 285

Pro Lys Glu Gly Thr Lys Thr Ala Glu Arg Ala Lys Arg Ala Glu Glu
    290                 295                 300

His Ile Tyr Arg Glu Met Met Asp Met Cys Phe Ile Ile Cys Thr Met
305                 310                 315                 320

Ala Arg His Arg Arg Asp Gly Lys Ile Gln Val Thr Phe Gly Asp Leu
                325                 330                 335
```

```
Phe Asp Arg Tyr Val Arg Ile Ser Asp Lys Val Val Gly Ile Leu Met
            340                 345                 350

Arg Ala Arg Lys His Gly Leu Val Asp Phe Glu Gly Glu Met Leu Trp
        355                 360                 365

Gln Gly Arg Asp Asp His Val Val Ile Thr Leu Leu Lys
    370                 375                 380


<210> 1439
<211> 730
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 423; "

<220>
<221> source
<223> /note="Gene Symbol: AFAP1; "

<220>
<221> source
<223> /note="Gene Name:
      actin filament associated prt 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N556; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000351245"

<400> 1439
Met Glu Glu Leu Ile Val Glu Leu Arg Leu Phe Leu Glu Leu Leu Asp
1               5                  10                  15

His Glu Tyr Leu Thr Ser Thr Val Arg Glu Lys Lys Ala Val Ile Thr
            20                  25                  30

Asn Ile Leu Leu Arg Ile Gln Ser Ser Lys Gly Phe Asp Val Lys Asp
        35                  40                  45

His Ala Gln Lys Gln Glu Thr Ala Asn Ser Leu Pro Ala Pro Pro Gln
    50                  55                  60
```

```
Met Pro Leu Pro Glu Ile Pro Gln Pro Trp Leu Pro Pro Asp Ser Gly
65                  70                  75                  80

Pro Pro Pro Leu Pro Thr Ser Ser Leu Pro Glu Gly Tyr Tyr Glu Glu
                85                  90                  95

Ala Val Pro Leu Ser Pro Gly Lys Ala Pro Glu Tyr Ile Thr Ser Asn
            100                 105                 110

Tyr Asp Ser Asp Ala Met Ser Ser Ser Tyr Glu Ser Tyr Asp Glu Glu
        115                 120                 125

Glu Glu Asp Gly Lys Gly Lys Lys Thr Arg His Gln Trp Pro Ser Glu
    130                 135                 140

Glu Ala Ser Met Asp Leu Val Lys Asp Ala Lys Ile Cys Ala Phe Leu
145                 150                 155                 160

Leu Arg Lys Lys Arg Phe Gly Gln Trp Thr Lys Leu Leu Cys Val Ile
                165                 170                 175

Lys Asp Thr Lys Leu Leu Cys Tyr Lys Ser Ser Lys Asp Gln Gln Pro
            180                 185                 190

Gln Met Glu Leu Pro Leu Gln Gly Cys Asn Ile Thr Tyr Ile Pro Lys
        195                 200                 205

Asp Ser Lys Lys Lys Lys His Glu Leu Lys Ile Thr Gln Gln Gly Thr
    210                 215                 220

Asp Pro Leu Val Leu Ala Val Gln Ser Lys Glu Gln Ala Glu Gln Trp
225                 230                 235                 240

Leu Lys Val Ile Lys Glu Ala Tyr Ser Gly Cys Ser Gly Pro Val Asp
                245                 250                 255

Ser Glu Cys Pro Pro Pro Pro Ser Ser Pro Val His Lys Ala Glu Leu
            260                 265                 270

Glu Lys Lys Leu Ser Ser Glu Arg Pro Ser Ser Asp Gly Glu Gly Val
        275                 280                 285

Val Glu Asn Gly Ile Thr Thr Cys Asn Gly Lys Glu Gln Val Lys Arg
```

```
    290                 295                 300

Lys Lys Ser Ser Lys Ser Glu Ala Lys Gly Thr Val Ser Lys Val Thr
305                 310                 315                 320

Gly Lys Lys Ile Thr Lys Ile Ile Ser Leu Gly Lys Lys Lys Pro Ser
                325                 330                 335

Thr Asp Glu Gln Thr Ser Ser Ala Glu Glu Asp Val Pro Thr Cys Gly
            340                 345                 350

Tyr Leu Asn Val Leu Ser Asn Ser Arg Trp Arg Glu Arg Trp Cys Arg
        355                 360                 365

Val Lys Asp Asn Lys Leu Ile Phe His Lys Asp Arg Thr Asp Leu Lys
    370                 375                 380

Thr His Ile Val Ser Ile Pro Leu Arg Gly Cys Glu Val Ile Pro Gly
385                 390                 395                 400

Leu Asp Ser Lys His Pro Leu Thr Phe Arg Leu Leu Arg Asn Gly Gln
                405                 410                 415

Glu Val Ala Val Leu Glu Ala Ser Ser Ser Glu Asp Met Gly Arg Trp
            420                 425                 430

Ile Gly Ile Leu Leu Ala Glu Thr Gly Ser Ser Thr Asp Pro Glu Ala
        435                 440                 445

Leu His Tyr Asp Tyr Ile Asp Val Glu Met Ser Ala Ser Val Ile Gln
    450                 455                 460

Thr Ala Lys Gln Thr Phe Cys Phe Met Asn Arg Arg Val Ile Ser Ala
465                 470                 475                 480

Asn Pro Tyr Leu Gly Gly Thr Ser Asn Gly Tyr Ala His Pro Ser Gly
                485                 490                 495

Thr Ala Leu His Tyr Asp Asp Val Pro Cys Ile Asn Gly Ser Leu Lys
            500                 505                 510

Gly Lys Lys Pro Pro Val Ala Ser Asn Gly Val Thr Gly Lys Gly Lys
        515                 520                 525
```

```
Thr Leu Ser Ser Gln Pro Lys Lys Ala Asp Pro Ala Ala Val Val Lys
    530                 535                 540

Arg Thr Gly Ser Asn Ala Ala Gln Tyr Lys Tyr Gly Lys Asn Arg Val
545                 550                 555                 560

Glu Ala Asp Ala Lys Arg Leu Gln Thr Lys Glu Glu Glu Leu Leu Lys
                565                 570                 575

Arg Lys Glu Ala Leu Arg Asn Arg Leu Ala Gln Leu Arg Lys Glu Arg
            580                 585                 590

Lys Asp Leu Arg Ala Ala Ile Glu Val Asn Ala Gly Arg Lys Pro Gln
        595                 600                 605

Ala Ile Leu Glu Glu Lys Leu Lys Gln Leu Glu Glu Glu Cys Arg Gln
    610                 615                 620

Lys Glu Ala Glu Arg Val Ser Leu Glu Leu Glu Leu Thr Glu Val Lys
625                 630                 635                 640

Glu Ser Leu Lys Lys Ala Leu Ala Gly Gly Val Thr Leu Gly Leu Ala
                645                 650                 655

Ile Glu Pro Lys Ser Gly Thr Ser Ser Pro Gln Ser Pro Val Phe Arg
            660                 665                 670

His Arg Thr Leu Glu Asn Ser Pro Ile Ser Ser Cys Asp Thr Ser Asp
        675                 680                 685

Thr Glu Gly Pro Val Pro Val Asn Ser Ala Ala Val Leu Lys Lys Ser
    690                 695                 700

Gln Ala Ala Pro Gly Ser Ser Pro Cys Arg Gly His Val Leu Arg Lys
705                 710                 715                 720

Ala Lys Glu Trp Glu Leu Lys Asn Gly Thr
                725                 730
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<210> 1440
<211> 730
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 423; "

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<221> source
<223> /note="Gene Symbol: AFAP1; "

<220>
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<223> /note="Gene Name:
actin filament associated prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N556; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000353402"

<400> 1440

Met	Glu	Glu	Leu	Ile	Val	Glu	Leu	Arg	Leu	Phe	Leu	Glu	Leu	Leu	Asp
1				5				10						15	
His	Glu	Tyr	Leu	Thr	Ser	Thr	Val	Arg	Glu	Lys	Lys	Ala	Val	Ile	Thr
			20					25					30		
Asn	Ile	Leu	Leu	Arg	Ile	Gln	Ser	Ser	Lys	Gly	Phe	Asp	Val	Lys	Asp
		35					40					45			
His	Ala	Gln	Lys	Gln	Glu	Thr	Ala	Asn	Ser	Leu	Pro	Ala	Pro	Pro	Gln
	50					55					60				
Met	Pro	Leu	Pro	Glu	Ile	Pro	Gln	Pro	Trp	Leu	Pro	Pro	Asp	Ser	Gly
65					70					75					80
Pro	Pro	Pro	Leu	Pro	Thr	Ser	Ser	Leu	Pro	Glu	Gly	Tyr	Tyr	Glu	Glu
				85					90					95	
Ala	Val	Pro	Leu	Ser	Pro	Gly	Lys	Ala	Pro	Glu	Tyr	Ile	Thr	Ser	Asn
			100					105					110		
Tyr	Asp	Ser	Asp	Ala	Met	Ser	Ser	Ser	Tyr	Glu	Ser	Tyr	Asp	Glu	Glu
		115					120					125			
Glu	Glu	Asp	Gly	Lys	Gly	Lys	Lys	Thr	Arg	His	Gln	Trp	Pro	Ser	Glu

```
    130                 135                 140

Glu Ala Ser Met Asp Leu Val Lys Asp Ala Lys Ile Cys Ala Phe Leu
145                 150                 155                 160

Leu Arg Lys Lys Arg Phe Gly Gln Trp Thr Lys Leu Leu Cys Val Ile
                165                 170                 175

Lys Asp Thr Lys Leu Leu Cys Tyr Lys Ser Ser Lys Asp Gln Gln Pro
            180                 185                 190

Gln Met Glu Leu Pro Leu Gln Gly Cys Asn Ile Thr Tyr Ile Pro Lys
        195                 200                 205

Asp Ser Lys Lys Lys Lys His Glu Leu Lys Ile Thr Gln Gln Gly Thr
    210                 215                 220

Asp Pro Leu Val Leu Ala Val Gln Ser Lys Glu Gln Ala Glu Gln Trp
225                 230                 235                 240

Leu Lys Val Ile Lys Glu Ala Tyr Ser Gly Cys Ser Gly Pro Val Asp
                245                 250                 255

Ser Glu Cys Pro Pro Pro Pro Ser Ser Pro Val His Lys Ala Glu Leu
            260                 265                 270

Glu Lys Lys Leu Ser Ser Glu Arg Pro Ser Ser Asp Gly Glu Gly Val
        275                 280                 285

Val Glu Asn Gly Ile Thr Thr Cys Asn Gly Lys Glu Gln Val Lys Arg
    290                 295                 300

Lys Lys Ser Ser Lys Ser Glu Ala Lys Gly Thr Val Ser Lys Val Thr
305                 310                 315                 320

Gly Lys Lys Ile Thr Lys Ile Ile Ser Leu Gly Lys Lys Lys Pro Ser
                325                 330                 335

Thr Asp Glu Gln Thr Ser Ser Ala Glu Glu Asp Val Pro Thr Cys Gly
            340                 345                 350

Tyr Leu Asn Val Leu Ser Asn Ser Arg Trp Arg Glu Arg Trp Cys Arg
        355                 360                 365
```

```
Val Lys Asp Asn Lys Leu Ile Phe His Lys Asp Arg Thr Asp Leu Lys
    370                 375                 380

Thr His Ile Val Ser Ile Pro Leu Arg Gly Cys Glu Val Ile Pro Gly
385                 390                 395                 400

Leu Asp Ser Lys His Pro Leu Thr Phe Arg Leu Leu Arg Asn Gly Gln
                405                 410                 415

Glu Val Ala Val Leu Glu Ala Ser Ser Ser Glu Asp Met Gly Arg Trp
            420                 425                 430

Ile Gly Ile Leu Leu Ala Glu Thr Gly Ser Ser Thr Asp Pro Glu Ala
        435                 440                 445

Leu His Tyr Asp Tyr Ile Asp Val Glu Met Ser Ala Ser Val Ile Gln
    450                 455                 460

Thr Ala Lys Gln Thr Phe Cys Phe Met Asn Arg Arg Val Ile Ser Ala
465                 470                 475                 480

Asn Pro Tyr Leu Gly Gly Thr Ser Asn Gly Tyr Ala His Pro Ser Gly
                485                 490                 495

Thr Ala Leu His Tyr Asp Asp Val Pro Cys Ile Asn Gly Ser Leu Lys
            500                 505                 510

Gly Lys Lys Pro Pro Val Ala Ser Asn Gly Val Thr Gly Lys Gly Lys
        515                 520                 525

Thr Leu Ser Ser Gln Pro Lys Lys Ala Asp Pro Ala Ala Val Val Lys
    530                 535                 540

Arg Thr Gly Ser Asn Ala Ala Gln Tyr Lys Tyr Gly Lys Asn Arg Val
545                 550                 555                 560

Glu Ala Asp Ala Lys Arg Leu Gln Thr Lys Glu Glu Glu Leu Leu Lys
                565                 570                 575

Arg Lys Glu Ala Leu Arg Asn Arg Leu Ala Gln Leu Arg Lys Glu Arg
            580                 585                 590
```

```
Lys Asp Leu Arg Ala Ala Ile Glu Val Asn Ala Gly Arg Lys Pro Gln
        595                 600                 605

Ala Ile Leu Glu Glu Lys Leu Lys Gln Leu Glu Glu Glu Cys Arg Gln
    610                 615                 620

Lys Glu Ala Glu Arg Val Ser Leu Glu Leu Glu Leu Thr Glu Val Lys
625                 630                 635                 640

Glu Ser Leu Lys Lys Ala Leu Ala Gly Gly Val Thr Leu Gly Leu Ala
                645                 650                 655

Ile Glu Pro Lys Ser Gly Thr Ser Ser Pro Gln Ser Pro Val Phe Arg
            660                 665                 670

His Arg Thr Leu Glu Asn Ser Pro Ile Ser Ser Cys Asp Thr Ser Asp
        675                 680                 685

Thr Glu Gly Pro Val Pro Val Asn Ser Ala Ala Val Leu Lys Lys Ser
    690                 695                 700

Gln Ala Ala Pro Gly Ser Ser Pro Cys Arg Gly His Val Leu Arg Lys
705                 710                 715                 720

Ala Lys Glu Trp Glu Leu Lys Asn Gly Thr
                725                 730


<210> 1441
<211> 814
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AFAP1; "

<220>
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<223> /note="Gene Name:
      actin filament associated prt 1; "

<220>
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<223> /note="Uniprot ID: Q8N556; "

<220>
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<223> /note="ENSP ID: ENSP00000371983"

<400> 1441
Met Glu Glu Leu Ile Val Glu Leu Arg Leu Phe Leu Glu Leu Leu Asp
1   5   10   15

His Glu Tyr Leu Thr Ser Thr Val Arg Glu Lys Lys Ala Val Ile Thr
            20   25   30

Asn Ile Leu Leu Arg Ile Gln Ser Ser Lys Gly Phe Asp Val Lys Asp
        35   40   45

His Ala Gln Lys Gln Glu Thr Ala Asn Ser Leu Pro Ala Pro Pro Gln
    50   55   60

Met Pro Leu Pro Glu Ile Pro Gln Pro Trp Leu Pro Pro Asp Ser Gly
65   70   75   80

Pro Pro Pro Leu Pro Thr Ser Ser Leu Pro Glu Gly Tyr Tyr Glu Glu
                85   90   95

Ala Val Pro Leu Ser Pro Gly Lys Ala Pro Glu Tyr Ile Thr Ser Asn
            100   105   110

Tyr Asp Ser Asp Ala Met Ser Ser Ser Tyr Glu Ser Tyr Asp Glu Glu
        115   120   125

Glu Glu Asp Gly Lys Gly Lys Lys Thr Arg His Gln Trp Pro Ser Glu
    130   135   140

Glu Ala Ser Met Asp Leu Val Lys Asp Ala Lys Ile Cys Ala Phe Leu
145   150   155   160

Leu Arg Lys Lys Arg Phe Gly Gln Trp Thr Lys Leu Leu Cys Val Ile
                165   170   175

Lys Asp Thr Lys Leu Leu Cys Tyr Lys Ser Ser Lys Asp Gln Gln Pro
            180   185   190

Gln Met Glu Leu Pro Leu Gln Gly Cys Asn Ile Thr Tyr Ile Pro Lys
        195   200   205

Asp Ser Lys Lys Lys Lys His Glu Leu Lys Ile Thr Gln Gln Gly Thr
210 215 220

Asp Pro Leu Val Leu Ala Val Gln Ser Lys Glu Gln Ala Glu Gln Trp
225 230 235 240

Leu Lys Val Ile Lys Glu Ala Tyr Ser Gly Cys Ser Gly Pro Val Asp
245 250 255

Ser Glu Cys Pro Pro Pro Pro Ser Ser Pro Val His Lys Ala Glu Leu
260 265 270

Glu Lys Lys Leu Ser Ser Glu Arg Pro Ser Ser Asp Gly Glu Gly Val
275 280 285

Val Glu Asn Gly Ile Thr Thr Cys Asn Gly Lys Glu Gln Val Lys Arg
290 295 300

Lys Lys Ser Ser Lys Ser Glu Ala Lys Gly Thr Val Ser Lys Val Thr
305 310 315 320

Gly Lys Lys Ile Thr Lys Ile Ile Ser Leu Gly Lys Lys Lys Pro Ser
325 330 335

Thr Asp Glu Gln Thr Ser Ser Ala Glu Glu Asp Val Pro Thr Cys Gly
340 345 350

Tyr Leu Asn Val Leu Ser Asn Ser Arg Trp Arg Glu Arg Trp Cys Arg
355 360 365

Val Lys Asp Asn Lys Leu Ile Phe His Lys Asp Arg Thr Asp Leu Lys
370 375 380

Thr His Ile Val Ser Ile Pro Leu Arg Gly Cys Glu Val Ile Pro Gly
385 390 395 400

Leu Asp Ser Lys His Pro Leu Thr Phe Arg Leu Leu Arg Asn Gly Gln
405 410 415

Glu Val Ala Val Leu Glu Ala Ser Ser Ser Glu Asp Met Gly Arg Trp
420 425 430

Ile Gly Ile Leu Leu Ala Glu Thr Gly Ser Ser Thr Asp Pro Glu Ala
435 440 445

Leu His Tyr Asp Tyr Ile Asp Val Glu Met Ser Ala Ser Val Ile Gln
450 455 460

Thr Ala Lys Gln Thr Phe Cys Phe Met Asn Arg Arg Val Ile Ser Ala
465 470 475 480

Asn Pro Tyr Leu Gly Gly Thr Ser Asn Gly Tyr Ala His Pro Ser Gly
485 490 495

Thr Ala Leu His Tyr Asp Asp Val Pro Cys Ile Asn Gly Ser Trp Glu
500 505 510

Pro Glu Asp Gly Phe Pro Ala Ser Cys Ser Arg Gly Leu Gly Glu Glu
515 520 525

Val Leu Tyr Asp Asn Ala Gly Leu Tyr Asp Asn Leu Pro Pro Pro His
530 535 540

Ile Phe Ala Arg Tyr Ser Pro Ala Asp Arg Lys Ala Ser Arg Leu Ser
545 550 555 560

Ala Asp Lys Leu Ser Ser Asn His Tyr Lys Tyr Pro Ala Ser Ala Gln
565 570 575

Ser Val Thr Asn Thr Ser Ser Val Gly Arg Ala Ser Leu Gly Leu Asn
580 585 590

Ser Gln Leu Lys Gly Lys Lys Pro Pro Val Ala Ser Asn Gly Val Thr
595 600 605

Gly Lys Gly Lys Thr Leu Ser Ser Gln Pro Lys Lys Ala Asp Pro Ala
610 615 620

Ala Val Val Lys Arg Thr Gly Ser Asn Ala Ala Gln Tyr Lys Tyr Gly
625 630 635 640

Lys Asn Arg Val Glu Ala Asp Ala Lys Arg Leu Gln Thr Lys Glu Glu
645 650 655

```
Glu Leu Leu Lys Arg Lys Glu Ala Leu Arg Asn Arg Leu Ala Gln Leu
            660                 665                 670

Arg Lys Glu Arg Lys Asp Leu Arg Ala Ala Ile Glu Val Asn Ala Gly
        675                 680                 685

Arg Lys Pro Gln Ala Ile Leu Glu Glu Lys Leu Lys Gln Leu Glu Glu
    690                 695                 700

Glu Cys Arg Gln Lys Glu Ala Glu Arg Val Ser Leu Glu Leu Glu Leu
705                 710                 715                 720

Thr Glu Val Lys Glu Ser Leu Lys Lys Ala Leu Ala Gly Gly Val Thr
                725                 730                 735

Leu Gly Leu Ala Ile Glu Pro Lys Ser Gly Thr Ser Ser Pro Gln Ser
            740                 745                 750

Pro Val Phe Arg His Arg Thr Leu Glu Asn Ser Pro Ile Ser Ser Cys
        755                 760                 765

Asp Thr Ser Asp Thr Glu Gly Pro Val Pro Val Asn Ser Ala Ala Val
    770                 775                 780

Leu Lys Lys Ser Gln Ala Ala Pro Gly Ser Ser Pro Cys Arg Gly His
785                 790                 795                 800

Val Leu Arg Lys Ala Lys Glu Trp Glu Leu Lys Asn Gly Thr
                805                 810
```

<210> 1442
<211> 814
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 423; "

<220>
<221> source
<223> /note="Gene Symbol: AFAP1; "

<220>
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<223> /note="Gene Name:
actin filament associated prt 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N556; "

<220>
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<223> /note="ENSP ID: ENSP00000410689"

<400> 1442
Met Glu Glu Leu Ile Val Glu Leu Arg Leu Phe Leu Glu Leu Leu Asp
1   5   10   15

His Glu Tyr Leu Thr Ser Thr Val Arg Glu Lys Lys Ala Val Ile Thr
            20   25   30

Asn Ile Leu Leu Arg Ile Gln Ser Ser Lys Gly Phe Asp Val Lys Asp
        35   40   45

His Ala Gln Lys Gln Glu Thr Ala Asn Ser Leu Pro Ala Pro Pro Gln
    50   55   60

Met Pro Leu Pro Glu Ile Pro Gln Pro Trp Leu Pro Pro Asp Ser Gly
65   70   75   80

Pro Pro Pro Leu Pro Thr Ser Ser Leu Pro Glu Gly Tyr Tyr Glu Glu
                85   90   95

Ala Val Pro Leu Ser Pro Gly Lys Ala Pro Glu Tyr Ile Thr Ser Asn
            100   105   110

Tyr Asp Ser Asp Ala Met Ser Ser Ser Tyr Glu Ser Tyr Asp Glu Glu
        115   120   125

Glu Glu Asp Gly Lys Gly Lys Lys Thr Arg His Gln Trp Pro Ser Glu
    130   135   140

Glu Ala Ser Met Asp Leu Val Lys Asp Ala Lys Ile Cys Ala Phe Leu
145   150   155   160

Leu Arg Lys Lys Arg Phe Gly Gln Trp Thr Lys Leu Leu Cys Val Ile
                165   170   175

Lys Asp Thr Lys Leu Leu Cys Tyr Lys Ser Ser Lys Asp Gln Gln Pro
            180   185   190

```
Gln Met Glu Leu Pro Leu Gln Gly Cys Asn Ile Thr Tyr Ile Pro Lys
        195                 200                 205

Asp Ser Lys Lys Lys Lys His Glu Leu Lys Ile Thr Gln Gln Gly Thr
    210                 215                 220

Asp Pro Leu Val Leu Ala Val Gln Ser Lys Glu Gln Ala Glu Gln Trp
225                 230                 235                 240

Leu Lys Val Ile Lys Glu Ala Tyr Ser Gly Cys Ser Gly Pro Val Asp
                245                 250                 255

Ser Glu Cys Pro Pro Pro Pro Ser Ser Pro Val His Lys Ala Glu Leu
            260                 265                 270

Glu Lys Lys Leu Ser Ser Glu Arg Pro Ser Ser Asp Gly Glu Gly Val
        275                 280                 285

Val Glu Asn Gly Ile Thr Thr Cys Asn Gly Lys Glu Gln Val Lys Arg
    290                 295                 300

Lys Lys Ser Ser Lys Ser Glu Ala Lys Gly Thr Val Ser Lys Val Thr
305                 310                 315                 320

Gly Lys Lys Ile Thr Lys Ile Ile Ser Leu Gly Lys Lys Lys Pro Ser
                325                 330                 335

Thr Asp Glu Gln Thr Ser Ser Ala Glu Glu Asp Val Pro Thr Cys Gly
            340                 345                 350

Tyr Leu Asn Val Leu Ser Asn Ser Arg Trp Arg Glu Arg Trp Cys Arg
        355                 360                 365

Val Lys Asp Asn Lys Leu Ile Phe His Lys Asp Arg Thr Asp Leu Lys
    370                 375                 380

Thr His Ile Val Ser Ile Pro Leu Arg Gly Cys Glu Val Ile Pro Gly
385                 390                 395                 400

Leu Asp Ser Lys His Pro Leu Thr Phe Arg Leu Leu Arg Asn Gly Gln
                405                 410                 415
```

```
Glu Val Ala Val Leu Glu Ala Ser Ser Ser Glu Asp Met Gly Arg Trp
            420                 425                 430

Ile Gly Ile Leu Leu Ala Glu Thr Gly Ser Ser Thr Asp Pro Glu Ala
        435                 440                 445

Leu His Tyr Asp Tyr Ile Asp Val Glu Met Ser Ala Ser Val Ile Gln
    450                 455                 460

Thr Ala Lys Gln Thr Phe Cys Phe Met Asn Arg Arg Val Ile Ser Ala
465                 470                 475                 480

Asn Pro Tyr Leu Gly Gly Thr Ser Asn Gly Tyr Ala His Pro Ser Gly
                485                 490                 495

Thr Ala Leu His Tyr Asp Asp Val Pro Cys Ile Asn Gly Ser Trp Glu
            500                 505                 510

Pro Glu Asp Gly Phe Pro Ala Ser Cys Ser Arg Gly Leu Gly Glu Glu
        515                 520                 525

Val Leu Tyr Asp Asn Ala Gly Leu Tyr Asp Asn Leu Pro Pro Pro His
    530                 535                 540

Ile Phe Ala Arg Tyr Ser Pro Ala Asp Arg Lys Ala Ser Arg Leu Ser
545                 550                 555                 560

Ala Asp Lys Leu Ser Ser Asn His Tyr Lys Tyr Pro Ala Ser Ala Gln
                565                 570                 575

Ser Val Thr Asn Thr Ser Ser Val Gly Arg Ala Ser Leu Gly Leu Asn
            580                 585                 590

Ser Gln Leu Lys Gly Lys Lys Pro Pro Val Ala Ser Asn Gly Val Thr
        595                 600                 605

Gly Lys Gly Lys Thr Leu Ser Ser Gln Pro Lys Lys Ala Asp Pro Ala
    610                 615                 620

Ala Val Val Lys Arg Thr Gly Ser Asn Ala Ala Gln Tyr Lys Tyr Gly
625                 630                 635                 640

Lys Asn Arg Val Glu Ala Asp Ala Lys Arg Leu Gln Thr Lys Glu Glu
```

645 650 655

Glu Leu Leu Lys Arg Lys Glu Ala Leu Arg Asn Arg Leu Ala Gln Leu
660 665 670

Arg Lys Glu Arg Lys Asp Leu Arg Ala Ala Ile Glu Val Asn Ala Gly
675 680 685

Arg Lys Pro Gln Ala Ile Leu Glu Glu Lys Leu Lys Gln Leu Glu Glu
690 695 700

Glu Cys Arg Gln Lys Glu Ala Glu Arg Val Ser Leu Glu Leu Glu Leu
705 710 715 720

Thr Glu Val Lys Glu Ser Leu Lys Lys Ala Leu Ala Gly Gly Val Thr
725 730 735

Leu Gly Leu Ala Ile Glu Pro Lys Ser Gly Thr Ser Ser Pro Gln Ser
740 745 750

Pro Val Phe Arg His Arg Thr Leu Glu Asn Ser Pro Ile Ser Ser Cys
755 760 765

Asp Thr Ser Asp Thr Glu Gly Pro Val Pro Val Asn Ser Ala Ala Val
770 775 780

Leu Lys Lys Ser Gln Ala Ala Pro Gly Ser Ser Pro Cys Arg Gly His
785 790 795 800

Val Leu Arg Lys Ala Lys Glu Trp Glu Leu Lys Asn Gly Thr
805 810

<210> 1443
<211> 92
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>

<221> source
<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000483962"

<400> 1443
Gly Ile Thr Thr Cys Asn Gly Lys Glu Gln Val Lys Arg Lys Lys Ser
1 5 10 15

Ser Lys Ser Glu Ala Lys Gly Thr Val Ser Lys Val Thr Gly Lys Lys
20 25 30

Ile Thr Lys Ile Ile Ser Leu Gly Lys Lys Lys Pro Ser Thr Asp Glu
35 40 45

Gln Thr Ser Ser Ala Glu Glu Asp Val Pro Thr Cys Gly Lys Thr Ala
50 55 60

Leu Pro Gly Asp Glu Gln Arg Ala Pro Lys Trp Val Ser Phe Ser Pro
65 70 75 80

Ala Val Val Ser Val Pro Ser Ser Ser Lys Ala Arg
85 90

<210> 1444
<211> 768
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 424; "

<220>
<221> source
<223> /note="Gene Symbol: AFAP1L1; "

<220>
<221> source
<223> /note="Gene Name:
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1-like
1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TED9; "

<220>
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<223> /note="ENSP ID: ENSP00000296721"

<400> 1444
Met Asp Arg Gly Gln Val Leu Glu Gln Leu Leu Pro Glu Leu Thr Gly
1   5   10   15

Leu Leu Ser Leu Leu Asp His Glu Tyr Leu Ser Asp Thr Thr Leu Glu
            20   25   30

Lys Lys Met Ala Val Ala Ser Ile Leu Gln Ser Leu Gln Pro Leu Pro
        35   40   45

Ala Lys Glu Val Ser Tyr Leu Tyr Val Asn Thr Ala Asp Leu His Ser
    50   55   60

Gly Pro Ser Phe Val Glu Ser Leu Phe Glu Glu Phe Asp Cys Asp Leu
65   70   75   80

Ser Asp Leu Arg Asp Met Pro Glu Asp Asp Gly Glu Pro Ser Lys Gly
                85   90   95

Ala Ser Pro Glu Leu Ala Lys Ser Pro Arg Leu Arg Asn Ala Ala Asp
            100   105   110

Leu Pro Pro Pro Leu Pro Asn Lys Pro Pro Pro Glu Asp Tyr Tyr Glu
        115   120   125

Glu Ala Leu Pro Leu Gly Pro Gly Lys Ser Pro Glu Tyr Ile Ser Ser
    130   135   140

His Asn Gly Cys Ser Pro Ser His Ser Ile Val Asp Gly Tyr Tyr Glu
145   150   155   160

Asp Ala Asp Ser Ser Tyr Pro Ala Thr Arg Val Asn Gly Glu Leu Lys
                165   170   175

Ser Ser Tyr Asn Asp Ser Asp Ala Met Ser Ser Ser Tyr Glu Ser Tyr
            180   185   190

Asp Glu Glu Glu Glu Glu Gly Lys Ser Pro Gln Pro Arg His Gln Trp
        195   200   205

```
Pro Ser Glu Glu Ala Ser Met His Leu Val Arg Glu Cys Arg Ile Cys
    210                 215                 220

Ala Phe Leu Leu Arg Lys Lys Arg Phe Gly Gln Trp Ala Lys Gln Leu
225                 230                 235                 240

Thr Val Ile Arg Glu Asp Gln Leu Leu Cys Tyr Lys Ser Ser Lys Asp
                245                 250                 255

Arg Gln Pro His Leu Arg Leu Ala Leu Asp Thr Cys Ser Ile Ile Tyr
            260                 265                 270

Val Pro Lys Asp Ser Arg His Lys Arg His Glu Leu Arg Phe Thr Gln
        275                 280                 285

Gly Ala Thr Glu Val Leu Val Leu Ala Leu Gln Ser Arg Glu Gln Ala
    290                 295                 300

Glu Glu Trp Leu Lys Val Ile Arg Glu Val Ser Lys Pro Val Gly Gly
305                 310                 315                 320

Ala Glu Gly Val Glu Val Pro Arg Ser Pro Val Leu Leu Cys Lys Leu
                325                 330                 335

Asp Leu Asp Lys Arg Leu Ser Gln Glu Lys Gln Thr Ser Asp Ser Asp
            340                 345                 350

Ser Val Gly Val Gly Asp Asn Cys Ser Thr Leu Gly Arg Arg Glu Thr
        355                 360                 365

Cys Asp His Gly Lys Gly Lys Lys Ser Ser Leu Ala Glu Leu Lys Gly
    370                 375                 380

Ser Met Ser Arg Ala Ala Gly Arg Lys Ile Thr Arg Ile Ile Gly Phe
385                 390                 395                 400

Ser Lys Lys Lys Thr Leu Ala Asp Asp Leu Gln Thr Ser Ser Thr Glu
                405                 410                 415

Glu Glu Val Pro Cys Cys Gly Tyr Leu Asn Val Leu Val Asn Gln Gly
            420                 425                 430

Trp Lys Glu Arg Trp Cys Arg Leu Lys Cys Asn Thr Leu Tyr Phe His
```

435 440 445

Lys Asp His Met Asp Leu Arg Thr His Val Asn Ala Ile Ala Leu Gln
450 455 460

Gly Cys Glu Val Ala Pro Gly Phe Gly Pro Arg His Pro Phe Ala Phe
465 470 475 480

Arg Ile Leu Arg Asn Arg Gln Glu Val Ala Ile Leu Glu Ala Ser Cys
485 490 495

Ser Glu Asp Met Gly Arg Trp Leu Gly Leu Leu Leu Val Glu Met Gly
500 505 510

Ser Arg Val Thr Pro Glu Ala Leu His Tyr Asp Tyr Val Asp Val Glu
515 520 525

Thr Leu Thr Ser Ile Val Ser Ala Gly Arg Asn Ser Phe Leu Tyr Ala
530 535 540

Arg Ser Cys Gln Asn Gln Trp Pro Glu Pro Arg Val Tyr Asp Asp Val
545 550 555 560

Pro Tyr Glu Lys Met Gln Asp Glu Glu Pro Glu Arg Pro Thr Gly Ala
565 570 575

Gln Val Lys Arg His Ala Ser Ser Cys Ser Glu Lys Ser His Arg Val
580 585 590

Asp Pro Gln Val Lys Val Lys Arg His Ala Ser Ser Ala Asn Gln Tyr
595 600 605

Lys Tyr Gly Lys Asn Arg Ala Glu Glu Asp Ala Arg Arg Tyr Leu Val
610 615 620

Glu Lys Glu Lys Leu Glu Lys Glu Lys Glu Thr Ile Arg Thr Glu Leu
625 630 635 640

Ile Ala Leu Arg Gln Glu Lys Arg Glu Leu Lys Glu Ala Ile Arg Ser
645 650 655

Ser Pro Gly Ala Lys Leu Lys Ala Leu Glu Glu Ala Val Ala Thr Leu
660 665 670

```
Glu Ala Gln Cys Arg Ala Lys Glu Glu Arg Arg Ile Asp Leu Glu Leu
        675                 680                 685

Lys Leu Val Ala Val Lys Glu Arg Leu Gln Gln Ser Leu Ala Gly Gly
    690                 695                 700

Pro Ala Leu Gly Leu Ser Val Ser Ser Lys Pro Lys Ser Gly Glu Thr
705                 710                 715                 720

Ala Asn Lys Pro Gln Asn Ser Val Pro Glu Gln Pro Leu Pro Val Asn
                725                 730                 735

Cys Val Ser Glu Leu Arg Lys Arg Ser Pro Ser Ile Val Ala Ser Asn
            740                 745                 750

Gln Gly Arg Val Leu Gln Lys Ala Lys Glu Trp Glu Met Lys Lys Thr
        755                 760                 765


<210> 1445
<211> 725
<212> PRT
<213> Homo sapiens

<220>
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      actin filament associated prt
      1-like
      1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TED9; "

<220>
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<223> /note="ENSP ID: ENSP00000424427"

<400> 1445
Met Asp Arg Gly Gln Val Leu Glu Gln Leu Leu Pro Glu Leu Thr Gly
1               5                   10                  15
```

```
Leu Leu Ser Leu Leu Asp His Glu Tyr Leu Ser Asp Thr Thr Leu Glu
            20                  25                  30

Lys Lys Met Ala Val Ala Ser Ile Leu Gln Ser Leu Gln Pro Leu Pro
        35                  40                  45

Ala Lys Glu Val Ser Tyr Leu Tyr Val Asn Thr Ala Asp Leu His Ser
    50                  55                  60

Gly Pro Ser Phe Val Glu Ser Leu Phe Glu Glu Phe Asp Cys Asp Leu
65                  70                  75                  80

Ser Asp Leu Arg Asp Met Pro Glu Asp Asp Gly Glu Pro Ser Lys Gly
                85                  90                  95

Ala Ser Pro Glu Leu Ala Lys Ser Pro Arg Leu Arg Asn Ala Ala Asp
            100                 105                 110

Leu Pro Pro Pro Leu Pro Asn Lys Pro Pro Pro Glu Asp Tyr Tyr Glu
        115                 120                 125

Glu Ala Leu Pro Leu Gly Pro Gly Lys Ser Pro Glu Tyr Ile Ser Ser
    130                 135                 140

His Asn Gly Cys Ser Pro Ser His Ser Ile Val Asp Gly Tyr Tyr Glu
145                 150                 155                 160

Asp Ala Asp Ser Ser Tyr Pro Ala Thr Arg Val Asn Gly Glu Leu Lys
                165                 170                 175

Ser Ser Tyr Asn Asp Ser Asp Ala Met Ser Ser Ser Tyr Glu Ser Tyr
            180                 185                 190

Asp Glu Glu Glu Glu Glu Gly Lys Ser Pro Gln Pro Arg His Gln Trp
        195                 200                 205

Pro Ser Glu Glu Ala Ser Met His Leu Val Arg Glu Cys Arg Ile Cys
    210                 215                 220

Ala Phe Leu Leu Arg Lys Lys Arg Phe Gly Gln Trp Ala Lys Gln Leu
225                 230                 235                 240
```

```
Thr Val Ile Arg Glu Asp Gln Leu Leu Cys Tyr Lys Ser Ser Lys Asp
                245                 250                 255

Arg Gln Pro His Leu Arg Leu Ala Leu Asp Thr Cys Ser Ile Ile Tyr
            260                 265                 270

Val Pro Lys Asp Ser Arg His Lys Arg His Glu Leu Arg Phe Thr Gln
        275                 280                 285

Gly Ala Thr Glu Val Leu Val Leu Ala Leu Gln Ser Arg Glu Gln Ala
    290                 295                 300

Glu Glu Trp Leu Lys Val Ile Arg Glu Val Ser Lys Pro Val Gly Gly
305                 310                 315                 320

Ala Glu Gly Val Glu Val Pro Arg Ser Pro Val Leu Leu Cys Lys Leu
                325                 330                 335

Asp Leu Asp Lys Arg Leu Ser Gln Glu Lys Gln Thr Ser Asp Ser Asp
            340                 345                 350

Ser Val Gly Val Gly Asp Asn Cys Ser Thr Leu Gly Arg Arg Glu Thr
        355                 360                 365

Cys Asp His Gly Lys Gly Lys Lys Ser Ser Leu Ala Glu Leu Lys Gly
    370                 375                 380

Ser Met Ser Arg Ala Ala Gly Arg Lys Ile Thr Arg Ile Ile Gly Phe
385                 390                 395                 400

Ser Lys Lys Lys Thr Leu Ala Asp Asp Leu Gln Thr Ser Ser Thr Glu
                405                 410                 415

Glu Glu Val Pro Cys Cys Gly Tyr Leu Asn Val Leu Val Asn Gln Gly
            420                 425                 430

Trp Lys Glu Arg Trp Cys Arg Leu Lys Cys Asn Thr Leu Tyr Phe His
        435                 440                 445

Lys Asp His Met Asp Leu Arg Thr His Val Asn Ala Ile Ala Leu Gln
    450                 455                 460
```

```
Gly Cys Glu Val Ala Pro Gly Phe Gly Pro Arg His Pro Phe Ala Phe
465                 470                 475                 480

Arg Ile Leu Arg Asn Arg Gln Glu Val Ala Ile Leu Glu Ala Ser Cys
                485                 490                 495

Ser Glu Asp Met Gly Arg Trp Leu Gly Leu Leu Leu Val Glu Met Gly
            500                 505                 510

Ser Arg Val Thr Pro Glu Ala Leu His Tyr Asp Tyr Val Asp Val Glu
        515                 520                 525

Thr Leu Thr Ser Ile Val Ser Ala Gly Arg Asn Ser Phe Leu Tyr Ala
    530                 535                 540

Arg Ser Cys Gln Asn Gln Trp Pro Glu Pro Arg Val Tyr Asp Asp Val
545                 550                 555                 560

Pro Tyr Glu Lys Met Gln Asp Glu Glu Pro Glu Arg Pro Thr Gly Ala
                565                 570                 575

Gln Val Lys Arg His Ala Ser Ser Cys Ser Glu Lys Ser His Arg Val
            580                 585                 590

Asp Pro Gln Val Lys Val Lys Arg His Ala Ser Ser Ala Asn Gln Tyr
        595                 600                 605

Lys Tyr Gly Lys Asn Arg Ala Glu Glu Asp Ala Arg Arg Tyr Leu Val
    610                 615                 620

Glu Lys Glu Lys Leu Glu Lys Glu Lys Glu Thr Ile Arg Thr Glu Leu
625                 630                 635                 640

Ile Ala Leu Arg Gln Glu Lys Arg Glu Leu Lys Glu Ala Ile Arg Ser
                645                 650                 655

Ser Pro Gly Ala Lys Leu Lys Ala Leu Glu Glu Ala Val Ala Thr Leu
            660                 665                 670

Glu Ala Gln Cys Arg Ala Lys Glu Glu Arg Arg Ile Asp Leu Glu Leu
        675                 680                 685

Lys Leu Val Ala Val Lys Glu Arg Leu Gln Gln Ser Leu Ala Gly Gly
```

690 695 700

Pro Ala Leu Gly Leu Ser Val Ser Ser Lys Pro Lys Ser Gly Glu Trp
705 710 715 720

Glu Met Lys Lys Thr
725

<210> 1446
<211> 818
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 425; "

<220>
<221> source
<223> /note="Gene Symbol: AFAP1L2; "

<220>
<221> source
<223> /note="Gene Name:
actin filament associated prt
1-like 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N4X5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000303042"

<400> 1446
Met Glu Arg Tyr Lys Ala Leu Glu Gln Leu Leu Thr Glu Leu Asp Asp
1 5 10 15

Phe Leu Lys Ile Leu Asp Gln Glu Asn Leu Ser Ser Thr Ala Leu Val
20 25 30

Lys Lys Ser Cys Leu Ala Glu Leu Leu Arg Leu Tyr Thr Lys Ser Ser
35 40 45

Ser Ser Asp Glu Glu Tyr Ile Tyr Met Asn Lys Val Thr Ile Asn Lys
50 55 60

Gln Gln Asn Ala Glu Ser Gln Gly Lys Ala Pro Glu Glu Gln Gly Leu
65 70 75 80

```
Leu Pro Asn Gly Glu Pro Ser Gln His Ser Ser Ala Pro Gln Lys Ser
                85                  90                  95

Leu Pro Asp Leu Pro Pro Pro Lys Met Ile Pro Glu Arg Lys Gln Leu
            100                 105                 110

Ala Ile Pro Lys Thr Glu Ser Pro Glu Gly Tyr Tyr Glu Glu Ala Glu
        115                 120                 125

Pro Tyr Asp Thr Ser Leu Asn Glu Asp Gly Glu Ala Val Ser Ser Ser
    130                 135                 140

Tyr Glu Ser Tyr Asp Glu Glu Asp Gly Ser Lys Gly Lys Ser Ala Pro
145                 150                 155                 160

Tyr Gln Trp Pro Ser Pro Glu Ala Gly Ile Glu Leu Met Arg Asp Ala
                165                 170                 175

Arg Ile Cys Ala Phe Leu Trp Arg Lys Lys Trp Leu Gly Gln Trp Ala
            180                 185                 190

Lys Gln Leu Cys Val Ile Lys Asp Asn Arg Leu Leu Cys Tyr Lys Ser
        195                 200                 205

Ser Lys Asp His Ser Pro Gln Leu Asp Val Asn Leu Leu Gly Ser Ser
    210                 215                 220

Val Ile His Lys Glu Lys Gln Val Arg Lys Lys Glu His Lys Leu Lys
225                 230                 235                 240

Ile Thr Pro Met Asn Ala Asp Val Ile Val Leu Gly Leu Gln Ser Lys
                245                 250                 255

Asp Gln Ala Glu Gln Trp Leu Arg Val Ile Gln Glu Val Ser Gly Leu
            260                 265                 270

Pro Ser Glu Gly Ala Ser Glu Gly Asn Gln Tyr Thr Pro Asp Ala Gln
        275                 280                 285

Arg Phe Asn Cys Gln Lys Pro Asp Ile Ala Glu Lys Tyr Leu Ser Ala
    290                 295                 300
```

Ser Glu Tyr Gly Ser Ser Val Asp Gly His Pro Glu Val Pro Glu Thr
305 310 315 320

Lys Asp Val Lys Lys Lys Cys Ser Ala Gly Leu Lys Leu Ser Asn Leu
325 330 335

Met Asn Leu Gly Arg Lys Lys Ser Thr Ser Leu Glu Pro Val Glu Arg
340 345 350

Ser Leu Glu Thr Ser Ser Tyr Leu Asn Val Leu Val Asn Ser Gln Trp
355 360 365

Lys Ser Arg Trp Cys Ser Val Arg Asp Asn His Leu His Phe Tyr Gln
370 375 380

Asp Arg Asn Arg Ser Lys Val Ala Gln Gln Pro Leu Ser Leu Val Gly
385 390 395 400

Cys Glu Val Val Pro Asp Pro Ser Pro Asp His Leu Tyr Ser Phe Arg
405 410 415

Ile Leu His Lys Gly Glu Glu Leu Ala Lys Leu Glu Ala Lys Ser Ser
420 425 430

Glu Glu Met Gly His Trp Leu Gly Leu Leu Leu Ser Glu Ser Gly Ser
435 440 445

Lys Thr Asp Pro Glu Glu Phe Thr Tyr Asp Tyr Val Asp Ala Asp Arg
450 455 460

Val Ser Cys Ile Val Ser Ala Ala Lys Asn Ser Leu Leu Leu Met Gln
465 470 475 480

Arg Lys Phe Ser Glu Pro Asn Thr Tyr Ile Asp Gly Leu Pro Ser Gln
485 490 495

Asp Arg Gln Glu Glu Leu Tyr Asp Asp Val Asp Leu Ser Glu Leu Thr
500 505 510

Ala Ala Val Glu Pro Thr Glu Glu Ala Thr Pro Val Ala Asp Asp Pro
515 520 525

```
Asn Glu Arg Glu Ser Asp Arg Val Tyr Leu Asp Leu Thr Pro Val Lys
    530                 535                 540

Ser Phe Leu His Gly Pro Ser Ser Ala Gln Ala Gln Ala Ser Ser Pro
545                 550                 555                 560

Thr Leu Ser Cys Leu Asp Asn Ala Thr Glu Ala Leu Pro Ala Asp Ser
                565                 570                 575

Gly Pro Gly Pro Thr Pro Asp Glu Pro Cys Ile Lys Cys Pro Glu Asn
            580                 585                 590

Leu Gly Glu Gln Gln Leu Glu Ser Leu Glu Pro Glu Asp Pro Ser Leu
        595                 600                 605

Arg Ile Thr Thr Val Lys Ile Gln Thr Glu Gln Gln Arg Ile Ser Phe
    610                 615                 620

Pro Pro Ser Cys Pro Asp Ala Val Val Ala Thr Pro Pro Gly Ala Ser
625                 630                 635                 640

Pro Pro Val Lys Asp Arg Leu Arg Val Thr Ser Ala Glu Ile Lys Leu
                645                 650                 655

Gly Lys Asn Arg Thr Glu Ala Glu Val Lys Arg Tyr Thr Glu Glu Lys
            660                 665                 670

Glu Arg Leu Glu Lys Lys Lys Glu Glu Ile Arg Gly His Leu Ala Gln
        675                 680                 685

Leu Arg Lys Glu Lys Arg Glu Leu Lys Glu Thr Leu Leu Lys Cys Thr
    690                 695                 700

Asp Lys Glu Val Leu Ala Ser Leu Glu Gln Lys Leu Lys Glu Ile Asp
705                 710                 715                 720

Glu Glu Cys Arg Gly Glu Glu Ser Arg Arg Val Asp Leu Glu Leu Ser
                725                 730                 735

Ile Met Glu Val Lys Asp Asn Leu Lys Lys Ala Glu Ala Gly Pro Val
            740                 745                 750

Thr Leu Gly Thr Thr Val Asp Thr Thr His Leu Glu Asn Val Ser Pro
```

```
        755                 760                 765

Arg Pro Lys Ala Val Thr Pro Ala Ser Ala Pro Asp Cys Thr Pro Val
    770                 775                 780

Asn Ser Ala Thr Thr Leu Lys Asn Arg Pro Leu Ser Val Val Val Thr
785                 790                 795                 800

Gly Lys Gly Thr Val Leu Gln Lys Ala Lys Glu Trp Glu Lys Lys Gly
                805                 810                 815

Ala Ser
```

<210> 1447
<211> 814
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 425; "

<220>
<221> source
<223> /note="Gene Symbol: AFAP1L2; "

<220>
<221> source
<223> /note="Gene Name:
actin filament associated prt
1-like 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N4X5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358276"

<400> 1447

```
Met Glu Arg Tyr Lys Ala Leu Glu Gln Leu Leu Thr Glu Leu Asp Asp
1               5                  10                  15

Phe Leu Lys Ile Leu Asp Gln Glu Asn Leu Ser Ser Thr Ala Leu Val
            20                  25                  30

Lys Lys Ser Cys Leu Ala Glu Leu Leu Arg Leu Tyr Thr Lys Ser Ser
        35                  40                  45
```

```
Ser Ser Asp Glu Glu Tyr Ile Tyr Met Asn Lys Val Thr Ile Asn Lys
    50                  55                  60

Gln Gln Asn Ala Glu Ser Gln Gly Lys Ala Pro Glu Glu Gln Gly Leu
65                  70                  75                  80

Leu Pro Asn Gly Glu Pro Ser Gln His Ser Ser Ala Pro Gln Lys Ser
                85                  90                  95

Leu Pro Asp Leu Pro Pro Pro Lys Met Ile Pro Glu Arg Lys Gln Leu
            100                 105                 110

Ala Ile Pro Lys Thr Glu Ser Pro Glu Gly Tyr Tyr Glu Glu Ala Glu
        115                 120                 125

Pro Tyr Asp Thr Ser Leu Asn Glu Asp Gly Glu Ala Val Ser Ser Ser
    130                 135                 140

Tyr Glu Ser Tyr Asp Glu Glu Asp Gly Ser Lys Gly Lys Ser Ala Pro
145                 150                 155                 160

Tyr Gln Trp Pro Ser Pro Glu Ala Gly Ile Glu Leu Met Arg Asp Ala
                165                 170                 175

Arg Ile Cys Ala Phe Leu Trp Arg Lys Lys Trp Leu Gly Gln Trp Ala
            180                 185                 190

Lys Gln Leu Cys Val Ile Lys Asp Asn Arg Leu Leu Cys Tyr Lys Ser
        195                 200                 205

Ser Lys Asp His Ser Pro Gln Leu Asp Val Asn Leu Leu Gly Ser Ser
    210                 215                 220

Val Ile His Lys Glu Lys Gln Val Arg Lys Lys Glu His Lys Leu Lys
225                 230                 235                 240

Ile Thr Pro Met Asn Ala Asp Val Ile Val Leu Gly Leu Gln Ser Lys
                245                 250                 255

Asp Gln Ala Glu Gln Trp Leu Arg Val Ile Gln Glu Val Ser Gly Leu
            260                 265                 270
```

```
Pro Ser Glu Gly Ala Ser Glu Gly Asn Gln Tyr Thr Pro Asp Ala Gln
        275                 280                 285

Arg Phe Asn Cys Gln Lys Pro Asp Ile Ala Glu Lys Tyr Leu Ser Ala
    290                 295                 300

Ser Glu Tyr Gly Ser Ser Val Asp Gly His Pro Glu Val Pro Glu Thr
305                 310                 315                 320

Lys Asp Val Lys Lys Lys Cys Ser Ala Gly Leu Lys Leu Ser Asn Leu
                325                 330                 335

Met Asn Leu Gly Arg Lys Lys Ser Thr Ser Leu Glu Pro Val Glu Arg
            340                 345                 350

Ser Leu Glu Thr Ser Ser Tyr Leu Asn Val Leu Val Asn Ser Gln Trp
        355                 360                 365

Lys Ser Arg Trp Cys Ser Val Arg Asp Asn His Leu His Phe Tyr Gln
    370                 375                 380

Asp Arg Asn Arg Ser Lys Val Ala Gln Gln Pro Leu Ser Leu Val Gly
385                 390                 395                 400

Cys Glu Val Val Pro Asp Pro Ser Pro Asp His Leu Tyr Ser Phe Arg
                405                 410                 415

Ile Leu His Lys Gly Glu Glu Leu Ala Lys Leu Glu Ala Lys Ser Ser
            420                 425                 430

Glu Glu Met Gly His Trp Leu Gly Leu Leu Leu Ser Glu Ser Gly Ser
        435                 440                 445

Lys Thr Asp Pro Glu Glu Phe Thr Tyr Asp Tyr Val Asp Ala Asp Arg
    450                 455                 460

Val Ser Cys Ile Val Ser Ala Ala Lys Asn Ser Leu Leu Leu Met Gln
465                 470                 475                 480

Arg Lys Phe Ser Glu Pro Asn Thr Tyr Ile Asp Gly Leu Pro Ser Gln
                485                 490                 495
```

```
Asp Arg Gln Glu Glu Leu Tyr Asp Asp Val Asp Leu Ser Glu Leu Thr
            500                 505                 510

Ala Ala Val Glu Pro Thr Glu Glu Ala Thr Pro Val Ala Asp Asp Pro
        515                 520                 525

Asn Glu Arg Glu Ser Asp Arg Val Tyr Leu Asp Leu Thr Pro Val Lys
    530                 535                 540

Ser Phe Leu His Gly Pro Ser Ser Ala Gln Ala Gln Ala Ser Ser Pro
545                 550                 555                 560

Thr Leu Ser Cys Leu Asp Asn Ala Thr Glu Ala Leu Pro Ala Asp Ser
                565                 570                 575

Gly Pro Gly Pro Thr Pro Asp Glu Pro Cys Ile Lys Cys Pro Glu Asn
            580                 585                 590

Leu Gly Glu Gln Gln Leu Glu Ser Leu Glu Pro Glu Asp Pro Ser Leu
        595                 600                 605

Arg Ile Thr Thr Val Lys Ile Gln Thr Glu Gln Gln Arg Ile Ser Phe
    610                 615                 620

Pro Pro Ser Cys Pro Asp Ala Val Val Ala Thr Pro Pro Gly Ala Ser
625                 630                 635                 640

Pro Pro Val Lys Asp Arg Leu Arg Val Thr Ser Ala Glu Ile Lys Leu
                645                 650                 655

Gly Lys Asn Arg Thr Glu Ala Glu Val Lys Arg Tyr Thr Glu Glu Lys
            660                 665                 670

Glu Arg Leu Glu Lys Lys Lys Glu Glu Ile Arg Gly His Leu Ala Gln
        675                 680                 685

Leu Arg Lys Glu Lys Arg Glu Leu Lys Glu Thr Leu Leu Lys Cys Thr
    690                 695                 700

Asp Lys Glu Val Leu Ala Ser Leu Glu Gln Lys Leu Lys Glu Ile Asp
705                 710                 715                 720

Glu Glu Cys Arg Gly Glu Glu Ser Arg Arg Val Asp Leu Glu Leu Ser
```

725 730 735

Ile Met Glu Val Lys Asp Asn Leu Lys Lys Ala Glu Ala Gly Pro Val
740 745 750

Thr Leu Gly Thr Thr Val Asp Thr Thr His Leu Glu Asn Pro Lys Ala
755 760 765

Val Thr Pro Ala Ser Ala Pro Asp Cys Thr Pro Val Asn Ser Ala Thr
770 775 780

Thr Leu Lys Asn Arg Pro Leu Ser Val Val Val Thr Gly Lys Gly Thr
785 790 795 800

Val Leu Gln Lys Ala Lys Glu Trp Glu Lys Lys Gly Ala Ser
805 810

<210> 1448
<211> 312
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 425; "

<220>
<221> source
<223> /note="Gene Symbol: AFAP1L2; "

<220>
<221> source
<223> /note="Gene Name:
actin filament associated prt
1-like 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396781"

<400> 1448
Met Glu Arg Tyr Lys Ala Gln Gly Cys Cys Cys Leu Val Val Gln Arg
1 5 10 15

Arg Ile Arg Gln Val Ser Ala Ser Leu Glu Gln Leu Leu Thr Glu Leu
20 25 30

Asp Asp Phe Leu Lys Ile Leu Asp Gln Glu Asn Leu Ser Ser Thr Ala
35 40 45

```
Leu Val Lys Lys Ser Cys Leu Ala Glu Leu Leu Arg Leu Tyr Thr Lys
    50                  55                  60

Ser Ser Ser Ser Asp Glu Glu Tyr Ile Tyr Met Asn Lys Val Thr Ile
65                  70                  75                  80

Asn Lys Gln Gln Asn Ala Glu Ser Gln Gly Lys Ala Pro Glu Glu Gln
                85                  90                  95

Gly Leu Leu Pro Asn Gly Glu Pro Ser Gln His Ser Ser Ala Pro Gln
            100                 105                 110

Lys Ser Leu Pro Asp Leu Pro Pro Pro Lys Met Ile Pro Glu Arg Lys
        115                 120                 125

Gln Leu Ala Ile Pro Lys Thr Glu Ser Pro Glu Gly Tyr Tyr Glu Glu
    130                 135                 140

Ala Glu Pro Tyr Asp Thr Ser Leu Asn Glu Asp Gly Glu Ala Val Ser
145                 150                 155                 160

Ser Ser Tyr Glu Ser Tyr Asp Glu Glu Asp Gly Ser Lys Gly Lys Ser
                165                 170                 175

Ala Pro Tyr Gln Trp Pro Ser Pro Glu Ala Gly Ile Glu Leu Met Arg
            180                 185                 190

Asp Ala Arg Ile Cys Ala Phe Leu Trp Arg Lys Lys Trp Leu Gly Gln
        195                 200                 205

Trp Ala Lys Gln Leu Cys Val Ile Lys Asp Asn Arg Leu Leu Cys Tyr
    210                 215                 220

Lys Ser Ser Lys Asp His Ser Pro Gln Leu Asp Val Asn Leu Leu Gly
225                 230                 235                 240

Ser Ser Val Ile His Lys Glu Lys Gln Val Arg Lys Lys Glu His Lys
                245                 250                 255

Leu Lys Ile Thr Pro Met Asn Ala Asp Val Ile Val Leu Gly Leu Gln
            260                 265                 270
```

Ser Lys Asp Gln Ala Glu Gln Trp Leu Arg Val Ile Gln Glu Val Ser
        275   280   285

Gly Leu Pro Ser Glu Gly Ala Ser Glu Gly Asn Gln Tyr Thr Pro Asp
    290   295   300

Ala Gln Arg Phe Asn Cys Gln Lys
305   310

<210> 1449
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "

<220>
<221> source
<223> /note="Uniprot ID: P63261; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000331514"

<400> 1449
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp

65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
85 90 95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
100 105 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
115 120 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
130 135 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145 150 155 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
165 170 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
180 185 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
195 200 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
210 215 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225 230 235 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
245 250 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
260 265 270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
275 280 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
290 295 300

```
Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320


Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335


Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350


Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365


Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1450
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P63261; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458162"

<400> 1450
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1               5                   10                  15


Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20                  25                  30
```

```
Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35                  40                  45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50                  55                  60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65                  70                  75                  80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85                  90                  95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100                 105                 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115                 120                 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130                 135                 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145                 150                 155                 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165                 170                 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180                 185                 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195                 200                 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
    210                 215                 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225                 230                 235                 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
                245                 250                 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
```

```
            260                 265                 270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
        275                 280                 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
    290                 295                 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365

Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1451
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P63261; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458435"
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<400> 1451
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
20 25 30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
35 40 45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
85 90 95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
100 105 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
115 120 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
130 135 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145 150 155 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
165 170 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
180 185 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
195 200 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
210 215 220

```
Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225                 230                 235                 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
                245                 250                 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
            260                 265                 270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
        275                 280                 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
    290                 295                 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365

Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1452
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000459119"

<400> 1452
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65   70   75   80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85   90   95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100   105   110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115   120   125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130   135   140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145   150   155   160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165   170   175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180   185   190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195   200   205

Val Arg Asp Ile Lys Glu
    210

<210> 1453
<211> 375
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 426; "

<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID: P63261; "

<220>
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<400> 1453
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65   70   75   80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85   90   95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro

```
            100                 105                 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115                 120                 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130                 135                 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145                 150                 155                 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165                 170                 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180                 185                 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195                 200                 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
    210                 215                 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225                 230                 235                 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
                245                 250                 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
            260                 265                 270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
        275                 280                 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
    290                 295                 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335
```

```
Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365

Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1454
<211> 214
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460464"

<400> 1454
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1               5                   10                  15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20                  25                  30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35                  40                  45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50                  55                  60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65                  70                  75                  80
```

```
Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85                  90                  95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100                 105                 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115                 120                 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130                 135                 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145                 150                 155                 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165                 170                 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180                 185                 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195                 200                 205

Val Arg Asp Ile Lys Glu
    210


<210> 1455
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
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<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "

<220>
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<223> /note="ENSP ID: ENSP00000460660"
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<400> 1455
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65   70   75   80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85   90   95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100   105   110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115   120   125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130   135   140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145   150   155   160

His Thr Val Pro

<210> 1456
<211> 241
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
actin gamma 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461407"

<400> 1456

```
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1               5                  10                  15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20                  25                  30

Ser Ile Val Gly Arg Pro Arg His Gln Asp Ser Tyr Val Gly Asp Glu
        35                  40                  45

Ala Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His
    50                  55                  60

Gly Ile Val Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr
65                  70                  75                  80

Phe Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu
                85                  90                  95

Thr Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln
            100                 105                 110

Ile Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln
        115                 120                 125

Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Met
    130                 135                 140

Asp Ser Gly Asp Gly Val Thr His Thr Val Pro Ile Tyr Glu Gly Tyr
145                 150                 155                 160

Ala Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu
                165                 170                 175

Thr Asp Tyr Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr
```

```
            180                 185                 190

Thr Thr Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys
        195                 200                 205

Tyr Val Ala Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser Ser
    210                 215                 220

Ser Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr
225                 230                 235                 240

Ile
```

<210> 1457
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
actin gamma 1; "

<220>
<221> source
<223> /note="Uniprot ID: P63261; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461672"

<400> 1457

```
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1               5                   10                  15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20                  25                  30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35                  40                  45
```

```
Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50                  55                  60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65                  70                  75                  80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85                  90                  95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100                 105                 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115                 120                 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130                 135                 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145                 150                 155                 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165                 170                 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180                 185                 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195                 200                 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
    210                 215                 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225                 230                 235                 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
                245                 250                 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
            260                 265                 270
```

```
Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
        275                 280                 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
    290                 295                 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365

Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1458
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
      actin gamma 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462823"

<400> 1458
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1               5                   10                  15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20                  25                  30
```

```
Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35                  40                  45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50                  55                  60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65                  70                  75                  80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85                  90                  95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100                 105                 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ala Leu Phe Leu Ser Arg His
        115                 120                 125

Phe Leu Pro Glu Ala Ser Arg Leu Cys Leu Arg Pro Ser Thr Pro Arg
    130                 135                 140

Pro Cys Thr Trp Pro Ser Arg Pro Cys Cys Pro Ser Thr Pro Leu Gly
145                 150                 155                 160

Ala Pro Leu Ala Leu Ser Trp Thr Leu Glu Thr Gly Ser Pro Thr Arg
                165                 170                 175

Cys Pro Ser Thr Arg Ala Thr Pro Ser Pro Thr Pro Ser Cys Val Trp
            180                 185                 190

Thr Trp Leu Ala Gly Thr
        195


<210> 1459
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
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<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
actin gamma 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466346"

<400> 1459
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
20 25 30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
35 40 45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
85 90 95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
100 105 110

Lys Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val
115 120 125

Met Asp Ser Gly Asp
130

<210> 1460
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 426; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG1; "

<220>
<221> source
<223> /note="Gene Name:
actin gamma 1; "

<220>
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<223> /note="Uniprot ID: P63261; "

<220>
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<223> /note="ENSP ID: ENSP00000477968"

<400> 1460
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65   70   75   80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85   90   95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100   105   110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115   120   125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130   135   140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145   150   155   160

```
His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165                 170                 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180                 185                 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195                 200                 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
    210                 215                 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225                 230                 235                 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
                245                 250                 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
            260                 265                 270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
        275                 280                 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
    290                 295                 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365

Ile Val His Arg Lys Cys Phe
    370                 375
```

<210> 1461
<211> 370
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 427; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1A; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1A, 41kDa; "

<220>
<221> source
<223> /note="Uniprot ID: Q92747; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000262942"

<400> 1461

```
Met Ser Leu His Gln Phe Leu Leu Glu Pro Ile Thr Cys His Ala Trp
1               5                  10                  15

Asn Arg Asp Arg Thr Gln Ile Ala Leu Ser Pro Asn Asn His Glu Val
            20                  25                  30

His Ile Tyr Lys Lys Asn Gly Ser Gln Trp Val Lys Ala His Glu Leu
        35                  40                  45

Lys Glu His Asn Gly His Ile Thr Gly Ile Asp Trp Ala Pro Lys Ser
    50                  55                  60

Asp Arg Ile Val Thr Cys Gly Ala Asp Arg Asn Ala Tyr Val Trp Ser
65                  70                  75                  80

Gln Lys Asp Gly Val Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85                  90                  95

Arg Ala Ala Thr Phe Val Lys Trp Ser Pro Leu Glu Asn Lys Phe Ala
            100                 105                 110
```

```
Val Gly Ser Gly Ala Arg Leu Ile Ser Val Cys Tyr Phe Glu Ser Glu
        115                 120                 125

Asn Asp Trp Trp Val Ser Lys His Ile Lys Lys Pro Ile Arg Ser Thr
    130                 135                 140

Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
145                 150                 155                 160

Ser Cys Asp Phe Lys Cys Arg Val Phe Ser Ala Tyr Ile Lys Glu Val
                165                 170                 175

Asp Glu Lys Pro Ala Ser Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
            180                 185                 190

Gln Leu Met Ser Glu Phe Gly Gly Ser Gly Thr Gly Gly Trp Val His
        195                 200                 205

Gly Val Ser Phe Ser Ala Ser Gly Ser Arg Leu Ala Trp Val Ser His
    210                 215                 220

Asp Ser Thr Val Ser Val Ala Asp Ala Ser Lys Ser Val Gln Val Ser
225                 230                 235                 240

Thr Leu Lys Thr Glu Phe Leu Pro Leu Leu Ser Val Ser Phe Val Ser
                245                 250                 255

Glu Asn Ser Val Val Ala Ala Gly His Asp Cys Cys Pro Met Leu Phe
            260                 265                 270

Asn Tyr Asp Asp Arg Gly Cys Leu Thr Phe Val Ser Lys Leu Asp Ile
        275                 280                 285

Pro Lys Gln Ser Ile Gln Arg Asn Met Ser Ala Met Glu Arg Phe Arg
    290                 295                 300

Asn Met Asp Lys Arg Ala Thr Thr Glu Asp Arg Asn Thr Ala Leu Glu
305                 310                 315                 320

Thr Leu His Gln Asn Ser Ile Thr Gln Val Ser Ile Tyr Glu Val Asp
                325                 330                 335

Lys Gln Asp Cys Arg Lys Phe Cys Thr Thr Gly Ile Asp Gly Ala Met
```

340 345 350

Thr Ile Trp Asp Phe Lys Thr Leu Glu Ser Ser Ile Gln Gly Leu Arg
355 360 365

Ile Met
370

<210> 1462
<211> 279
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 427; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1A; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1A, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408711"

<400> 1462
Met Ser Leu His Gln Phe Leu Leu Glu Pro Ile Thr Cys His Ala Trp
1 5 10 15

Asn Arg Asp Arg Thr Gln Ile Ala Leu Ser Pro Asn Asn His Glu Val
20 25 30

His Ile Tyr Lys Lys Asn Gly Ser Gln Trp Val Lys Ala His Glu Leu
35 40 45

Lys Glu His Asn Gly His Ile Thr Gly Ile Asp Trp Ala Pro Lys Ser
50 55 60

Asp Arg Ile Val Thr Cys Gly Ala Asp Arg Asn Ala Tyr Val Trp Ser
65 70 75 80

Gln Lys Asp Gly Val Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn

```
                85                  90                  95

Arg Ala Ala Thr Phe Val Lys Trp Ser Pro Leu Glu Asn Lys Phe Ala
            100                 105                 110

Val Gly Ser Gly Ala Arg Leu Ile Ser Val Cys Tyr Phe Glu Ser Glu
        115                 120                 125

Asn Asp Trp Trp Val Ser Lys His Ile Lys Lys Pro Ile Arg Ser Thr
    130                 135                 140

Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
145                 150                 155                 160

Ser Cys Asp Phe Lys Cys Arg Val Phe Ser Ala Tyr Ile Lys Glu Val
                165                 170                 175

Asp Glu Lys Pro Ala Ser Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
            180                 185                 190

Gln Leu Met Ser Glu Phe Gly Gly Ser Gly Thr Gly Gly Trp Val His
        195                 200                 205

Gly Val Ser Phe Ser Ala Ser Gly Ser Arg Leu Ala Trp Val Ser His
    210                 215                 220

Asp Ser Thr Val Ser Val Ala Asp Ala Ser Lys Ser Val Gln Val Ser
225                 230                 235                 240

Thr Leu Lys Thr Glu Phe Leu Pro Leu Leu Ser Val Ser Phe Val Ser
                245                 250                 255

Glu Asn Ser Ser Cys Phe Arg Ala Met Thr Ala Ala Gln Cys Ser Leu
            260                 265                 270

Thr Thr Met Thr Ala Ala Ala
        275
```

<210> 1463
<211> 53
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 427; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1A; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1A, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412879"

<400> 1463
Met Ser Leu His Gln Phe Leu Leu Glu Pro Ile Thr Cys His Ala Trp
1 5 10 15

Asn Arg Asp Arg Thr Arg Pro Val Cys Leu Asp Tyr Tyr Ser Leu Val
20 25 30

Arg Leu Pro Ser Val Pro Ile Ile Thr Lys Cys Thr Ser Ile Arg Arg
35 40 45

Thr Gly Ala Ser Gly
50

<210> 1464
<211> 372
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source

<223> /note="Uniprot ID: O15143; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000252725"

<400> 1464
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1   5   10   15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
            20   25   30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35   40   45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50   55   60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65   70   75   80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85   90   95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
            100   105   110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
        115   120   125

Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
    130   135   140

Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
145   150   155   160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
                165   170   175

Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
            180   185   190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
        195   200   205

```
Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
    210                 215                 220

Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
225                 230                 235                 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
                245                 250                 255

Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
            260                 265                 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
        275                 280                 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
    290                 295                 300

Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
305                 310                 315                 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
                325                 330                 335

Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
            340                 345                 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
        355                 360                 365

Leu Lys Ile Lys
    370
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<210> 1465
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source

<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388802"

<400> 1465
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
50 55 60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
85 90 95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
115 120 125

Asn Asp Trp Trp
130

<210> 1466
<211> 372
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="Uniprot ID: O15143; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389631"

<400> 1466

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Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1               5                  10                  15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
            20                  25                  30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35                  40                  45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50                  55                  60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65                  70                  75                  80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85                  90                  95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
            100                 105                 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
        115                 120                 125

Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
    130                 135                 140
```

```
Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
145                 150                 155                 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
                165                 170                 175

Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
            180                 185                 190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
        195                 200                 205

Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
    210                 215                 220

Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
225                 230                 235                 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
                245                 250                 255

Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
            260                 265                 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
        275                 280                 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
    290                 295                 300

Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
305                 310                 315                 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
                325                 330                 335

Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
            340                 345                 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
        355                 360                 365
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Leu Lys Ile Lys
370

<210> 1467
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398110"

<400> 1467
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
50 55 60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
85 90 95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
115 120 125

Asn Asp Trp Trp
130

<210> 1468
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398620"

<400> 1468
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
50 55 60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
85 90 95

```
Arg Ala Ala Arg Cys Val
            100


<210> 1469
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399955"

<400> 1469
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1               5                  10                  15


Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
            20                  25                  30


His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35                  40                  45


Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50                  55                  60


Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65                  70                  75                  80


Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85                  90                  95


Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
            100                 105                 110
```

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
115 120 125

Asn Asp
130

<210> 1470
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403211"

<400> 1470
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
50 55 60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
85 90 95

```
Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
            100                 105                 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
        115                 120                 125

Asn Asp Trp Trp
    130


<210> 1471
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403324"

<400> 1471
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1               5                   10                  15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
            20                  25                  30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35                  40                  45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50                  55                  60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65                  70                  75                  80
```

```
Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85                  90                  95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
            100                 105                 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
        115                 120                 125

Asn Asp
    130
```

<210> 1472
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408508"

<400> 1472

```
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1               5                   10                  15

Asn Lys Asp Arg Thr Arg Gln Pro Val Pro Gly Glu Asp Arg Val Ala
            20                  25                  30
```

<210> 1473
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408758"

<400> 1473
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

Asn Lys Asp Arg Thr
20

<210> 1474
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410238"

<400> 1474
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
20 25 30

```
His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35                  40                  45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50                  55                  60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65                  70                  75                  80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85                  90                  95

Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
            100                 105                 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
        115                 120                 125


<210> 1475
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413067"

<400> 1475
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1               5                   10                  15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
            20                  25                  30
```

```
His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35                  40                  45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50                  55                  60

Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65                  70                  75                  80

Leu Lys
```

<210> 1476
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 428; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC1B; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 1B, 41kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413173"

<400> 1476

```
Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1               5                   10                  15

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
            20                  25                  30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
        35                  40                  45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
    50                  55                  60
```

```
Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
65                  70                  75                  80


Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
                85                  90                  95


Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu
            100                 105


<210> 1477
<211> 300
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 429; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC2; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 2, 34kDa; "

<220>
<221> source
<223> /note="Uniprot ID:  O15144; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000295685"

<400> 1477
Met Ile Leu Leu Glu Val Asn Asn Arg Ile Ile Glu Glu Thr Leu Ala
1               5                   10                  15


Leu Lys Phe Glu Asn Ala Ala Ala Gly Asn Lys Pro Glu Ala Val Glu
            20                  25                  30


Val Thr Phe Ala Asp Phe Asp Gly Val Leu Tyr His Ile Ser Asn Pro
        35                  40                  45


Asn Gly Asp Lys Thr Lys Val Met Val Ser Ile Ser Leu Lys Phe Tyr
    50                  55                  60
```

```
Lys Glu Leu Gln Ala His Gly Ala Asp Glu Leu Leu Lys Arg Val Tyr
65                  70                  75                  80

Gly Ser Phe Leu Val Asn Pro Glu Ser Gly Tyr Asn Val Ser Leu Leu
                85                  90                  95

Tyr Asp Leu Glu Asn Leu Pro Ala Ser Lys Asp Ser Ile Val His Gln
            100                 105                 110

Ala Gly Met Leu Lys Arg Asn Cys Phe Ala Ser Val Phe Glu Lys Tyr
        115                 120                 125

Phe Gln Phe Gln Glu Glu Gly Lys Glu Gly Glu Asn Arg Ala Val Ile
    130                 135                 140

His Tyr Arg Asp Asp Glu Thr Met Tyr Val Glu Ser Lys Lys Asp Arg
145                 150                 155                 160

Val Thr Val Val Phe Ser Thr Val Phe Lys Asp Asp Asp Asp Val Val
                165                 170                 175

Ile Gly Lys Val Phe Met Gln Glu Phe Lys Glu Gly Arg Arg Ala Ser
            180                 185                 190

His Thr Ala Pro Gln Val Leu Phe Ser His Arg Glu Pro Pro Leu Glu
        195                 200                 205

Leu Lys Asp Thr Asp Ala Ala Val Gly Asp Asn Ile Gly Tyr Ile Thr
    210                 215                 220

Phe Val Leu Phe Pro Arg His Thr Asn Ala Ser Ala Arg Asp Asn Thr
225                 230                 235                 240

Ile Asn Leu Ile His Thr Phe Arg Asp Tyr Leu His Tyr His Ile Lys
                245                 250                 255

Cys Ser Lys Ala Tyr Ile His Thr Arg Met Arg Ala Lys Thr Ser Asp
            260                 265                 270

Phe Leu Lys Val Leu Asn Arg Ala Arg Pro Asp Ala Glu Lys Lys Glu
        275                 280                 285
```

```
Met Lys Thr Ile Thr Gly Lys Thr Phe Ser Ser Arg
    290                 295                 300


<210> 1478
<211> 300
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 429; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC2; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 2, 34kDa; "

<220>
<221> source
<223> /note="Uniprot ID:  O15144; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000327137"

<400> 1478
Met Ile Leu Leu Glu Val Asn Asn Arg Ile Ile Glu Glu Thr Leu Ala
1               5                  10                  15


Leu Lys Phe Glu Asn Ala Ala Ala Gly Asn Lys Pro Glu Ala Val Glu
            20                  25                  30


Val Thr Phe Ala Asp Phe Asp Gly Val Leu Tyr His Ile Ser Asn Pro
        35                  40                  45


Asn Gly Asp Lys Thr Lys Val Met Val Ser Ile Ser Leu Lys Phe Tyr
    50                  55                  60


Lys Glu Leu Gln Ala His Gly Ala Asp Glu Leu Leu Lys Arg Val Tyr
65                  70                  75                  80


Gly Ser Phe Leu Val Asn Pro Glu Ser Gly Tyr Asn Val Ser Leu Leu
                85                  90                  95
```

```
Tyr Asp Leu Glu Asn Leu Pro Ala Ser Lys Asp Ser Ile Val His Gln
            100                 105                 110

Ala Gly Met Leu Lys Arg Asn Cys Phe Ala Ser Val Phe Glu Lys Tyr
        115                 120                 125

Phe Gln Phe Gln Glu Glu Gly Lys Glu Gly Glu Asn Arg Ala Val Ile
    130                 135                 140

His Tyr Arg Asp Asp Glu Thr Met Tyr Val Glu Ser Lys Lys Asp Arg
145                 150                 155                 160

Val Thr Val Val Phe Ser Thr Val Phe Lys Asp Asp Asp Asp Val Val
                165                 170                 175

Ile Gly Lys Val Phe Met Gln Glu Phe Lys Glu Gly Arg Arg Ala Ser
            180                 185                 190

His Thr Ala Pro Gln Val Leu Phe Ser His Arg Glu Pro Pro Leu Glu
        195                 200                 205

Leu Lys Asp Thr Asp Ala Ala Val Gly Asp Asn Ile Gly Tyr Ile Thr
    210                 215                 220

Phe Val Leu Phe Pro Arg His Thr Asn Ala Ser Ala Arg Asp Asn Thr
225                 230                 235                 240

Ile Asn Leu Ile His Thr Phe Arg Asp Tyr Leu His Tyr His Ile Lys
                245                 250                 255

Cys Ser Lys Ala Tyr Ile His Thr Arg Met Arg Ala Lys Thr Ser Asp
            260                 265                 270

Phe Leu Lys Val Leu Asn Arg Ala Arg Pro Asp Ala Glu Lys Lys Glu
        275                 280                 285

Met Lys Thr Ile Thr Gly Lys Thr Phe Ser Ser Arg
    290                 295                 300
```

<210> 1479
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 429; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC2; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 2, 34kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396475"

<400> 1479
Met Ile Leu Leu Glu Val Asn Asn Arg Ile Ile Glu Glu Thr Leu Ala
1 5 10 15

Leu Lys Phe Glu Asn Ala Ala Ala Gly Asn Lys Pro Glu Ala Val Glu
20 25 30

Val Thr Phe Ala Asp Phe Asp Gly Val Leu Tyr His Ile Ser Asn Pro
35 40 45

Asn Gly Asp Lys Thr Lys Val Met Val Ser Ile Ser Leu Lys Phe Tyr
50 55 60

Lys Glu Leu Gln Ala His Gly Ala Asp Glu Leu Leu Lys Arg Val Tyr
65 70 75 80

Gly Ser Phe Leu Val Asn Pro Glu Ser Val Phe
85 90

<210> 1480
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 429; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC2; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 2, 34kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401070"

<400> 1480
Met Ile Leu Leu Glu Val Asn Asn Arg Ile Ile Glu Glu Thr Leu Ala
1 5 10 15

Leu Lys Phe Glu Asn Ala Ala Ala Gly Asn Lys Pro Glu Ala Val Glu
20 25 30

Val Thr Phe Ala Asp Phe Asp Gly Val Leu Tyr His Ile Ser Asn Pro
35 40 45

Asn Gly Asp Lys Thr Lys Val Met Val Ser Ile Ser Leu Lys Phe Tyr
50 55 60

Lys Glu Leu Gln Ala His Gly Ala Asp Glu Leu Leu Lys Arg Val Tyr
65 70 75 80

Gly Ser Phe Leu Val Asn Pro Glu Ser
85

<210> 1481
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 429; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC2; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 2, 34kDa; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000411612"

<400> 1481
Lys Glu Gly Arg Arg Ala Ser His Thr Ala Pro Gln Val Leu Phe Ser
1   5   10   15

His Arg Glu Pro Pro Leu Glu Leu Lys Asp Thr Asp Ala Ala Val Gly
            20   25   30

Asp Asn Ile Gly Tyr Ile Thr Phe Val Leu Phe Pro Arg His Thr Asn
        35   40   45

Ala Ser Ala Arg Asp Asn Thr Ile Asn Leu Ile His Thr Phe Arg Asp
    50   55   60

Tyr Leu His Tyr His Ile Lys Cys Ser Lys Ala Tyr Ile His Thr Arg
65   70   75   80

Met Arg Ala Lys Thr Ser Asp Phe Leu Lys Val Leu Asn Arg Ala Arg
                85   90   95

Pro Asp Ala Glu Lys Lys Glu Met Lys Thr Ile Thr Phe Ser Leu Ala
            100   105   110

Glu Leu Gly Pro Arg Lys Glu Lys Gln Glu Thr Asn Ser Cys Ile His
        115   120   125

Pro Glu Asn Gln Ile Met Leu Leu Met Gly Glu Asp Val Phe Ile Pro
    130   135   140

Leu Ile Leu Gly Ile Arg Gly Gly Ser Gly Trp Gln Leu Lys Ala Gly
145   150   155   160

Thr Leu Ala Thr Gly
                165

<210> 1482
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 429; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC2; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 2, 34kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412632"

<400> 1482
Met Ile Leu Leu Glu Val Asn Asn Arg Ile Ile Glu Glu Thr Leu Ala
1 5 10 15

Leu Lys Phe Glu Asn Ala Ala Ala Gly Asn Lys Pro Glu Ala Val Glu
20 25 30

Val Thr Phe Ala Gly Glu
35

<210> 1483
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 430; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC3; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 3, 21kDa; "

<220>
<221> source
<223> /note="Uniprot ID: O15145; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000228825"

<400> 1483

```
Met Pro Ala Tyr His Ser Ser Leu Met Asp Pro Asp Thr Lys Leu Ile
1               5                  10                  15

Gly Asn Met Ala Leu Leu Pro Ile Arg Ser Gln Phe Lys Gly Pro Ala
            20                  25                  30

Pro Arg Glu Thr Lys Asp Thr Asp Ile Val Asp Glu Ala Ile Tyr Tyr
        35                  40                  45

Phe Lys Ala Asn Val Phe Phe Lys Asn Tyr Glu Ile Lys Asn Glu Ala
    50                  55                  60

Asp Arg Thr Leu Ile Tyr Ile Thr Leu Tyr Ile Ser Glu Cys Leu Lys
65                  70                  75                  80

Lys Leu Gln Lys Cys Asn Ser Lys Ser Gln Gly Glu Lys Glu Met Tyr
                85                  90                  95

Thr Leu Gly Ile Thr Asn Phe Pro Ile Pro Gly Glu Pro Gly Phe Pro
            100                 105                 110

Leu Asn Ala Ile Tyr Ala Lys Pro Ala Asn Lys Gln Glu Asp Glu Val
        115                 120                 125

Met Arg Ala Tyr Leu Gln Gln Leu Arg Gln Glu Thr Gly Leu Arg Leu
    130                 135                 140

Cys Glu Lys Val Phe Asp Pro Gln Asn Asp Lys Pro Ser Lys Trp Trp
145                 150                 155                 160

Thr Cys Phe Val Lys Arg Gln Phe Met Asn Lys Ser Leu Ser Gly Pro
                165                 170                 175

Gly Gln
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<210> 1484
<211> 99
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 430; "

<220>
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<220>
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<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 3, 21kDa; "

<220>
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<223> /note="ENSP ID: ENSP00000413221"

<400> 1484
Met Pro Ala Tyr His Ser Ser Leu Met Asp Pro Asp Thr Lys Leu Ile
1 5 10 15

Gly Asn Met Ala Leu Leu Pro Ile Arg Ser Gln Phe Lys Gly Pro Ala
20 25 30

Pro Arg Glu Thr Lys Asp Thr Asp Ile Val Asp Glu Ala Ile Tyr Tyr
35 40 45

Phe Lys Ala Asn Val Phe Phe Lys Asn Tyr Glu Ile Lys Asn Glu Ala
50 55 60

Asp Arg Thr Leu Ile Tyr Ile Thr Leu Tyr Ile Ser Glu Cys Leu Lys
65 70 75 80

Lys Leu Gln Lys Cys Asn Ser Lys Ser Gln Glu Val Met Arg Ala Tyr
85 90 95

Leu Gln Gln

<210> 1485
<211> 84
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ARPC3; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 3, 21kDa; "

<220>
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<223> /note="ENSP ID: ENSP00000446598"

<400> 1485
Met Asp Pro Asp Thr Lys Leu Ile Gly Asn Met Ala Leu Leu Pro Ile
1 5 10 15

Arg Ser Gln Phe Lys Gly Pro Ala Pro Arg Glu Thr Lys Asp Thr Asp
20 25 30

Ile Val Asp Glu Ala Ile Tyr Tyr Phe Lys Ala Asn Val Phe Phe Lys
35 40 45

Asn Tyr Glu Ile Lys Asn Glu Ala Asp Arg Thr Leu Ile Tyr Ile Thr
50 55 60

Leu Tyr Ile Ser Glu Cys Leu Lys Lys Leu Gln Lys Cys Asn Ser Lys
65 70 75 80

Ser Gln Gly Glu

<210> 1486
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 431; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC4; "

<220>
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<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 4, 20kDa; "

<220>

<221> source
<223> /note="Uniprot ID: P59998; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000380431"

<400> 1486
Met Thr Ala Thr Leu Arg Pro Tyr Leu Ser Ala Val Arg Ala Thr Leu
1   5   10   15

Gln Ala Ala Leu Cys Leu Glu Asn Phe Ser Ser Gln Val Val Glu Arg
            20   25   30

His Asn Lys Pro Glu Val Glu Val Arg Ser Ser Lys Glu Leu Leu Leu
        35   40   45

Gln Pro Val Thr Ile Ser Arg Asn Glu Lys Glu Lys Val Leu Ile Glu
    50   55   60

Gly Ser Ile Asn Ser Val Arg Val Ser Ile Ala Val Lys Gln Ala Asp
65   70   75   80

Glu Ile Glu Lys Ile Leu Cys His Lys Phe Met Arg Phe Met Met Met
                85   90   95

Arg Ala Glu Asn Phe Phe Ile Leu Arg Arg Lys Pro Val Glu Gly Tyr
            100   105   110

Asp Ile Ser Phe Leu Ile Thr Asn Phe His Thr Glu Gln Met Tyr Lys
        115   120   125

His Lys Leu Val Asp Phe Val Ile His Phe Met Glu Glu Ile Asp Lys
    130   135   140

Glu Ile Ser Glu Met Lys Leu Ser Val Asn Ala Arg Ala Arg Ile Val
145   150   155   160

Ala Glu Glu Phe Leu Lys Asn Phe
                165

<210> 1487
<211> 187
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 4, 20kDa; "

<220>
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<223> /note="Uniprot ID: P59998; "

<220>
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<400> 1487

```
Met Val Arg Glu Pro Gly Pro Arg Pro Gly Thr Pro Gly Cys Ser Ala
1               5                  10                  15

Ser Gly Gln Trp Thr Ala Thr Leu Arg Pro Tyr Leu Ser Ala Val Arg
            20                  25                  30

Ala Thr Leu Gln Ala Ala Leu Cys Leu Glu Asn Phe Ser Ser Gln Val
        35                  40                  45

Val Glu Arg His Asn Lys Pro Glu Val Glu Val Arg Ser Ser Lys Glu
    50                  55                  60

Leu Leu Leu Gln Pro Val Thr Ile Ser Arg Asn Glu Lys Glu Lys Val
65                  70                  75                  80

Leu Ile Glu Gly Ser Ile Asn Ser Val Arg Val Ser Ile Ala Val Lys
                85                  90                  95

Gln Ala Asp Glu Ile Glu Lys Ile Leu Cys His Lys Phe Met Arg Phe
            100                 105                 110

Met Met Met Arg Ala Glu Asn Phe Phe Ile Leu Arg Arg Lys Pro Val
        115                 120                 125

Glu Gly Tyr Asp Ile Ser Phe Leu Ile Thr Asn Phe His Thr Glu Gln
```

```
    130                 135                 140

Met Tyr Lys His Lys Leu Val Asp Phe Val Ile His Phe Met Glu Glu
145                 150                 155                 160

Ile Asp Lys Glu Ile Ser Glu Met Lys Leu Ser Val Asn Ala Arg Ala
                165                 170                 175

Arg Ile Val Ala Glu Glu Phe Leu Lys Asn Phe
            180                 185


<210> 1488
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 431; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC4; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 4, 20kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000395085"

<400> 1488
Met Thr Ala Thr Leu Arg Pro Tyr Leu Ser Ala Val Arg Ala Thr Leu
1               5                   10                  15

Gln Ala Ala Leu Cys Leu Glu Asn Phe Ser Ser Gln Val Val Glu Arg
            20                  25                  30

His Asn Lys Pro Glu Val Glu Val Arg Ser Ser Lys Glu Leu Leu Leu
        35                  40                  45

Gln Pro Val Thr Ile Ser Arg Asn Glu Lys Glu Lys Val Leu Ile Glu
    50                  55                  60

Gly Ser Ile Asn Ser Val Arg Val Ser Ile Ala Val Lys Gln Ala Asp
```

65 70 75 80

Glu Ile Glu Lys Ile Leu Cys His Lys Phe Met Arg Phe Met Met Met
85 90 95

Arg Ala Glu Asn Phe Phe Ile Leu Arg Arg Lys Pro Val Glu Ile Ile
100 105 110

Leu

<210> 1489
<211> 44
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 431; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC4; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 4, 20kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414751"

<400> 1489
Met Thr Ala Thr Leu Arg Pro Tyr Leu Ser Ala Val Arg Ala Thr Leu
1 5 10 15

Gln Ala Ala Leu Cys Leu Glu Asn Phe Ser Ser Gln Val Val Glu Arg
20 25 30

His Asn Lys Pro Glu Val Glu Val Ser Pro Arg Gln
35 40

<210> 1490
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 431; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC4; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 4, 20kDa; "

<220>
<221> source
<223> /note="Uniprot ID: P59998; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432235"

<400> 1490
Met Arg Phe Met Met Met Arg Ala Glu Asn Phe Phe Ile Leu Arg Arg
1   5   10   15

Lys Pro Val Glu Gly Tyr Asp Ile Ser Phe Leu Ile Thr Asn Phe His
            20   25   30

Thr Glu Gln Met Tyr Lys His Lys Leu Val Asp Phe Val Ile His Phe
        35   40   45

Met Glu Glu Ile Asp Lys Glu Ile Ser Glu Met Lys Leu Ser Val Asn
    50   55   60

Ala Arg Ala Arg Ile Val Ala Glu Glu Phe Leu Lys Asn Phe
65   70   75

<210> 1491
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 431; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC4; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 4, 20kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000473435"

<400> 1491
Met Arg Phe Met Met Met Arg Ala Glu Asn Phe Phe Ile Leu Arg Arg
1 5 10 15

Lys Pro Val Glu Gly Tyr Asp Ile Ser Phe Leu Ile Thr Asn Phe His
20 25 30

Thr Glu Gln Met Tyr Lys His Lys Leu Val Asp Phe Val Ile His Phe
35 40 45

Met Glu Glu Ile Asp Lys Glu Ile Ser Glu Met Lys Leu Ser Val Asn
50 55 60

Ala Arg Ala Arg Ile Val Ala Glu Glu Phe Leu Lys Asn
65 70 75

<210> 1492
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 432; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC5; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 5, 16kDa; "

<220>
<221> source
<223> /note="Uniprot ID: O15511; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000294742"

<400> 1492
Met Ser Lys Asn Thr Val Ser Ser Ala Arg Phe Arg Lys Val Asp Val
1   5   10   15

Asp Glu Tyr Asp Glu Asn Lys Phe Val Asp Glu Glu Asp Gly Gly Asp
            20   25   30

Gly Gln Ala Gly Pro Asp Glu Gly Glu Val Asp Ser Cys Leu Arg His
        35   40   45

Ser Ile Thr Gly Asn Met Thr Ala Ala Leu Gln Ala Ala Leu Lys Asn
    50   55   60

Pro Pro Ile Asn Thr Lys Ser Gln Ala Val Lys Asp Arg Ala Gly Ser
65   70   75   80

Ile Val Leu Lys Val Leu Ile Ser Phe Lys Ala Asn Asp Ile Glu Lys
                85   90   95

Ala Val Gln Ser Leu Asp Lys Asn Gly Val Asp Leu Leu Met Lys Tyr
            100   105   110

Ile Tyr Lys Gly Phe Glu Ser Pro Ser Asp Asn Ser Ser Ala Met Leu
        115   120   125

Leu Gln Trp His Glu Lys Ala Leu Ala Ala Gly Gly Val Gly Ser Ile
    130   135   140

Val Arg Val Leu Thr Ala Arg Lys Thr Val
145   150

<210> 1493
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 432; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC5; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 5, 16kDa; "

<220>
<221> source
<223> /note="Uniprot ID: O15511; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000352918"

<400> 1493

Met	Ser	Lys	Asn	Thr	Val	Ser	Ser	Ala	Arg	Phe	Arg	Lys	Val	Asp	Val
1				5				10					15		
Asp	Glu	Tyr	Asp	Glu	Asn	Lys	Phe	Val	Asp	Glu	Glu	Asp	Gly	Gly	Asp
			20				25					30			
Gly	Gln	Ala	Gly	Pro	Asp	Glu	Gly	Glu	Val	Asp	Ser	Cys	Leu	Arg	Gln
		35				40					45				
Gly	Asn	Met	Thr	Ala	Ala	Leu	Gln	Ala	Ala	Leu	Lys	Asn	Pro	Pro	Ile
	50				55					60					
Asn	Thr	Lys	Ser	Gln	Ala	Val	Lys	Asp	Arg	Ala	Gly	Ser	Ile	Val	Leu
65				70					75					80	
Lys	Val	Leu	Ile	Ser	Phe	Lys	Ala	Asn	Asp	Ile	Glu	Lys	Ala	Val	Gln
			85					90					95		
Ser	Leu	Asp	Lys	Asn	Gly	Val	Asp	Leu	Leu	Met	Lys	Tyr	Ile	Tyr	Lys
		100					105					110			
Gly	Phe	Glu	Ser	Pro	Ser	Asp	Asn	Ser	Ser	Ala	Met	Leu	Leu	Gln	Trp
	115					120					125				
His	Glu	Lys	Ala	Leu	Ala	Ala	Gly	Gly	Val	Gly	Ser	Ile	Val	Arg	Val
	130				135					140					
Leu	Thr	Ala	Arg	Lys	Thr	Val									
145				150											

<210> 1494

<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 432; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC5; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 5, 16kDa; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356504"

<400> 1494

Met	Ser	Lys	Asn	Thr	Val	Ser	Ser	Ala	Arg	Phe	Arg	Lys	Val	Asp	Val
1				5				10					15		

Asp	Glu	Tyr	Asp	Glu	Asn	Lys	Phe	Val	Asp	Glu	Glu	Asp	Gly	Gly	Asp
			20					25					30		

Gly	Gln	Ala	Gly	Pro	Asp	Glu	Gly	Glu	Val	Asp	Ser	Cys	Leu	Arg	Gln
		35					40					45			

Gly	Asn	Met	Thr	Ala	Ala	Leu	Gln	Ala	Ala	Leu	Lys	Asn	Pro	Pro	Ile
	50					55					60				

Asn	Thr	Lys	Ser	Gln	Ala	Val	Lys	Asp	Arg	Ala	Gly	Ser	Ile	Val	Leu
65				70					75					80	

Lys	Val	Leu	Ile	Ser	Phe	Lys	Ala	Asn	Asp	Ile	Glu	Lys	Ala	Val	Gln
				85					90					95	

Ser	Leu	Asp	Lys	Asn	Gly	Val	Asp	Leu	Leu	Met	Lys	Tyr	Ile	Tyr	Lys
			100					105					110		

Gly	Phe	Glu	Ser	Pro	Ser	Asp	Asn	Ser	Ser	Ala	Met	Leu	Leu	Gln	Trp
		115					120					125			

His	Glu	Lys	Val	Pro	Leu	Val

130 135

<210> 1495
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 433; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC5L; "

<220>
<221> source
<223> /note="Gene Name:
actin related prt 2/3
complex,
subunit 5-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BPX5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000259477"

<400> 1495
Met Ala Arg Asn Thr Leu Ser Ser Arg Phe Arg Arg Val Asp Ile Asp
1 5 10 15

Glu Phe Asp Glu Asn Lys Phe Val Asp Glu Gln Glu Glu Ala Ala Ala
20 25 30

Ala Ala Ala Glu Pro Gly Pro Asp Pro Ser Glu Val Asp Gly Leu Leu
35 40 45

Arg Gln Gly Asp Met Leu Arg Ala Phe His Ala Ala Leu Arg Asn Ser
50 55 60

Pro Val Asn Thr Lys Asn Gln Ala Val Lys Glu Arg Ala Gln Gly Val
65 70 75 80

Val Leu Lys Val Leu Thr Asn Phe Lys Ser Ser Glu Ile Glu Gln Ala
85 90 95

Val Gln Ser Leu Asp Arg Asn Gly Val Asp Leu Leu Met Lys Tyr Ile

```
            100                 105                 110

Tyr Lys Gly Phe Glu Lys Pro Thr Glu Asn Ser Ser Ala Val Leu Leu
        115                 120                 125

Gln Trp His Glu Lys Ala Leu Ala Val Gly Gly Leu Gly Ser Ile Ile
    130                 135                 140

Arg Val Leu Thr Ala Arg Lys Thr Val
145                 150


<210> 1496
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 433; "

<220>
<221> source
<223> /note="Gene Symbol: ARPC5L; "

<220>
<221> source
<223> /note="Gene Name:
      actin related prt 2/3
      complex,
      subunit 5-like; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9BPX5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000345361"

<400> 1496
Met Ala Arg Asn Thr Leu Ser Ser Arg Phe Arg Arg Val Asp Ile Asp
1               5                   10                  15

Glu Phe Asp Glu Asn Lys Phe Val Asp Glu Gln Glu Glu Ala Ala Ala
            20                  25                  30

Ala Ala Ala Glu Pro Gly Pro Asp Pro Ser Glu Val Asp Gly Leu Leu
        35                  40                  45

Arg Gln Gly Asp Met Leu Arg Ala Phe His Ala Ala Leu Arg Asn Ser
```

```
    50                  55                  60

Pro Val Asn Thr Lys Asn Gln Ala Val Lys Glu Arg Ala Gln Gly Val
65                  70                  75                  80

Val Leu Lys Val Leu Thr Asn Phe Lys Ser Ser Glu Ile Glu Gln Ala
                85                  90                  95

Val Gln Ser Leu Asp Arg Asn Gly Val Asp Leu Leu Met Lys Tyr Ile
            100                 105                 110

Tyr Lys Gly Phe Glu Lys Pro Thr Glu Asn Ser Ser Ala Val Leu Leu
        115                 120                 125

Gln Trp His Glu Lys Ala Leu Ala Val Gly Gly Leu Gly Ser Ile Ile
    130                 135                 140

Arg Val Leu Thr Ala Arg Lys Thr Val
145                 150


<210> 1497
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 434; "

<220>
<221> source
<223> /note="Gene Symbol: ACTA1; "

<220>
<221> source
<223> /note="Gene Name:
      actin, alpha 1, skeletal muscle; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355644"

<400> 1497
Met Cys Asp Glu Asp Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser
1               5                   10                  15

Gly Leu Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20                  25                  30
```

```
Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35                  40                  45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50                  55                  60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65                  70                  75                  80

Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu
                85                  90                  95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100                 105                 110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115                 120                 125

Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130                 135                 140

Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly
145                 150                 155                 160

Ile Met Lys Cys Asp Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn
                165                 170                 175

Val Met Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met
            180                 185                 190

Gln Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile
        195                 200                 205

Ile Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile
    210                 215                 220

Leu Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Thr Lys Gln Glu
225                 230                 235                 240

Tyr Asp Glu Ala Gly Pro Ser Ile Val His Arg Lys Cys Phe
                245                 250
```

<210> 1498
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 434; "

<220>
<221> source
<223> /note="Gene Symbol: ACTA1; "

<220>
<221> source
<223> /note="Gene Name:
actin, alpha 1, skeletal muscle; "

<220>
<221> source
<223> /note="Uniprot ID: P68133; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355645"

<400> 1498
Met Cys Asp Glu Asp Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser
1   5   10   15

Gly Leu Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20   25   30

Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35   40   45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50   55   60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65   70   75   80

Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu
                85   90   95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100   105   110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115   120   125

```
Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130                 135                 140

Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly
145                 150                 155                 160

Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala
                165                 170                 175

Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met
            180                 185                 190

Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg
        195                 200                 205

Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp
    210                 215                 220

Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys
225                 230                 235                 240

Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg
                245                 250                 255

Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu
            260                 265                 270

Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp
        275                 280                 285

Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Met Ser Gly Gly
    290                 295                 300

Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr
305                 310                 315                 320

Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu
                325                 330                 335

Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser
            340                 345                 350
```

```
Thr Phe Gln Gln Met Trp Ile Thr Lys Gln Glu Tyr Asp Glu Ala Gly
        355                 360                 365


Pro Ser Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1499
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 435; "

<220>
<221> source
<223> /note="Gene Symbol: ACTA2; "

<220>
<221> source
<223> /note="Gene Name:
      actin, alpha 2, smooth muscle, aorta; "

<220>
<221> source
<223> /note="Uniprot ID:  P62736; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000224784"

<400> 1499
Met Cys Glu Glu Glu Asp Ser Thr Ala Leu Val Cys Asp Asn Gly Ser
1               5                   10                  15


Gly Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20                  25                  30


Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35                  40                  45


Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50                  55                  60


Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65                  70                  75                  80


Trp Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu
```

```
                85                  90                  95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100                 105                 110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115                 120                 125

Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130                 135                 140

Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly
145                 150                 155                 160

Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala
                165                 170                 175

Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met
            180                 185                 190

Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg
        195                 200                 205

Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp
    210                 215                 220

Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys
225                 230                 235                 240

Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg
                245                 250                 255

Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu
            260                 265                 270

Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp
        275                 280                 285

Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly
    290                 295                 300

Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr
305                 310                 315                 320
```

```
Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu
                325                 330                 335

Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser
            340                 345                 350

Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly
        355                 360                 365

Pro Ser Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1500
<211> 151
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 435; "

<220>
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<223> /note="Gene Symbol: ACTA2; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
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<400> 1500
Met Cys Glu Glu Glu Asp Ser Thr Ala Leu Val Cys Asp Asn Gly Ser
1               5                   10                  15

Gly Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20                  25                  30

Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35                  40                  45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50                  55                  60
```

```
Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65                  70                  75                  80


Trp Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu
                85                  90                  95


Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100                 105                 110


Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115                 120                 125


Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130                 135                 140


Tyr Ala Ser Gly Arg Thr Thr
145                 150


<210> 1501
<211> 151
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACTA2; "

<220>
<221> source
<223> /note="Gene Name:
      actin, alpha 2, smooth muscle, aorta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398239"

<400> 1501
Met Cys Glu Glu Glu Asp Ser Thr Ala Leu Val Cys Asp Asn Gly Ser
1               5                   10                  15


Gly Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20                  25                  30


Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35                  40                  45
```

```
Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50                  55                  60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65                  70                  75                  80

Trp Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu
                85                  90                  95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100                 105                 110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115                 120                 125

Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130                 135                 140

Tyr Ala Ser Gly Arg Thr Thr
145                 150
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<210> 1502
<211> 377
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACTA2; "

<220>
<221> source
<223> /note="Gene Name:
actin, alpha 2, smooth muscle, aorta; "

<220>
<221> source
<223> /note="Uniprot ID: P62736; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402373"

<400> 1502

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Met Cys Glu Glu Glu Asp Ser Thr Ala Leu Val Cys Asp Asn Gly Ser
1               5                  10                  15

Gly Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20                  25                  30

Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35                  40                  45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50                  55                  60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65                  70                  75                  80

Trp Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu
                85                  90                  95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100                 105                 110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115                 120                 125

Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130                 135                 140

Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly
145                 150                 155                 160

Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala
                165                 170                 175

Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met
            180                 185                 190

Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg
        195                 200                 205

Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp
    210                 215                 220

Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys
```

```
225                 230                 235                 240

Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg
                245                 250                 255

Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu
            260                 265                 270

Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp
        275                 280                 285

Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly
    290                 295                 300

Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr
305                 310                 315                 320

Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu
                325                 330                 335

Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser
            340                 345                 350

Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly
        355                 360                 365

Pro Ser Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1503
<211> 377
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 436; "

<220>
<221> source
<223> /note="Gene Symbol: ACTC1; "

<220>
<221> source
<223> /note="Gene Name:
      actin, alpha, cardiac muscle 1; "
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<220>
<221> source
<223> /note="Uniprot ID: P68032; "

<220>
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<223> /note="ENSP ID: ENSP00000290378"

<400> 1503
Met Cys Asp Asp Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser
1   5   10   15

Gly Leu Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
            20   25   30

Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly
        35   40   45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
    50   55   60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn
65   70   75   80

Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu
                85   90   95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu
            100   105   110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
        115   120   125

Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
    130   135   140

Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly
145   150   155   160

Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala
                165   170   175

Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met
            180   185   190

```
Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg
        195                 200                 205

Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp
    210                 215                 220

Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys
225                 230                 235                 240

Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg
                245                 250                 255

Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu
            260                 265                 270

Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp
        275                 280                 285

Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly
    290                 295                 300

Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr
305                 310                 315                 320

Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu
                325                 330                 335

Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser
            340                 345                 350

Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly
        355                 360                 365

Pro Ser Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1504
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 437; "
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<220>
<221> source
<223> /note="Gene Symbol: ACTB; "

<220>
<221> source
<223> /note="Gene Name:
actin, beta; "

<220>
<221> source
<223> /note="Uniprot ID: P60709; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000349960"

<400> 1504
Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65   70   75   80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85   90   95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100   105   110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115   120   125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130   135   140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145   150   155   160

```
His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
                165                 170                 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
            180                 185                 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
        195                 200                 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
    210                 215                 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225                 230                 235                 240

Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
                245                 250                 255

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
            260                 265                 270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
        275                 280                 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
    290                 295                 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
305                 310                 315                 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
                325                 330                 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
            340                 345                 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
        355                 360                 365

Ile Val His Arg Lys Cys Phe
    370                 375
```

<210> 1505
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 437; "

<220>
<221> source
<223> /note="Gene Symbol: ACTB; "

<220>
<221> source
<223> /note="Gene Name:
actin, beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393951"

<400> 1505
Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
20 25 30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
35 40 45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
85 90 95

Ala Pro Glu Glu His Pro
100

<210> 1506
<211> 99
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 437; "

<220>
<221> source
<223> /note="Gene Symbol: ACTB; "

<220>
<221> source
<223> /note="Gene Name:
actin, beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399487"

<400> 1506
Met Leu Thr Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly
1 5 10 15

Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala
20 25 30

Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val
35 40 45

Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys
50 55 60

Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr
65 70 75 80

Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu
85 90 95

Leu Arg Val

<210> 1507
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 437; "

<220>
<221> source
<223> /note="Gene Symbol: ACTB; "

<220>
<221> source
<223> /note="Gene Name:
actin, beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401032"

<400> 1507
Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
20 25 30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
35 40 45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65 70 75 80

<210> 1508
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 437; "

<220>
<221> source
<223> /note="Gene Symbol: ACTB; "

<220>
<221> source
<223> /note="Gene Name:
actin, beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000407473"

<400> 1508
Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
1 5 10 15

```
Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20                  25                  30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35                  40                  45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50                  55                  60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65                  70                  75                  80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85                  90                  95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100                 105                 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
        115                 120                 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
    130                 135                 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145                 150                 155                 160

His Thr Val
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<210> 1509
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 437; "

<220>
<221> source
<223> /note="Gene Symbol: ACTB; "

<220>
<221> source
<223> /note="Gene Name:

actin, beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000409264"

<400> 1509
Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
1   5   10   15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
            20   25   30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
        35   40   45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
    50   55   60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65   70   75   80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
                85   90   95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
            100   105   110

Lys Ala Asn Arg Glu Lys Met Thr Gln Asp Ser Leu Leu
        115   120   125

<210> 1510
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 438; "

<220>
<221> source
<223> /note="Gene Symbol: ACTBL2; "

<220>
<221> source
<223> /note="Gene Name:
actin, beta-like 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q562R1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416706"

<400> 1510
Met Thr Asp Asn Glu Leu Ser Ala Leu Val Val Asp Asn Gly Ser Gly
1   5   10   15

Met Cys Lys Ala Gly Phe Gly Gly Asp Asp Ala Pro Arg Ala Val Phe
            20   25   30

Pro Ser Met Ile Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
        35   40   45

Gly Gln Lys Asp Cys Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
    50   55   60

Val Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Val Val Thr Asn Trp
65   70   75   80

Asp Asp Met Glu Lys Ile Trp Tyr His Thr Phe Tyr Asn Glu Leu Arg
                85   90   95

Val Ala Pro Asp Glu His Pro Ile Leu Leu Thr Glu Ala Pro Leu Asn
            100   105   110

Pro Lys Ile Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Ala Phe
        115   120   125

Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr
    130   135   140

Ala Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val
145   150   155   160

Thr His Ile Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile
                165   170   175

Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys
            180   185   190

```
Ile Leu Thr Glu Arg Gly Tyr Asn Phe Thr Thr Thr Ala Glu Arg Glu
        195                 200                 205

Ile Val Arg Asp Val Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe
    210                 215                 220

Glu Gln Glu Met Val Arg Ala Ala Ala Ser Ser Ser Pro Glu Arg Ser
225                 230                 235                 240

Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe
                245                 250                 255

Arg Cys Pro Glu Ala Ile Phe Gln Pro Ser Phe Leu Gly Ile Glu Ser
            260                 265                 270

Ser Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val
        275                 280                 285

Asp Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Ser
    290                 295                 300

Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Ile Thr
305                 310                 315                 320

Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg
                325                 330                 335

Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
            340                 345                 350

Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Pro
        355                 360                 365

Pro Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1511
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 439; "
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<220>
<221> source
<223> /note="Gene Symbol: ACTG2; "

<220>
<221> source
<223> /note="Gene Name:
actin, gamma 2, smooth muscle, enteric; "

<220>
<221> source
<223> /note="Uniprot ID: P63267; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000295137"

<400> 1511
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1 5 10 15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
20 25 30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
35 40 45

Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
50 55 60

Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn Trp
65 70 75 80

Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu Arg
85 90 95

Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu Asn
100 105 110

Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe
115 120 125

Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr
130 135 140

Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly Val
145 150 155 160

```
Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile
                165                 170                 175

Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys
            180                 185                 190

Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg Glu
        195                 200                 205

Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe
    210                 215                 220

Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser
225                 230                 235                 240

Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe
                245                 250                 255

Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu Ser
            260                 265                 270

Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp Ile
        275                 280                 285

Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly Thr
    290                 295                 300

Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala
305                 310                 315                 320

Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg
                325                 330                 335

Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
            340                 345                 350

Phe Gln Gln Met Trp Ile Ser Lys Pro Glu Tyr Asp Glu Ala Gly Pro
        355                 360                 365

Ser Ile Val His Arg Lys Cys Phe
    370                 375
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<210> 1512
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 439; "

<220>
<221> source
<223> /note="Gene Symbol: ACTG2; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID: P63267; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000386857"

<400> 1512
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1 5 10 15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
            20 25 30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
        35 40 45

Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
    50 55 60

Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn Trp
65 70 75 80

Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu Arg
                85 90 95

Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu Asn
            100 105 110

Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe
        115 120 125

```
Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr
    130                 135                 140

Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly Val
145                 150                 155                 160

Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile
                165                 170                 175

Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys
            180                 185                 190

Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg Glu
        195                 200                 205

Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe
    210                 215                 220

Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser
225                 230                 235                 240

Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe
                245                 250                 255

Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu Ser
            260                 265                 270

Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp Ile
        275                 280                 285

Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly Thr
    290                 295                 300

Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala
305                 310                 315                 320

Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg
                325                 330                 335

Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
            340                 345                 350
```

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Phe Gln Gln Met Trp Ile Ser Lys Pro Glu Tyr Asp Glu Ala Gly Pro
        355                 360                 365


Ser Ile Val His Arg Lys Cys Phe
    370                 375


<210> 1513
<211> 333
<212> PRT
<213> Homo sapiens

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<220>
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<400> 1513
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1               5                   10                  15


Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
            20                  25                  30


Pro Ser Ile Val Gly Arg Pro Arg His Gln Ile Trp His His Ser Phe
        35                  40                  45


Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr
    50                  55                  60


Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile
65                  70                  75                  80


Met Phe Glu Thr Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala
```

```
                85                  90                  95

Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp
            100                 105                 110

Ser Gly Asp Gly Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala
        115                 120                 125

Leu Pro His Ala Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr
    130                 135                 140

Asp Tyr Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr
145                 150                 155                 160

Thr Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr
                165                 170                 175

Val Ala Leu Asp Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser
            180                 185                 190

Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
        195                 200                 205

Gly Asn Glu Arg Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe
    210                 215                 220

Ile Gly Met Glu Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile
225                 230                 235                 240

Met Lys Cys Asp Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val
                245                 250                 255

Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln
            260                 265                 270

Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile
        275                 280                 285

Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu
    290                 295                 300

Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Pro Glu Tyr
305                 310                 315                 320
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Asp Glu Ala Gly Pro Ser Ile Val His Arg Lys Cys Phe
325 330

<210> 1514
<211> 119
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<400> 1514
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1 5 10 15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
20 25 30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
35 40 45

Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
50 55 60

Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn Trp
65 70 75 80

Asp Asp Met Glu Lys Pro His Asp His Phe Ser Asn Leu Gly Cys Gln
85 90 95

His Leu Ser Leu Asp Tyr Cys Asn Gly Phe Leu Ala Asp Phe Leu Val
100 105 110

Ser Cys Pro His Ser Pro Asn
        115

<210> 1515
<211> 52
<212> PRT
<213> Homo sapiens

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<400> 1515
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1   5   10   15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
            20   25   30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Val Arg Ala His Leu Asp
        35   40   45

Thr Thr Arg Leu
    50

<210> 1516
<211> 144
<212> PRT
<213> Homo sapiens

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<223> /note="ENSP ID: ENSP00000410020"

<400> 1516
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1 5 10 15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
20 25 30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
35 40 45

Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
50 55 60

Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn Trp
65 70 75 80

Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu Arg
85 90 95

Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu Asn
100 105 110

Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Val Arg Ser Gln Glu Asp
115 120 125

Leu Asn Thr Gly Ile Arg Met Gln His Gly Cys Leu Ala Arg Tyr Phe
130 135 140

<210> 1517
<211> 105
<212> PRT
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<400> 1517
Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1 5 10 15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
20 25 30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
35 40 45

Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
50 55 60

Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn Trp
65 70 75 80

Asp Asp Met Glu Lys Pro Leu Ala Gly Ile Phe Tyr Gln Pro Asn Ile
85 90 95

Ala Arg Ser Gln Lys Ala Met Asn Thr
100 105

<210> 1518
<211> 892
<212> PRT
<213> Homo sapiens

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<223> /note="Gene Symbol: ACTN1; "

<220>
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<223> /note="Gene Name:
actinin, alpha 1; "

<220>
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<223> /note="Uniprot ID: P12814; "

<220>
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<400> 1518
Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
1   5   10   15

Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
            20   25   30

Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
        35   40   45

Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
    50   55   60

Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro
65   70   75   80

Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala
                85   90   95

Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
            100   105   110

Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
        115   120   125

Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
    130   135   140

Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
145   150   155   160

Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
                165   170   175

Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
            180   185   190

```
Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
        195                 200                 205

Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
    210                 215                 220

Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
225                 230                 235                 240

Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
                245                 250                 255

Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
            260                 265                 270

Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
        275                 280                 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn
    290                 295                 300

Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg
305                 310                 315                 320

Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile
                325                 330                 335

Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala
            340                 345                 350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp
        355                 360                 365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn
    370                 375                 380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg
385                 390                 395                 400

Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met
                405                 410                 415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala
```

```
            420                 425                 430

Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln
        435                 440                 445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu
    450                 455                 460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys
465                 470                 475                 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala
                485                 490                 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu
            500                 505                 510

Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala
        515                 520                 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile
    530                 535                 540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp
545                 550                 555                 560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser
                565                 570                 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr
            580                 585                 590

Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg
        595                 600                 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
    610                 615                 620

Gln Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn
625                 630                 635                 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
                645                 650                 655
```

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
660 665 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
675 680 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
690 695 700

His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
705 710 715 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
725 730 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
740 745 750

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro
755 760 765

Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn
770 775 780

Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp
785 790 795 800

Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met
805 810 815

Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser
820 825 830

Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu
835 840 845

Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met
850 855 860

Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met
865 870 875 880

Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
885 890

<210> 1519
<211> 822
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 440; "

<220>
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<220>
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<223> /note="Gene Name:
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<220>
<221> source
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<400> 1519
Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro Glu
1 5 10 15

Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala Leu
20 25 30

Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala Glu
35 40 45

Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp Thr
50 55 60

Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser
65 70 75 80

Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr
85 90 95

Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly Leu
100 105 110

Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp Tyr

115 120 125

Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala Phe
130 135 140

Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu
145 150 155 160

Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr
165 170 175

Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu Thr
180 185 190

Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn Glu
195 200 205

Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp
210 215 220

Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn Thr
225 230 235 240

Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg
245 250 255

Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn
260 265 270

Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe
275 280 285

Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp Gly
290 295 300

Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn Glu
305 310 315 320

Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg Gln
325 330 335

Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met Leu
340 345 350

```
Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala Leu
        355                 360                 365

Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp
    370                 375                 380

Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu Asp
385                 390                 395                 400

Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys Asp
                405                 410                 415

Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala Leu
            420                 425                 430

Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu Glu
        435                 440                 445

Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala Met
    450                 455                 460

Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile Gln
465                 470                 475                 480

Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp Ala
                485                 490                 495

Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser Lys
            500                 505                 510

Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr Thr
        515                 520                 525

Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg Gln
    530                 535                 540

Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg Gln
545                 550                 555                 560

Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn Val
                565                 570                 575
```

```
Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser
            580                 585                 590

Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg Gln
        595                 600                 605

Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu Glu
    610                 615                 620

Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His
625                 630                 635                 640

Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu
                645                 650                 655

Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr
            660                 665                 670

Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg Ala
        675                 680                 685

Ser Phe Asn His Phe Asp Arg Lys Lys Thr Gly Met Met Asp Thr Asp
    690                 695                 700

Asp Phe Arg Ala Cys Leu Ile Ser Met Gly Tyr Asn Met Gly Glu Ala
705                 710                 715                 720

Glu Phe Ala Arg Ile Met Ser Ile Val Asp Pro Asn Arg Leu Gly Val
                725                 730                 735

Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Ala Asp
            740                 745                 750

Thr Asp Thr Ala Asp Gln Val Met Ala Ser Phe Lys Ile Leu Ala Gly
        755                 760                 765

Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu Arg Arg Glu Leu Pro Pro
    770                 775                 780

Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Thr Gly Pro
785                 790                 795                 800
```

```
Asp Ser Val Pro Gly Ala Leu Asp Tyr Met Ser Phe Ser Thr Ala Leu
                805                 810                 815


Tyr Gly Glu Ser Asp Leu
            820


<210> 1520
<211> 914
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 440; "

<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000377941"

<400> 1520
Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
1               5                   10                  15


Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
            20                  25                  30


Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
        35                  40                  45


Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
    50                  55                  60


Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro
65                  70                  75                  80


Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala
                85                  90                  95
```

```
Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
            100                 105                 110

Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
        115                 120                 125

Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
    130                 135                 140

Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
145                 150                 155                 160

Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
                165                 170                 175

Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
            180                 185                 190

Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
        195                 200                 205

Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
    210                 215                 220

Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
225                 230                 235                 240

Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
                245                 250                 255

Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
            260                 265                 270

Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
        275                 280                 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn
    290                 295                 300

Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg
305                 310                 315                 320
```

Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile
325 330 335

Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala
340 345 350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp
355 360 365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn
370 375 380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg
385 390 395 400

Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met
405 410 415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala
420 425 430

Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln
435 440 445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu
450 455 460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys
465 470 475 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala
485 490 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu
500 505 510

Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala
515 520 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile
530 535 540

```
Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp
545                 550                 555                 560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser
                565                 570                 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr
            580                 585                 590

Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg
        595                 600                 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
    610                 615                 620

Gln Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn
625                 630                 635                 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
                645                 650                 655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
            660                 665                 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
        675                 680                 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
    690                 695                 700

His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
705                 710                 715                 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
                725                 730                 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
            740                 745                 750

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro
        755                 760                 765

Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn
```

```
    770                 775                 780

Asp Pro Gln Lys Lys Thr Gly Met Met Asp Thr Asp Asp Phe Arg Ala
785                 790                 795                 800

Cys Leu Ile Ser Met Gly Tyr Asn Met Gly Glu Ala Glu Phe Ala Arg
                805                 810                 815

Ile Met Ser Ile Val Asp Pro Asn Arg Leu Gly Val Val Thr Phe Gln
            820                 825                 830

Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala
        835                 840                 845

Asp Gln Val Met Ala Ser Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr
    850                 855                 860

Ile Thr Met Asp Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu
865                 870                 875                 880

Tyr Cys Ile Ala Arg Met Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro
                885                 890                 895

Gly Ala Leu Asp Tyr Met Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser
            900                 905                 910

Asp Leu
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<210> 1521
<211> 887
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

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<223> /note="Gene Symbol: ACTN1; "

<220>
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<223> /note="Gene Name:
actinin, alpha 1; "

<220>
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<223> /note="Uniprot ID: P12814; "

<220>
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<400> 1521
Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
1   5   10   15

Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
            20   25   30

Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
        35   40   45

Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
    50   55   60

Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro
65   70   75   80

Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala
                85   90   95

Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
            100   105   110

Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
        115   120   125

Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
    130   135   140

Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
145   150   155   160

Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
                165   170   175

Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
            180   185   190

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Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
        195                 200                 205

Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
    210                 215                 220

Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
225                 230                 235                 240

Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
                245                 250                 255

Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
            260                 265                 270

Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
        275                 280                 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn
    290                 295                 300

Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg
305                 310                 315                 320

Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile
                325                 330                 335

Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala
            340                 345                 350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp
        355                 360                 365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn
    370                 375                 380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg
385                 390                 395                 400

Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met
                405                 410                 415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala
```

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            420                 425                 430

Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln
        435                 440                 445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu
    450                 455                 460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys
465                 470                 475                 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala
                485                 490                 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu
            500                 505                 510

Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala
        515                 520                 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile
    530                 535                 540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp
545                 550                 555                 560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser
                565                 570                 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr
            580                 585                 590

Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg
        595                 600                 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
    610                 615                 620

Gln Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn
625                 630                 635                 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
                645                 650                 655
```

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
660 665 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
675 680 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
690 695 700

His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
705 710 715 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
725 730 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
740 745 750

Ala Ser Phe Asn His Phe Asp Arg Lys Lys Thr Gly Met Met Asp Thr
755 760 765

Asp Asp Phe Arg Ala Cys Leu Ile Ser Met Gly Tyr Asn Met Gly Glu
770 775 780

Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp Pro Asn Arg Leu Gly
785 790 795 800

Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Ala
805 810 815

Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser Phe Lys Ile Leu Ala
820 825 830

Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu Arg Arg Glu Leu Pro
835 840 845

Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Thr Gly
850 855 860

Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met Ser Phe Ser Thr Ala
865 870 875 880

Leu Tyr Gly Glu Ser Asp Leu
885

<210> 1522
<211> 930
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 440; "

<220>
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<223> /note="Gene Name:
actinin, alpha 1; "

<220>
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<223> /note="Uniprot ID: P12814; "

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<400> 1522
Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
1 5 10 15

Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
20 25 30

Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
35 40 45

Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
50 55 60

Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro
65 70 75 80

Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala
85 90 95

Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala

```
            100                 105                 110

Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
        115                 120                 125

Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
    130                 135                 140

Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
145                 150                 155                 160

Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
                165                 170                 175

Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
            180                 185                 190

Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
        195                 200                 205

Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
    210                 215                 220

Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
225                 230                 235                 240

Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
                245                 250                 255

Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
            260                 265                 270

Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
        275                 280                 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn
    290                 295                 300

Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg
305                 310                 315                 320

Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile
                325                 330                 335
```

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Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala
            340                 345                 350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp
        355                 360                 365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn
    370                 375                 380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg
385                 390                 395                 400

Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met
                405                 410                 415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala
            420                 425                 430

Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln
        435                 440                 445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu
    450                 455                 460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys
465                 470                 475                 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala
                485                 490                 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu
            500                 505                 510

Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala
        515                 520                 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile
    530                 535                 540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp
545                 550                 555                 560
```

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser
565 570 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr
580 585 590

Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg
595 600 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
610 615 620

Gln Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn
625 630 635 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
645 650 655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
660 665 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
675 680 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
690 695 700

His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
705 710 715 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
725 730 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
740 745 750

Ala Ser Phe Asn His Phe Asp Arg Lys Lys Thr Gly Met Met Asp Thr
755 760 765

Asp Asp Phe Arg Ala Cys Leu Ile Ser Met Gly Tyr Asn Met Gly Glu
770 775 780

```
Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp Pro Asn Arg Leu Gly
785                 790                 795                 800

Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Ala
                805                 810                 815

Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser Phe Lys Ile Leu Ala
            820                 825                 830

Gly Asp Lys Leu Gln Glu Gly Gly Lys Met Gln Thr Ala His Ala Ala
        835                 840                 845

Phe Thr Pro Pro Gly Phe Ala Ala Val Ser Gly Arg Ala Ala Leu Arg
    850                 855                 860

Leu Leu Asp Phe Ala Ala Phe Leu Thr Thr Leu Ser Ser Gln Asn Tyr
865                 870                 875                 880

Ile Thr Met Asp Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu
                885                 890                 895

Tyr Cys Ile Ala Arg Met Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro
            900                 905                 910

Gly Ala Leu Asp Tyr Met Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser
        915                 920                 925

Asp Leu
    930


<210> 1523
<211> 297
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN1; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 1; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000444422"

<400> 1523
Asp Gly Lys Glu Ala Met Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr
1   5   10   15

Leu Ser Glu Ile Lys Ala Leu Leu Lys Lys His Glu Ala Phe Glu Ser
            20   25   30

Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala
        35   40   45

Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala
    50   55   60

Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr
65   70   75   80

Gln Lys Arg Arg Glu Ala Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr
                85   90   95

Ile Asp Gln Leu Tyr Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn
            100   105   110

Asn Trp Met Glu Gly Ala Met Glu Asp Leu Gln Asp Thr Phe Ile Val
        115   120   125

His Thr Ile Glu Glu Ile Gln Gly Leu Thr Thr Ala His Glu Gln Phe
    130   135   140

Lys Ala Thr Leu Pro Asp Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly
145   150   155   160

Ile His Asn Glu Val Ser Lys Ile Val Gln Thr Tyr His Val Asn Met
                165   170   175

Ala Gly Thr Asn Pro Tyr Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly
            180   185   190

Lys Trp Asp His Leu Ser His Leu Arg Gln Tyr Glu Lys Ser Ile Val
        195   200   205

```
Asn Tyr Lys Pro Lys Ile Asp Gln Leu Glu Gly Asp His Gln Leu Ile
    210                 215                 220

Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu
225                 230                 235                 240

His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr
                245                 250                 255

Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile
            260                 265                 270

Ser Gln Glu Gln Met Asn Glu Phe Arg Ala Ser Phe Asn His Phe Asp
        275                 280                 285

Arg Asp His Ser Gly Thr Leu Gly Pro
    290                 295


<210> 1524
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN1; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450618"

<400> 1524
Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro Glu
1               5                   10                  15

Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala Leu
            20                  25                  30

Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala Glu
```

```
        35                  40                  45

Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp Thr
    50                  55                  60

Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser
65                  70                  75                  80

Ala Lys Glu Gly Leu
                85


<210> 1525
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN1; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000450625"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1525
Xaa Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu Glu Tyr Ala
1               5                   10                  15

Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala Met Glu Asp
            20                  25                  30

Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile Gln Val Arg
        35                  40                  45

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
```

```
    50                  55                  60

Gln Gln His Asn Glu Arg Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn
65                  70                  75                  80

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
                85                  90                  95

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
            100                 105                 110

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
        115                 120                 125

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
    130                 135                 140

His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
145                 150                 155                 160

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
                165                 170                 175

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
            180                 185                 190

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly
        195                 200                 205


<210> 1526
<211> 260
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN1; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 1; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000450764"

<400> 1526
Met Gly Leu Arg Tyr Val Leu Pro Leu Arg Pro Pro Gly Lys Thr Phe
1   5   10   15

Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu
            20   25   30

Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu
        35   40   45

Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro Glu Arg Gly Lys Met
    50   55   60

Arg Val His Lys Ile Ser Asn Val Asn Lys Ala Leu Asp Phe Ile Ala
65   70   75   80

Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp
                85   90   95

Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg
            100   105   110

Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly
        115   120   125

Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn
    130   135   140

Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly Leu Gly Phe Cys Ala
145   150   155   160

Leu Ile His Arg His Arg Pro Glu Leu Ile Asp Tyr Gly Lys Leu Arg
                165   170   175

Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala Phe Asp Val Ala Glu
            180   185   190

Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Gly
        195   200   205

```
Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe
    210                 215                 220

Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg
225                 230                 235                 240

Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn Glu Gln Leu Met Glu
                245                 250                 255

Asp Tyr Glu Lys
            260
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<210> 1527
<211> 238
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 440; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN1; "

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<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000450903"

<400> 1527

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Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro Glu
1               5                   10                  15

Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala Leu
            20                  25                  30

Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala Glu
        35                  40                  45

Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp Thr
    50                  55                  60

Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser
65                  70                  75                  80
```

```
Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr
                85                  90                  95

Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly Leu
            100                 105                 110

Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp Tyr
        115                 120                 125

Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala Phe
    130                 135                 140

Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu
145                 150                 155                 160

Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr
                165                 170                 175

Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu Thr
            180                 185                 190

Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn Glu
        195                 200                 205

Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp
    210                 215                 220

Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu
225                 230                 235


<210> 1528
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACTN1; "

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<221> source
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000450925"

<400> 1528
Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro Glu
1 5 10 15

Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala Leu
20 25 30

Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala Glu
35 40 45

Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp Thr
50 55 60

Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser
65 70 75 80

Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr
85 90 95

Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly Leu
100 105 110

Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp Tyr
115 120 125

Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala Phe
130 135 140

<210> 1529
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

<220>
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<223> /note="Gene Symbol: ACTN1; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000451086"

<400> 1529
Met Gly Pro Gly His Ser Gly Gln Trp Gln Glu Glu Val Arg Asn His
1 5 10 15

Ser Trp Trp Trp Gly Glu Gly Ala Ser Thr Leu Pro Leu Leu Pro Ala
20 25 30

Cys Ala Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala Gly
35 40 45

Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys Leu
50 55 60

Met Leu Leu Leu Glu Val Ile Ser
65 70

<210> 1530
<211> 251
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 440; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN1; "

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<221> source
<223> /note="Gene Name:
actinin, alpha 1; "

<220>
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<223> /note="ENSP ID: ENSP00000452254"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1530
Xaa Gln Ala Leu Thr Glu Glu His Ala Arg Gln Gln His Asn Glu Arg
1 5 10 15

Leu Arg Lys Gln Phe Gly Ala Gln Ala Asn Val Ile Gly Pro Trp Ile
20 25 30

Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser Ile Glu Met His Gly
35 40 45

Thr Leu Glu Asp Gln Leu Ser His Leu Arg Gln Tyr Glu Lys Ser Ile
50 55 60

Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu Glu Gly Asp His Gln Leu
65 70 75 80

Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met
85 90 95

Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg
100 105 110

Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly
115 120 125

Ile Ser Gln Glu Gln Met Asn Glu Phe Arg Ala Ser Phe Asn His Phe
130 135 140

Asp Arg Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp Pro
145 150 155 160

Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser
165 170 175

Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser Phe
180 185 190

Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu Arg
195 200 205

Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala
210 215 220

```
Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met Ser
225                 230                 235                 240


Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
                245                 250


<210> 1531
<211> 126
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 440; "

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<223> /note="Gene Symbol: ACTN1; "

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<223> /note="Gene Name:
      actinin, alpha 1; "

<220>
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<223> /note="ENSP ID: ENSP00000452423"

<400> 1531
Met Gly Pro Gly His Ser Gly Gln Trp Gln Glu Glu Thr Phe Thr Ala
1               5                   10                  15


Trp Cys Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile
            20                  25                  30


Glu Glu Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val
        35                  40                  45


Ile Ser Gly Glu Arg Leu Ala Lys Pro Glu Arg Gly Lys Met Arg Val
    50                  55                  60


His Lys Ile Ser Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys
65                  70                  75                  80


Gly Val Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn
                85                  90                  95


Val Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala
```

```
            100                 105                 110

Ile Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly
        115                 120                 125


<210> 1532
<211> 894
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 441; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN2; "

<220>
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<223> /note="Gene Name:
      actinin, alpha 2; "

<220>
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<223> /note="Uniprot ID:  P35609; "

<220>
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<400> 1532
Met Asn Gln Ile Glu Pro Gly Val Gln Tyr Asn Tyr Val Tyr Asp Glu
1               5                   10                  15


Asp Glu Tyr Met Ile Gln Glu Glu Glu Trp Asp Arg Asp Leu Leu Leu
            20                  25                  30


Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys
        35                  40                  45


Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Glu Glu
    50                  55                  60


Asp Phe Arg Asn Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser
65                  70                  75                  80


Gly Glu Arg Leu Pro Lys Pro Asp Arg Gly Lys Met Arg Phe His Lys
                85                  90                  95
```

```
Ile Ala Asn Val Asn Lys Ala Leu Asp Tyr Ile Ala Ser Lys Gly Val
            100                 105                 110

Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Val Lys
        115                 120                 125

Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln
    130                 135                 140

Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp
145                 150                 155                 160

Cys Gln Arg Lys Thr Ala Pro Tyr Arg Asn Val Asn Ile Gln Asn Phe
                165                 170                 175

His Thr Ser Trp Lys Asp Gly Leu Gly Leu Cys Ala Leu Ile His Arg
            180                 185                 190

His Arg Pro Asp Leu Ile Asp Tyr Ser Lys Leu Asn Lys Asp Asp Pro
        195                 200                 205

Ile Gly Asn Ile Asn Leu Ala Met Glu Ile Ala Glu Lys His Leu Asp
    210                 215                 220

Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Pro Lys Pro
225                 230                 235                 240

Asp Glu Arg Ala Ile Met Thr Tyr Val Ser Cys Phe Tyr His Ala Phe
                245                 250                 255

Ala Gly Ala Glu Gln Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val
            260                 265                 270

Leu Ala Val Asn Gln Glu Asn Glu Arg Leu Met Glu Glu Tyr Glu Arg
        275                 280                 285

Leu Ala Ser Glu Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu
    290                 295                 300

Glu Asn Arg Thr Pro Glu Lys Thr Met Gln Ala Met Gln Lys Lys Leu
305                 310                 315                 320
```

```
Glu Asp Phe Arg Asp Tyr Arg Arg Lys His Lys Pro Pro Lys Val Gln
                325                 330                 335

Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu
            340                 345                 350

Arg Ile Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val
        355                 360                 365

Ser Asp Ile Ala Gly Ala Trp Gln Arg Leu Glu Gln Ala Glu Lys Gly
    370                 375                 380

Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Glu
385                 390                 395                 400

His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Thr His Glu Thr Trp
                405                 410                 415

Ala Tyr Gly Lys Glu Gln Ile Leu Leu Gln Lys Asp Tyr Glu Ser Ala
            420                 425                 430

Ser Leu Thr Glu Val Arg Ala Leu Leu Arg Lys His Glu Ala Phe Glu
        435                 440                 445

Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile
    450                 455                 460

Ala Gln Glu Leu Asn Glu Leu Asp Tyr His Asp Ala Val Asn Val Asn
465                 470                 475                 480

Asp Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Arg Leu Gly Thr Leu
                485                 490                 495

Thr Gln Lys Arg Arg Glu Ala Leu Glu Arg Met Glu Lys Leu Leu Glu
            500                 505                 510

Thr Ile Asp Gln Leu His Leu Glu Phe Ala Lys Arg Ala Ala Pro Phe
        515                 520                 525

Asn Asn Trp Met Glu Gly Ala Met Glu Asp Leu Gln Asp Met Phe Ile
    530                 535                 540

Val His Ser Ile Glu Glu Ile Gln Ser Leu Ile Thr Ala His Glu Gln
```

545 550 555 560

Phe Lys Ala Thr Leu Pro Glu Ala Asp Gly Glu Arg Gln Ser Ile Met
565 570 575

Ala Ile Gln Asn Glu Val Glu Lys Val Ile Gln Ser Tyr Asn Ile Arg
580 585 590

Ile Ser Ser Ser Asn Pro Tyr Ser Thr Val Thr Met Asp Glu Leu Arg
595 600 605

Thr Lys Trp Asp Lys Val Lys Gln Leu Val Pro Ile Arg Asp Gln Ser
610 615 620

Leu Gln Glu Glu Leu Ala Arg Gln His Ala Asn Glu Arg Leu Arg Arg
625 630 635 640

Gln Phe Ala Ala Gln Ala Asn Ala Ile Gly Pro Trp Ile Gln Asn Lys
645 650 655

Met Glu Glu Ile Ala Arg Ser Ser Ile Gln Ile Thr Gly Ala Leu Glu
660 665 670

Asp Gln Met Asn Gln Leu Lys Gln Tyr Glu His Asn Ile Ile Asn Tyr
675 680 685

Lys Asn Asn Ile Asp Lys Leu Glu Gly Asp His Gln Leu Ile Gln Glu
690 695 700

Ala Leu Val Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile
705 710 715 720

Arg Val Gly Trp Glu Leu Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn
725 730 735

Glu Val Glu Thr Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Thr Gln
740 745 750

Glu Gln Met Asn Glu Phe Arg Ala Ser Phe Asn His Phe Asp Arg Arg
755 760 765

Lys Asn Gly Leu Met Asp His Glu Asp Phe Arg Ala Cys Leu Ile Ser
770 775 780

```
Met Gly Tyr Asp Leu Gly Glu Ala Glu Phe Ala Arg Ile Met Thr Leu
785                 790                 795                 800

Val Asp Pro Asn Gly Gln Gly Thr Val Thr Phe Gln Ser Phe Ile Asp
                805                 810                 815

Phe Met Thr Arg Glu Thr Ala Asp Thr Asp Thr Ala Glu Gln Val Ile
            820                 825                 830

Ala Ser Phe Arg Ile Leu Ala Ser Asp Lys Pro Tyr Ile Leu Ala Glu
        835                 840                 845

Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Gln Tyr Cys Ile Lys
    850                 855                 860

Arg Met Pro Ala Tyr Ser Gly Pro Gly Ser Val Pro Gly Ala Leu Asp
865                 870                 875                 880

Tyr Ala Ala Phe Ser Ser Ala Leu Tyr Gly Glu Ser Asp Leu
                885                 890


<210> 1533
<211> 686
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 441; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN2; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438384"

<400> 1533
Met Thr Tyr Val Ser Cys Phe Tyr His Ala Phe Ala Gly Ala Glu Gln
1               5                   10                  15
```

```
Val Arg Gln Ser Leu Lys Ala His Ser Ala Leu Trp Lys Asp Pro Pro
            20                  25                  30

Pro Glu Ser Ser Thr Cys Ser Tyr Gln Glu Met Arg Arg Ser Ser Val
        35                  40                  45

Asn Ser Ser Ala Met Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val
    50                  55                  60

Leu Ala Val Asn Gln Glu Asn Glu Arg Leu Met Glu Glu Tyr Glu Arg
65                  70                  75                  80

Leu Ala Ser Glu Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu
                85                  90                  95

Glu Asn Arg Thr Pro Glu Lys Thr Met Gln Ala Met Gln Lys Lys Leu
            100                 105                 110

Glu Asp Phe Arg Asp Tyr Arg Arg Lys His Lys Pro Pro Lys Val Gln
        115                 120                 125

Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu
    130                 135                 140

Arg Ile Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val
145                 150                 155                 160

Ser Asp Ile Ala Gly Ala Trp Gln Arg Leu Glu Gln Ala Glu Lys Gly
                165                 170                 175

Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Glu
            180                 185                 190

His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Thr His Glu Thr Trp
        195                 200                 205

Ala Tyr Gly Lys Glu Gln Ile Leu Leu Gln Lys Asp Tyr Glu Ser Ala
    210                 215                 220

Ser Leu Thr Glu Val Arg Ala Leu Leu Arg Lys His Glu Ala Phe Glu
225                 230                 235                 240

Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile
```

245 250 255

Ala Gln Glu Leu Asn Glu Leu Asp Tyr His Asp Ala Val Asn Val Asn
260 265 270

Asp Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Arg Leu Gly Thr Leu
275 280 285

Thr Gln Lys Arg Arg Glu Ala Leu Glu Arg Met Glu Lys Leu Leu Glu
290 295 300

Thr Ile Asp Gln Leu His Leu Glu Phe Ala Lys Arg Ala Ala Pro Phe
305 310 315 320

Asn Asn Trp Met Glu Gly Ala Met Glu Asp Leu Gln Asp Met Phe Ile
325 330 335

Val His Ser Ile Glu Glu Ile Gln Ser Leu Ile Thr Ala His Glu Gln
340 345 350

Phe Lys Ala Thr Leu Pro Glu Ala Asp Gly Glu Arg Gln Ser Ile Met
355 360 365

Ala Ile Gln Asn Glu Val Glu Lys Val Ile Gln Ser Tyr Asn Ile Arg
370 375 380

Ile Ser Ser Ser Asn Pro Tyr Ser Thr Val Thr Met Asp Glu Leu Arg
385 390 395 400

Thr Lys Trp Asp Lys Val Lys Gln Leu Val Pro Ile Arg Asp Gln Ser
405 410 415

Leu Gln Glu Glu Leu Ala Arg Gln His Ala Asn Glu Arg Leu Arg Arg
420 425 430

Gln Phe Ala Ala Gln Ala Asn Ala Ile Gly Pro Trp Ile Gln Asn Lys
435 440 445

Met Glu Glu Ile Ala Arg Ser Ser Ile Gln Ile Thr Gly Ala Leu Glu
450 455 460

Asp Gln Met Asn Gln Leu Lys Gln Tyr Glu His Asn Ile Ile Asn Tyr
465 470 475 480

```
Lys Asn Asn Ile Asp Lys Leu Glu Gly Asp His Gln Leu Ile Gln Glu
                485                 490                 495

Ala Leu Val Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile
            500                 505                 510

Arg Val Gly Trp Glu Leu Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn
        515                 520                 525

Glu Val Glu Thr Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Thr Gln
    530                 535                 540

Glu Gln Met Asn Glu Phe Arg Ala Ser Phe Asn His Phe Asp Arg Arg
545                 550                 555                 560

Lys Asn Gly Leu Met Asp His Glu Asp Phe Arg Ala Cys Leu Ile Ser
                565                 570                 575

Met Gly Tyr Asp Leu Gly Glu Ala Glu Phe Ala Arg Ile Met Thr Leu
            580                 585                 590

Val Asp Pro Asn Gly Gln Gly Thr Val Thr Phe Gln Ser Phe Ile Asp
        595                 600                 605

Phe Met Thr Arg Glu Thr Ala Asp Thr Asp Thr Ala Glu Gln Val Ile
    610                 615                 620

Ala Ser Phe Arg Ile Leu Ala Ser Asp Lys Pro Tyr Ile Leu Ala Glu
625                 630                 635                 640

Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Gln Tyr Cys Ile Lys
                645                 650                 655

Arg Met Pro Ala Tyr Ser Gly Pro Gly Ser Val Pro Gly Ala Leu Asp
            660                 665                 670

Tyr Ala Ala Phe Ser Ser Ala Leu Tyr Gly Glu Ser Asp Leu
        675                 680                 685
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<210> 1534
<211> 894
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 441; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN2; "

<220>
<221> source
<223> /note="Gene Name:
actinin, alpha 2; "

<220>
<221> source
<223> /note="Uniprot ID: P35609; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443495"

<400> 1534

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Met Asn Gln Ile Glu Pro Gly Val Gln Tyr Asn Tyr Val Tyr Asp Glu
1               5                  10                  15

Asp Glu Tyr Met Ile Gln Glu Glu Glu Trp Asp Arg Asp Leu Leu Leu
            20                  25                  30

Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys
        35                  40                  45

Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Glu Glu
    50                  55                  60

Asp Phe Arg Asn Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser
65                  70                  75                  80

Gly Glu Arg Leu Pro Lys Pro Asp Arg Gly Lys Met Arg Phe His Lys
                85                  90                  95

Ile Ala Asn Val Asn Lys Ala Leu Asp Tyr Ile Ala Ser Lys Gly Val
            100                 105                 110

Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Val Lys
        115                 120                 125

Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln
```

130 135 140

Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp
145 150 155 160

Cys Gln Arg Lys Thr Ala Pro Tyr Arg Asn Val Asn Ile Gln Asn Phe
165 170 175

His Thr Ser Trp Lys Asp Gly Leu Gly Leu Cys Ala Leu Ile His Arg
180 185 190

His Arg Pro Asp Leu Ile Asp Tyr Ser Lys Leu Asn Lys Asp Asp Pro
195 200 205

Ile Gly Asn Ile Asn Leu Ala Met Glu Ile Ala Glu Lys His Leu Asp
210 215 220

Ile Pro Lys Met Leu Asp Ala Glu Asp Leu Val Tyr Thr Ala Arg Pro
225 230 235 240

Asp Glu Arg Ala Ile Met Thr Tyr Val Ser Cys Tyr Tyr His Ala Phe
245 250 255

Ala Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val
260 265 270

Leu Ala Val Asn Gln Glu Asn Glu Arg Leu Met Glu Glu Tyr Glu Arg
275 280 285

Leu Ala Ser Glu Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu
290 295 300

Glu Asn Arg Thr Pro Glu Lys Thr Met Gln Ala Met Gln Lys Lys Leu
305 310 315 320

Glu Asp Phe Arg Asp Tyr Arg Arg Lys His Lys Pro Pro Lys Val Gln
325 330 335

Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu
340 345 350

Arg Ile Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val
355 360 365

Ser Asp Ile Ala Gly Ala Trp Gln Arg Leu Glu Gln Ala Glu Lys Gly
370 375 380

Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Glu
385 390 395 400

His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Thr His Glu Thr Trp
405 410 415

Ala Tyr Gly Lys Glu Gln Ile Leu Leu Gln Lys Asp Tyr Glu Ser Ala
420 425 430

Ser Leu Thr Glu Val Arg Ala Leu Leu Arg Lys His Glu Ala Phe Glu
435 440 445

Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile
450 455 460

Ala Gln Glu Leu Asn Glu Leu Asp Tyr His Asp Ala Val Asn Val Asn
465 470 475 480

Asp Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Arg Leu Gly Thr Leu
485 490 495

Thr Gln Lys Arg Arg Glu Ala Leu Glu Arg Met Glu Lys Leu Leu Glu
500 505 510

Thr Ile Asp Gln Leu His Leu Glu Phe Ala Lys Arg Ala Ala Pro Phe
515 520 525

Asn Asn Trp Met Glu Gly Ala Met Glu Asp Leu Gln Asp Met Phe Ile
530 535 540

Val His Ser Ile Glu Glu Ile Gln Ser Leu Ile Thr Ala His Glu Gln
545 550 555 560

Phe Lys Ala Thr Leu Pro Glu Ala Asp Gly Glu Arg Gln Ser Ile Met
565 570 575

Ala Ile Gln Asn Glu Val Glu Lys Val Ile Gln Ser Tyr Asn Ile Arg
580 585 590

```
Ile Ser Ser Ser Asn Pro Tyr Ser Thr Val Thr Met Asp Glu Leu Arg
        595                 600                 605

Thr Lys Trp Asp Lys Val Lys Gln Leu Val Pro Ile Arg Asp Gln Ser
    610                 615                 620

Leu Gln Glu Glu Leu Ala Arg Gln His Ala Asn Glu Arg Leu Arg Arg
625                 630                 635                 640

Gln Phe Ala Ala Gln Ala Asn Ala Ile Gly Pro Trp Ile Gln Asn Lys
                645                 650                 655

Met Glu Glu Ile Ala Arg Ser Ser Ile Gln Ile Thr Gly Ala Leu Glu
            660                 665                 670

Asp Gln Met Asn Gln Leu Lys Gln Tyr Glu His Asn Ile Ile Asn Tyr
        675                 680                 685

Lys Asn Asn Ile Asp Lys Leu Glu Gly Asp His Gln Leu Ile Gln Glu
    690                 695                 700

Ala Leu Val Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile
705                 710                 715                 720

Arg Val Gly Trp Glu Leu Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn
                725                 730                 735

Glu Val Glu Thr Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Thr Gln
            740                 745                 750

Glu Gln Met Asn Glu Phe Arg Ala Ser Phe Asn His Phe Asp Arg Arg
        755                 760                 765

Lys Asn Gly Leu Met Asp His Glu Asp Phe Arg Ala Cys Leu Ile Ser
    770                 775                 780

Met Gly Tyr Asp Leu Gly Glu Ala Glu Phe Ala Arg Ile Met Thr Leu
785                 790                 795                 800

Val Asp Pro Asn Gly Gln Gly Thr Val Thr Phe Gln Ser Phe Ile Asp
                805                 810                 815
```

```
Phe Met Thr Arg Glu Thr Ala Asp Thr Asp Thr Ala Glu Gln Val Ile
            820                 825                 830

Ala Ser Phe Arg Ile Leu Ala Ser Asp Lys Pro Tyr Ile Leu Ala Glu
        835                 840                 845

Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Gln Tyr Cys Ile Lys
    850                 855                 860

Arg Met Pro Ala Tyr Ser Gly Pro Gly Ser Val Pro Gly Ala Leu Asp
865                 870                 875                 880

Tyr Ala Ala Phe Ser Ser Ala Leu Tyr Gly Glu Ser Asp Leu
                885                 890


<210> 1535
<211> 944
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 442; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN3; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 3
      (
      gene/pseudogene); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422007"

<400> 1535
Met Gly Ile Gly Leu Cys Val Pro Pro Ala Arg Cys Trp Lys Arg Leu
1               5                   10                  15

Thr Arg Ser Ser Arg Gly Gln Pro Leu Glu Arg Pro Ala Ala Thr Ile
            20                  25                  30

Ile Ile Gly Leu Ser Ile Val Glu Arg Ser Lys Gln Thr Gln Arg Gly
        35                  40                  45
```

```
Pro Val Asp Phe Ser Arg Ser His Ser Ala Pro Ala Ala Glu Gln Glu
    50                  55                  60

Cys Lys Pro Arg Ile Ser Ala Ala Arg Ser Thr Pro Ala Pro Pro Ser
65                  70                  75                  80

Pro Ala Val Pro Gly Phe Arg Thr Thr Pro Cys Gln Thr Phe Thr Ala
                85                  90                  95

Trp Cys Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile
            100                 105                 110

Glu Glu Asp Phe Arg Asn Gly Leu Lys Leu Met Leu Leu Leu Glu Val
        115                 120                 125

Ile Ser Gly Glu Arg Leu Pro Arg Pro Asp Lys Gly Lys Met Arg Phe
    130                 135                 140

His Lys Ile Ala Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys
145                 150                 155                 160

Gly Val Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn
                165                 170                 175

Leu Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala
            180                 185                 190

Ile Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu
        195                 200                 205

Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr Arg Asn Val Asn Val Gln
    210                 215                 220

Asn Phe His Thr Ser Trp Lys Asp Gly Leu Ala Leu Cys Ala Leu Ile
225                 230                 235                 240

His Arg His Arg Pro Asp Leu Ile Asp Tyr Ala Lys Leu Arg Lys Asp
                245                 250                 255

Asp Pro Ile Gly Asn Leu Asn Thr Ala Phe Glu Val Ala Glu Lys Tyr
            260                 265                 270

Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Pro
```

275 280 285

Lys Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Cys Phe Tyr His
290 295 300

Ala Phe Ala Gly Ala Glu Gln Ala Glu Thr Ala Ala Asn Arg Ile Cys
305 310 315 320

Lys Val Leu Ala Val Asn Gln Glu Asn Glu Lys Leu Met Glu Glu Tyr
325 330 335

Glu Lys Leu Ala Ser Glu Leu Leu Glu Trp Ile Arg Arg Thr Val Pro
340 345 350

Trp Leu Glu Asn Arg Val Gly Glu Pro Ser Met Ser Ala Met Gln Arg
355 360 365

Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Leu His Lys Pro Pro Arg
370 375 380

Ile Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr
385 390 395 400

Lys Leu Arg Leu Ser His Arg Pro Ala Phe Met Pro Ser Glu Gly Lys
405 410 415

Leu Val Ser Asp Ile Ala Asn Ala Trp Arg Gly Leu Glu Gln Val Glu
420 425 430

Lys Gly Tyr Glu Asp Trp Leu Leu Ser Glu Ile Arg Arg Leu Gln Arg
435 440 445

Leu Gln His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Leu His Glu
450 455 460

Ala Trp Thr Arg Gly Lys Glu Glu Met Leu Ser Gln Arg Asp Tyr Asp
465 470 475 480

Ser Ala Leu Leu Gln Glu Val Arg Ala Leu Leu Arg Arg His Glu Ala
485 490 495

Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu His Ile Ala
500 505 510

```
Ala Leu Ala Gln Glu Leu Asn Glu Leu Asp Tyr His Glu Ala Ala Ser
        515                 520                 525

Val Asn Ser Arg Cys Gln Ala Ile Cys Asp Gln Trp Asp Asn Leu Gly
    530                 535                 540

Thr Leu Thr Gln Lys Arg Arg Asp Ala Leu Glu Arg Met Glu Lys Leu
545                 550                 555                 560

Leu Glu Thr Ile Asp Arg Leu Gln Leu Glu Phe Ala Arg Arg Ala Ala
                565                 570                 575

Pro Phe Asn Asn Trp Leu Asp Gly Ala Val Glu Asp Leu Gln Asp Val
            580                 585                 590

Trp Leu Val His Ser Val Glu Glu Thr Gln Ser Leu Leu Thr Ala His
        595                 600                 605

Asp Gln Phe Lys Ala Thr Leu Pro Glu Ala Asp Arg Glu Arg Gly Ala
    610                 615                 620

Ile Met Gly Ile Gln Gly Glu Ile Gln Lys Ile Cys Gln Thr Tyr Gly
625                 630                 635                 640

Leu Arg Pro Cys Ser Thr Asn Pro Tyr Ile Thr Leu Ser Pro Gln Asp
                645                 650                 655

Ile Asn Thr Lys Trp Asp Met Val Arg Lys Leu Val Pro Ser Cys Asp
            660                 665                 670

Gln Thr Leu Gln Glu Glu Leu Ala Arg Gln Gln Val Asn Glu Arg Leu
        675                 680                 685

Arg Arg Gln Phe Ala Ala Gln Ala Asn Ala Ile Gly Pro Trp Ile Gln
    690                 695                 700

Ala Lys Val Glu Glu Val Gly Arg Leu Ala Ala Gly Leu Ala Gly Ser
705                 710                 715                 720

Leu Glu Glu Gln Met Ala Gly Leu Arg Gln Gln Glu Gln Asn Ile Ile
                725                 730                 735
```

```
Asn Tyr Lys Thr Asn Ile Asp Arg Leu Glu Gly Asp His Gln Leu Leu
            740                 745                 750

Gln Glu Ser Leu Val Phe Asp Asn Lys His Thr Val Tyr Ser Met Glu
        755                 760                 765

His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Ser Ile Ala Arg Thr
    770                 775                 780

Ile Asn Glu Val Glu Asn Gln Val Leu Thr Arg Asp Ala Lys Gly Leu
785                 790                 795                 800

Ser Gln Glu Gln Leu Asn Glu Phe Arg Ala Ser Phe Asn His Phe Asp
                805                 810                 815

Arg Lys Gln Asn Gly Met Met Glu Pro Asp Asp Phe Arg Ala Cys Leu
            820                 825                 830

Ile Ser Met Gly Tyr Asp Leu Gly Glu Val Glu Phe Ala Arg Ile Met
        835                 840                 845

Thr Met Val Asp Pro Asn Ala Ala Gly Val Val Thr Phe Gln Ala Phe
    850                 855                 860

Ile Asp Phe Met Thr Arg Glu Thr Ala Glu Thr Asp Thr Thr Glu Gln
865                 870                 875                 880

Val Val Ala Ser Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr
                885                 890                 895

Pro Glu Glu Leu Arg Arg Glu Leu Pro Ala Lys Gln Ala Glu Tyr Cys
            900                 905                 910

Ile Arg Arg Met Val Pro Tyr Lys Gly Ser Gly Ala Pro Ala Gly Ala
        915                 920                 925

Leu Asp Tyr Val Ala Phe Ser Ser Ala Leu Tyr Gly Glu Ser Asp Leu
    930                 935                 940
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<210> 1536
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 442; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN3; "

<220>
<221> source
<223> /note="Gene Name:
actinin, alpha 3
(
gene/pseudogene); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426236"

<400> 1536
Met Met Met Val Met Gln Pro Glu Gly Leu Gly Ala Gly Glu Gly Arg
1 5 10 15

Phe Ala Gly Gly Gly Gly Gly Gly Glu Tyr Met Glu Gln Glu Glu Asp
20 25 30

Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln Gln Arg
35 40 45

Lys Glu Asn Glu Ser Ser Glu Arg Glu Arg Asp Trp Pro Arg Met His
50 55 60

Ser Lys Ser Val Ala Glu Leu Ser
65 70

<210> 1537
<211> 901
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 442; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN3; "

<220>
<221> source
<223> /note="Gene Name:

actinin, alpha 3
(
gene/pseudogene); "

<220>
<221> source
<223> /note="Uniprot ID: Q08043; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426797"

<400> 1537
Met Met Met Val Met Gln Pro Glu Gly Leu Gly Ala Gly Glu Gly Arg
1   5   10   15

Phe Ala Gly Gly Gly Gly Gly Gly Glu Tyr Met Glu Gln Glu Glu Asp
            20   25   30

Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln Gln Arg
        35   40   45

Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala Gly Thr
    50   55   60

Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asn Gly Leu Lys Leu Met
65   70   75   80

Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Pro Arg Pro Asp Lys
                85   90   95

Gly Lys Met Arg Phe His Lys Ile Ala Asn Val Asn Lys Ala Leu Asp
            100   105   110

Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala Glu Glu
        115   120   125

Ile Val Asp Gly Asn Leu Lys Met Thr Leu Gly Met Ile Trp Thr Ile
    130   135   140

Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser Ala
145   150   155   160

Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr Arg
                165   170   175

```
Asn Val Asn Val Gln Asn Phe His Thr Ser Trp Lys Asp Gly Leu Ala
            180                 185                 190

Leu Cys Ala Leu Ile His Arg His Arg Pro Asp Leu Ile Asp Tyr Ala
        195                 200                 205

Lys Leu Arg Lys Asp Asp Pro Ile Gly Asn Leu Asn Thr Ala Phe Glu
    210                 215                 220

Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp
225                 230                 235                 240

Ile Val Asn Thr Pro Lys Pro Asp Glu Lys Ala Ile Met Thr Tyr Val
                245                 250                 255

Ser Cys Phe Tyr His Ala Phe Ala Gly Ala Glu Gln Ala Glu Thr Ala
            260                 265                 270

Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn Glu Lys
        275                 280                 285

Leu Met Glu Glu Tyr Glu Lys Leu Ala Ser Glu Leu Leu Glu Trp Ile
    290                 295                 300

Arg Arg Thr Val Pro Trp Leu Glu Asn Arg Val Gly Glu Pro Ser Met
305                 310                 315                 320

Ser Ala Met Gln Arg Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Leu
                325                 330                 335

His Lys Pro Pro Arg Ile Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe
            340                 345                 350

Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser His Arg Pro Ala Phe Met
        355                 360                 365

Pro Ser Glu Gly Lys Leu Val Ser Asp Ile Ala Asn Ala Trp Arg Gly
    370                 375                 380

Leu Glu Gln Val Glu Lys Gly Tyr Glu Asp Trp Leu Leu Ser Glu Ile
385                 390                 395                 400

Arg Arg Leu Gln Arg Leu Gln His Leu Ala Glu Lys Phe Arg Gln Lys
```

405 410 415

Ala Ser Leu His Glu Ala Trp Thr Arg Gly Lys Glu Glu Met Leu Ser
420 425 430

Gln Arg Asp Tyr Asp Ser Ala Leu Leu Gln Glu Val Arg Ala Leu Leu
435 440 445

Arg Arg His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg
450 455 460

Val Glu His Ile Ala Ala Leu Ala Gln Glu Leu Asn Glu Leu Asp Tyr
465 470 475 480

His Glu Ala Ala Ser Val Asn Ser Arg Cys Gln Ala Ile Cys Asp Gln
485 490 495

Trp Asp Asn Leu Gly Thr Leu Thr Gln Lys Arg Arg Asp Ala Leu Glu
500 505 510

Arg Met Glu Lys Leu Leu Glu Thr Ile Asp Arg Leu Gln Leu Glu Phe
515 520 525

Ala Arg Arg Ala Ala Pro Phe Asn Asn Trp Leu Asp Gly Ala Val Glu
530 535 540

Asp Leu Gln Asp Val Trp Leu Val His Ser Val Glu Glu Thr Gln Ser
545 550 555 560

Leu Leu Thr Ala His Asp Gln Phe Lys Ala Thr Leu Pro Glu Ala Asp
565 570 575

Arg Glu Arg Gly Ala Ile Met Gly Ile Gln Gly Glu Ile Gln Lys Ile
580 585 590

Cys Gln Thr Tyr Gly Leu Arg Pro Cys Ser Thr Asn Pro Tyr Ile Thr
595 600 605

Leu Ser Pro Gln Asp Ile Asn Thr Lys Trp Asp Met Val Arg Lys Leu
610 615 620

Val Pro Ser Cys Asp Gln Thr Leu Gln Glu Glu Leu Ala Arg Gln Gln
625 630 635 640

Val Asn Glu Arg Leu Arg Arg Gln Phe Ala Ala Gln Ala Asn Ala Ile
645 650 655

Gly Pro Trp Ile Gln Ala Lys Val Glu Glu Val Gly Arg Leu Ala Ala
660 665 670

Gly Leu Ala Gly Ser Leu Glu Glu Gln Met Ala Gly Leu Arg Gln Gln
675 680 685

Glu Gln Asn Ile Ile Asn Tyr Lys Thr Asn Ile Asp Arg Leu Glu Gly
690 695 700

Asp His Gln Leu Leu Gln Glu Ser Leu Val Phe Asp Asn Lys His Thr
705 710 715 720

Val Tyr Ser Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr
725 730 735

Ser Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Val Leu Thr Arg
740 745 750

Asp Ala Lys Gly Leu Ser Gln Glu Gln Leu Asn Glu Phe Arg Ala Ser
755 760 765

Phe Asn His Phe Asp Arg Lys Gln Asn Gly Met Met Glu Pro Asp Asp
770 775 780

Phe Arg Ala Cys Leu Ile Ser Met Gly Tyr Asp Leu Gly Glu Val Glu
785 790 795 800

Phe Ala Arg Ile Met Thr Met Val Asp Pro Asn Ala Ala Gly Val Val
805 810 815

Thr Phe Gln Ala Phe Ile Asp Phe Met Thr Arg Glu Thr Ala Glu Thr
820 825 830

Asp Thr Thr Glu Gln Val Val Ala Ser Phe Lys Ile Leu Ala Gly Asp
835 840 845

Lys Asn Tyr Ile Thr Pro Glu Glu Leu Arg Arg Glu Leu Pro Ala Lys
850 855 860

```
Gln Ala Glu Tyr Cys Ile Arg Arg Met Val Pro Tyr Lys Gly Ser Gly
865                 870                 875                 880


Ala Pro Ala Gly Ala Leu Asp Tyr Val Ala Phe Ser Ser Ala Leu Tyr
                885                 890                 895


Gly Glu Ser Asp Leu
            900


<210> 1538
<211> 911
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1               5                   10                  15


Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
            20                  25                  30


Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
        35                  40                  45


Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
    50                  55                  60


Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
```

65 70 75 80

Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu
85 90 95

Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val
100 105 110

Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser
115 120 125

Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly
130 135 140

Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val
145 150 155 160

Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys
165 170 175

Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp
180 185 190

Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu
195 200 205

Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu
210 215 220

Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met
225 230 235 240

Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala
245 250 255

Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln
260 265 270

Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn
275 280 285

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp
290 295 300

```
Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
305                 310                 315                 320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
                325                 330                 335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln
            340                 345                 350

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn
        355                 360                 365

Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn
    370                 375                 380

Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp
385                 390                 395                 400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu
                405                 410                 415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys
            420                 425                 430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp
        435                 440                 445

Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala
    450                 455                 460

Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu
465                 470                 475                 480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln
                485                 490                 495

Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg
            500                 505                 510

Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln
        515                 520                 525
```

Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met
530 535 540

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile
545 550 555 560

Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr
565 570 575

Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys
580 585 590

Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser
595 600 605

Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu
610 615 620

Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu
625 630 635 640

Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser
645 650 655

Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile
660 665 670

Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser
675 680 685

His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu
690 695 700

Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe
705 710 715 720

Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp
725 730 735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn
740 745 750

```
Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln
        755                 760                 765

Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala
    770                 775                 780

Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp
785                 790                 795                 800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser
                805                 810                 815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile
            820                 825                 830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val
        835                 840                 845

Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala
    850                 855                 860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile
865                 870                 875                 880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu
                885                 890                 895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
            900                 905                 910


<210> 1539
<211> 342
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<400> 1539
Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala
1   5   10   15

Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys Glu Ala Gln Arg
            20   25   30

Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr
        35   40   45

Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln
    50   55   60

Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln
65   70   75   80

Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val
                85   90   95

Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser
            100   105   110

Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln
        115   120   125

Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu
    130   135   140

Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His
145   150   155   160

Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu
                165   170   175

Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr
            180   185   190

Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala
        195   200   205

```
Ser Phe Asn His Phe Asp Lys Lys Gln Thr Gly Ser Met Asp Ser Asp
    210                 215                 220

Asp Phe Arg Ala Leu Leu Ile Ser Thr Gly Tyr Ser Leu Gly Glu Ala
225                 230                 235                 240

Glu Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu
                245                 250                 255

Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp
            260                 265                 270

Thr Asp Thr Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly
        275                 280                 285

Asp Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro
    290                 295                 300

Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro
305                 310                 315                 320

Asp Ala Val Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu
                325                 330                 335

Tyr Gly Glu Ser Asp Leu
            340


<210> 1540
<211> 521
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000411187"

<400> 1540

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Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1               5                  10                  15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
            20                  25                  30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
        35                  40                  45

Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
    50                  55                  60

Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
65                  70                  75                  80

Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Glu Leu Asp Tyr Tyr
                85                  90                  95

Asp Ser His Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp
            100                 105                 110

Asp Ala Leu Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys
        115                 120                 125

Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln Leu His Leu Glu Tyr Ala
    130                 135                 140

Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp
145                 150                 155                 160

Leu Gln Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu
                165                 170                 175

Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg
            180                 185                 190

Glu Arg Glu Ala Ile Leu Ala Ile His Lys Glu Ala Gln Arg Ile Ala
        195                 200                 205

Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val
    210                 215                 220
```

```
Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val
225                 230                 235                 240

Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser
                245                 250                 255

Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly
            260                 265                 270

Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser Ile Glu
        275                 280                 285

Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu
    290                 295                 300

Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln
305                 310                 315                 320

His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn
                325                 330                 335

Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr
            340                 345                 350

Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp
        355                 360                 365

Ala Lys Gly Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe
    370                 375                 380

Asn His Phe Asp Lys Asp His Gly Gly Ala Leu Gly Pro Glu Glu Phe
385                 390                 395                 400

Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln
                405                 410                 415

Gly Glu Ala Glu Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His
            420                 425                 430

Ser Gly Leu Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu
        435                 440                 445
```

```
Thr Thr Asp Thr Asp Thr Ala Asp Gln Val Ile Ala Ser Phe Lys Val
    450                 455                 460

Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu
465                 470                 475                 480

Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr
                485                 490                 495

Gln Gly Pro Asp Ala Val Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser
            500                 505                 510

Thr Ala Leu Tyr Gly Glu Ser Asp Leu
        515                 520


<210> 1541
<211> 692
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Uniprot ID:  O43707; "

<220>
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<400> 1541
Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1               5                   10                  15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
            20                  25                  30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
```

```
        35                  40                  45

Glu Lys Gln Gln Arg Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys
    50                  55                  60

Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu
65                  70                  75                  80

Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp
                85                  90                  95

Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys
            100                 105                 110

Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val
        115                 120                 125

Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys
    130                 135                 140

Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met
145                 150                 155                 160

Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys
                165                 170                 175

Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu
            180                 185                 190

Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala
        195                 200                 205

Trp Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr
    210                 215                 220

Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe
225                 230                 235                 240

Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala
                245                 250                 255

Ile Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val
            260                 265                 270
```

```
Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser
        275                 280                 285

Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu
    290                 295                 300

Glu Ala Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro
305                 310                 315                 320

Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe
                325                 330                 335

Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp
            340                 345                 350

Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile
        355                 360                 365

Leu Ala Ile His Lys Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile
    370                 375                 380

Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile
385                 390                 395                 400

Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His
                405                 410                 415

Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg
            420                 425                 430

Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr
        435                 440                 445

Lys Met Glu Glu Ile Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu
    450                 455                 460

Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp
465                 470                 475                 480

Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln
                485                 490                 495
```

```
Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His
            500                 505                 510

Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile
        515                 520                 525

Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser
    530                 535                 540

Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys
545                 550                 555                 560

Asp His Gly Gly Ala Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile
                565                 570                 575

Ser Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe
            580                 585                 590

Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr
        595                 600                 605

Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp
    610                 615                 620

Thr Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys
625                 630                 635                 640

Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln
                645                 650                 655

Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala
            660                 665                 670

Val Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly
        675                 680                 685

Glu Ser Asp Leu
    690
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<210> 1542
<211> 182
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
actinin, alpha 4; "

<220>
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<400> 1542
Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu
1 5 10 15

Arg Lys Asp Asp Pro Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala
20 25 30

Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val
35 40 45

Gly Thr Leu Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Cys
50 55 60

Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn
65 70 75 80

Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met
85 90 95

Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg
100 105 110

Thr Ile Pro Trp Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu
115 120 125

Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys
130 135 140

Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr
145 150 155 160

```
Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser
                165                 170                 175


Glu Gly Lys Met Val Ser
            180


<210> 1543
<211> 105
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000467190"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1543
Xaa Gly Gly Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr
1               5                   10                  15


Gly Pro Ser Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly
            20                  25                  30


Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp
        35                  40                  45


Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn
    50                  55                  60


Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp
65                  70                  75                  80
```

```
Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Glu
                85                  90                  95

Glu Leu Ser Trp Gln Thr Gly Pro Pro
            100                 105


<210> 1544
<211> 692
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
      actinin, alpha 4; "

<220>
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<223> /note="ENSP ID: ENSP00000488962"

<400> 1544
Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1               5                  10                  15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
            20                  25                  30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
        35                  40                  45

Glu Lys Gln Gln Arg Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys
    50                  55                  60

Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu
65                  70                  75                  80

Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp
                85                  90                  95
```

```
Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys
            100                 105                 110

Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val
        115                 120                 125

Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys
    130                 135                 140

Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met
145                 150                 155                 160

Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys
                165                 170                 175

Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu
            180                 185                 190

Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala
        195                 200                 205

Trp Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr
    210                 215                 220

Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe
225                 230                 235                 240

Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala
                245                 250                 255

Ile Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val
            260                 265                 270

Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser
        275                 280                 285

Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu
    290                 295                 300

Glu Ala Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro
305                 310                 315                 320

Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe
```

325 330 335

Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp
340 345 350

Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile
355 360 365

Leu Ala Ile His Lys Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile
370 375 380

Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile
385 390 395 400

Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His
405 410 415

Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg
420 425 430

Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr
435 440 445

Lys Met Glu Glu Ile Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu
450 455 460

Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp
465 470 475 480

Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln
485 490 495

Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His
500 505 510

Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile
515 520 525

Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser
530 535 540

Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys
545 550 555 560

```
Asp His Gly Gly Ala Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile
                565                 570                 575

Ser Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe
            580                 585                 590

Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr
        595                 600                 605

Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp
    610                 615                 620

Thr Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys
625                 630                 635                 640

Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln
                645                 650                 655

Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala
            660                 665                 670

Val Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly
        675                 680                 685

Glu Ser Asp Leu
    690


<210> 1545
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 443; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN4; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 4; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000489202"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1545
Xaa Gly Gly Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr
1 5 10 15

Gly Pro Ser Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly
20 25 30

Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp
35 40 45

Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn
50 55 60

Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp
65 70 75 80

Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Glu
85 90 95

Glu Leu Ser Trp Gln Thr Gly Pro Pro
100 105

<210> 1546
<211> 911
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 443; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN4; "

<220>
<221> source
<223> /note="Gene Name:
actinin, alpha 4; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000489220"

<400> 1546
Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1 5 10 15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
20 25 30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
35 40 45

Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
50 55 60

Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
65 70 75 80

Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu
85 90 95

Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val
100 105 110

Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser
115 120 125

Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly
130 135 140

Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val
145 150 155 160

Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys
165 170 175

Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp
180 185 190

Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu
195 200 205

Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu

```
    210                 215                 220

Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met
225                 230                 235                 240

Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala
                245                 250                 255

Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln
            260                 265                 270

Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn
        275                 280                 285

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp
    290                 295                 300

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
305                 310                 315                 320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
                325                 330                 335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln
            340                 345                 350

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn
        355                 360                 365

Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn
    370                 375                 380

Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp
385                 390                 395                 400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu
                405                 410                 415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys
            420                 425                 430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp
        435                 440                 445
```

```
Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala
    450                 455                 460

Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu
465                 470                 475                 480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln
                485                 490                 495

Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg
            500                 505                 510

Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln
        515                 520                 525

Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met
    530                 535                 540

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile
545                 550                 555                 560

Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr
                565                 570                 575

Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys
            580                 585                 590

Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser
        595                 600                 605

Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu
    610                 615                 620

Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu
625                 630                 635                 640

Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser
                645                 650                 655

Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile
            660                 665                 670
```

```
Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser
        675                 680                 685

His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu
    690                 695                 700

Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe
705                 710                 715                 720

Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp
                725                 730                 735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn
            740                 745                 750

Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln
        755                 760                 765

Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala
    770                 775                 780

Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp
785                 790                 795                 800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser
                805                 810                 815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile
            820                 825                 830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val
        835                 840                 845

Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala
    850                 855                 860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile
865                 870                 875                 880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu
                885                 890                 895
```

```
Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
            900                 905                 910


<210> 1547
<211> 342
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 443; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN4; "

<220>
<221> source
<223> /note="Gene Name:
      actinin, alpha 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489448"

<400> 1547
Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala
1               5                  10                  15


Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys Glu Ala Gln Arg
            20                  25                  30


Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr
        35                  40                  45


Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln
    50                  55                  60


Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln
65                  70                  75                  80


Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val
                85                  90                  95


Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser
            100                 105                 110


Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln
        115                 120                 125
```

```
Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu
    130                 135                 140

Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His
145                 150                 155                 160

Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu
                165                 170                 175

Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr
            180                 185                 190

Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala
        195                 200                 205

Ser Phe Asn His Phe Asp Lys Lys Gln Thr Gly Ser Met Asp Ser Asp
    210                 215                 220

Asp Phe Arg Ala Leu Leu Ile Ser Thr Gly Tyr Ser Leu Gly Glu Ala
225                 230                 235                 240

Glu Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu
                245                 250                 255

Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp
            260                 265                 270

Thr Asp Thr Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly
        275                 280                 285

Asp Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro
    290                 295                 300

Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro
305                 310                 315                 320

Asp Ala Val Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu
                325                 330                 335

Tyr Gly Glu Ser Asp Leu
            340
```

<210> 1548
<211> 521
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 443; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN4; "

<220>
<221> source
<223> /note="Gene Name:
actinin, alpha 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489474"

<400> 1548
Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1 5 10 15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
20 25 30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
35 40 45

Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
50 55 60

Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
65 70 75 80

Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Glu Leu Asp Tyr Tyr
85 90 95

Asp Ser His Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp
100 105 110

Asp Ala Leu Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys
115 120 125

Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln Leu His Leu Glu Tyr Ala

```
    130                 135                 140

Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp
145                 150                 155                 160

Leu Gln Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu
                165                 170                 175

Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg
            180                 185                 190

Glu Arg Glu Ala Ile Leu Ala Ile His Lys Glu Ala Gln Arg Ile Ala
        195                 200                 205

Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val
    210                 215                 220

Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val
225                 230                 235                 240

Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser
                245                 250                 255

Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly
            260                 265                 270

Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser Ile Glu
        275                 280                 285

Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu
    290                 295                 300

Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln
305                 310                 315                 320

His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn
                325                 330                 335

Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr
            340                 345                 350

Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp
        355                 360                 365
```

```
Ala Lys Gly Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe
    370                 375                 380

Asn His Phe Asp Lys Asp His Gly Gly Ala Leu Gly Pro Glu Glu Phe
385                 390                 395                 400

Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln
                405                 410                 415

Gly Glu Ala Glu Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His
            420                 425                 430

Ser Gly Leu Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu
        435                 440                 445

Thr Thr Asp Thr Asp Thr Ala Asp Gln Val Ile Ala Ser Phe Lys Val
    450                 455                 460

Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu
465                 470                 475                 480

Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr
                485                 490                 495

Gln Gly Pro Asp Ala Val Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser
            500                 505                 510

Thr Ala Leu Tyr Gly Glu Ser Asp Leu
        515                 520


<210> 1549
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 443; "

<220>
<221> source
<223> /note="Gene Symbol: ACTN4; "

<220>
<221> source
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<223> /note="Gene Name:
actinin, alpha 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000489516"

<400> 1549
Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu
1 5 10 15

Arg Lys Asp Asp Pro Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala
20 25 30

Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val
35 40 45

Gly Thr Leu Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Cys
50 55 60

Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn
65 70 75 80

Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met
85 90 95

Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg
100 105 110

Thr Ile Pro Trp Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu
115 120 125

Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys
130 135 140

Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr
145 150 155 160

Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser
165 170 175

Glu Gly Lys Met Val Ser
180

<210> 1550

<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 444; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL10; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 10; "

<220>
<221> source
<223> /note="Uniprot ID: Q5JWF8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000329647"

<400> 1550
Met Ala Ser Thr Ala Leu Leu Ala Leu Cys Ser Thr Gly Ala Phe Ser
1   5   10   15

Gly Leu Ala Val Glu Ala Gly Ala Gly Val Cys His Ala Thr Pro Ile
            20   25   30

Tyr Ala Gly His Ser Trp His Gln Ala Thr Phe Arg Leu Asn Val Ala
        35   40   45

Gly Ser Thr Leu Ser Arg Tyr Leu Arg Asp Leu Leu Val Ala Ala Asn
    50   55   60

Pro Asp Leu Leu Gln Gln Ala Leu Pro Arg Lys Ala Ile Thr His Leu
65   70   75   80

Lys Lys Arg Ser Cys Tyr Val Ser Leu Asp Phe Glu Gly Asp Leu Arg
                85   90   95

Asp Pro Ala Arg His His Pro Ala Ser Phe Ser Val Gly Asn Gly Cys
            100   105   110

Cys Val Cys Leu Ser Ser Glu Arg Phe Arg Cys Pro Glu Pro Ile Phe
        115   120   125

```
Gln Pro Gly Leu Leu Gly Gln Ala Glu Gln Gly Leu Pro Ala Leu Ala
    130                 135                 140

Phe Arg Ala Leu Gln Lys Met Pro Lys Thr Leu Arg Thr Arg Leu Ala
145                 150                 155                 160

Asp Thr Val Val Leu Ala Gly Gly Ser Thr Leu Phe Pro Gly Phe Ala
                165                 170                 175

Glu Arg Leu Asp Lys Glu Leu Glu Ala Gln Cys Arg Arg His Gly Tyr
            180                 185                 190

Ala Ala Leu Arg Pro His Leu Val Ala Lys His Gly Arg Gly Met Ala
        195                 200                 205

Val Trp Thr Gly Gly Ser Met Val Ala Ser Leu His Ser Phe Gln Arg
    210                 215                 220

Arg Trp Ile Thr Arg Ala Met Tyr Gln Glu Cys Gly Ser Arg Leu Leu
225                 230                 235                 240

Tyr Asp Val Phe Asn
                245
```

<210> 1551
<211> 387
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 445; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL6A; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 6A; "

<220>
<221> source
<223> /note="Uniprot ID: O96019; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000376430"

<400> 1551

```
Met Val Val Glu Arg Asp Asp Gly Ser Thr Leu Met Glu Ile Asp Gly
1               5                  10                  15

Asp Lys Gly Lys Gln Gly Gly Pro Thr Tyr Tyr Ile Asp Thr Asn Ala
            20                  25                  30

Leu Arg Val Pro Arg Glu Asn Met Glu Ala Ile Ser Pro Leu Lys Asn
        35                  40                  45

Gly Met Val Glu Asp Trp Asp Ser Phe Gln Ala Ile Leu Asp His Thr
    50                  55                  60

Tyr Lys Met His Val Lys Ser Glu Ala Ser Leu His Pro Val Leu Met
65                  70                  75                  80

Ser Glu Ala Pro Trp Asn Thr Arg Ala Lys Arg Glu Lys Leu Thr Glu
                85                  90                  95

Leu Met Phe Glu His Tyr Asn Ile Pro Ala Phe Phe Leu Cys Lys Thr
            100                 105                 110

Ala Val Leu Thr Ala Phe Ala Asn Gly Arg Ser Thr Gly Leu Ile Leu
        115                 120                 125

Asp Ser Gly Ala Thr His Thr Thr Ala Ile Pro Val His Asp Gly Tyr
    130                 135                 140

Val Leu Gln Gln Gly Ile Val Lys Ser Pro Leu Ala Gly Asp Phe Ile
145                 150                 155                 160

Thr Met Gln Cys Arg Glu Leu Phe Gln Glu Met Asn Ile Glu Leu Val
                165                 170                 175

Pro Pro Tyr Met Ile Ala Ser Lys Glu Ala Val Arg Glu Gly Ser Pro
            180                 185                 190

Ala Asn Trp Lys Arg Lys Glu Lys Leu Pro Gln Val Thr Arg Ser Trp
        195                 200                 205

His Asn Tyr Met Cys Asn Cys Val Ile Gln Asp Phe Gln Ala Ser Val
    210                 215                 220
```

```
Leu Gln Val Ser Asp Ser Thr Tyr Asp Glu Gln Val Ala Ala Gln Met
225                 230                 235                 240

Pro Thr Val His Tyr Glu Phe Pro Asn Gly Tyr Asn Cys Asp Phe Gly
                245                 250                 255

Ala Glu Arg Leu Lys Ile Pro Glu Gly Leu Phe Asp Pro Ser Asn Val
            260                 265                 270

Lys Gly Leu Ser Gly Asn Thr Met Leu Gly Val Ser His Val Val Thr
        275                 280                 285

Thr Ser Val Gly Met Cys Asp Ile Asp Ile Arg Pro Gly Leu Tyr Gly
    290                 295                 300

Ser Val Ile Val Ala Gly Gly Asn Thr Leu Ile Gln Ser Phe Thr Asp
305                 310                 315                 320

Arg Leu Asn Arg Glu Leu Ser Gln Lys Thr Pro Pro Ser Met Arg Leu
                325                 330                 335

Lys Leu Ile Ala Asn Asn Thr Thr Val Glu Arg Arg Phe Ser Ser Trp
            340                 345                 350

Ile Gly Gly Ser Ile Leu Ala Ser Leu Gly Thr Phe Gln Gln Met Trp
        355                 360                 365

Ile Ser Lys Gln Glu Tyr Glu Glu Gly Gly Lys Gln Cys Val Glu Arg
    370                 375                 380

Lys Cys Pro
385
```

<210> 1552
<211> 387
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 445; "

<220>
<221> source

<223> /note="Gene Symbol: ACTL6A; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 6A; "

<220>
<221> source
<223> /note="Uniprot ID: O96019; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394014"

<400> 1552

```
Met Val Val Glu Arg Asp Asp Gly Ser Thr Leu Met Glu Ile Asp Gly
1               5                  10                  15

Asp Lys Gly Lys Gln Gly Gly Pro Thr Tyr Tyr Ile Asp Thr Asn Ala
            20                  25                  30

Leu Arg Val Pro Arg Glu Asn Met Glu Ala Ile Ser Pro Leu Lys Asn
        35                  40                  45

Gly Met Val Glu Asp Trp Asp Ser Phe Gln Ala Ile Leu Asp His Thr
    50                  55                  60

Tyr Lys Met His Val Lys Ser Glu Ala Ser Leu His Pro Val Leu Met
65                  70                  75                  80

Ser Glu Ala Pro Trp Asn Thr Arg Ala Lys Arg Glu Lys Leu Thr Glu
                85                  90                  95

Leu Met Phe Glu His Tyr Asn Ile Pro Ala Phe Phe Leu Cys Lys Thr
            100                 105                 110

Ala Val Leu Thr Ala Phe Ala Asn Gly Arg Ser Thr Gly Leu Ile Leu
        115                 120                 125

Asp Ser Gly Ala Thr His Thr Thr Ala Ile Pro Val His Asp Gly Tyr
    130                 135                 140

Val Leu Gln Gln Gly Ile Val Lys Ser Pro Leu Ala Gly Asp Phe Ile
145                 150                 155                 160

Thr Met Gln Cys Arg Glu Leu Phe Gln Glu Met Asn Ile Glu Leu Val
```

```
                165                 170                 175

Pro Pro Tyr Met Ile Ala Ser Lys Glu Ala Val Arg Glu Gly Ser Pro
            180                 185                 190

Ala Asn Trp Lys Arg Lys Glu Lys Leu Pro Gln Val Thr Arg Ser Trp
        195                 200                 205

His Asn Tyr Met Cys Asn Cys Val Ile Gln Asp Phe Gln Ala Ser Val
    210                 215                 220

Leu Gln Val Ser Asp Ser Thr Tyr Asp Glu Gln Val Ala Ala Gln Met
225                 230                 235                 240

Pro Thr Val His Tyr Glu Phe Pro Asn Gly Tyr Asn Cys Asp Phe Gly
                245                 250                 255

Ala Glu Arg Leu Lys Ile Pro Glu Gly Leu Phe Asp Pro Ser Asn Val
            260                 265                 270

Lys Gly Leu Ser Gly Asn Thr Met Leu Gly Val Ser His Val Val Thr
        275                 280                 285

Thr Ser Val Gly Met Cys Asp Ile Asp Ile Arg Pro Gly Leu Tyr Gly
    290                 295                 300

Ser Val Ile Val Ala Gly Gly Asn Thr Leu Ile Gln Ser Phe Thr Asp
305                 310                 315                 320

Arg Leu Asn Arg Glu Leu Ser Gln Lys Thr Pro Pro Ser Met Arg Leu
                325                 330                 335

Lys Leu Ile Ala Asn Asn Thr Thr Val Glu Arg Arg Phe Ser Ser Trp
            340                 345                 350

Ile Gly Gly Ser Ile Leu Ala Ser Leu Gly Thr Phe Gln Gln Met Trp
        355                 360                 365

Ile Ser Lys Gln Glu Tyr Glu Glu Gly Gly Lys Gln Cys Val Glu Arg
    370                 375                 380

Lys Cys Pro
385
```

<210> 1553
<211> 429
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 445; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL6A; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 6A; "

<220>
<221> source
<223> /note="Uniprot ID: O96019; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397552"

<400> 1553
Met Ser Gly Gly Val Tyr Gly Gly Asp Glu Val Gly Ala Leu Val Phe
1   5   10   15

Asp Ile Gly Ser Tyr Thr Val Arg Ala Gly Tyr Ala Gly Glu Asp Cys
            20   25   30

Pro Lys Val Asp Phe Pro Thr Ala Ile Gly Met Val Val Glu Arg Asp
        35   40   45

Asp Gly Ser Thr Leu Met Glu Ile Asp Gly Asp Lys Gly Lys Gln Gly
    50   55   60

Gly Pro Thr Tyr Tyr Ile Asp Thr Asn Ala Leu Arg Val Pro Arg Glu
65   70   75   80

Asn Met Glu Ala Ile Ser Pro Leu Lys Asn Gly Met Val Glu Asp Trp
                85   90   95

Asp Ser Phe Gln Ala Ile Leu Asp His Thr Tyr Lys Met His Val Lys
            100   105   110

```
Ser Glu Ala Ser Leu His Pro Val Leu Met Ser Glu Ala Pro Trp Asn
        115                 120                 125

Thr Arg Ala Lys Arg Glu Lys Leu Thr Glu Leu Met Phe Glu His Tyr
    130                 135                 140

Asn Ile Pro Ala Phe Phe Leu Cys Lys Thr Ala Val Leu Thr Ala Phe
145                 150                 155                 160

Ala Asn Gly Arg Ser Thr Gly Leu Ile Leu Asp Ser Gly Ala Thr His
                165                 170                 175

Thr Thr Ala Ile Pro Val His Asp Gly Tyr Val Leu Gln Gln Gly Ile
            180                 185                 190

Val Lys Ser Pro Leu Ala Gly Asp Phe Ile Thr Met Gln Cys Arg Glu
        195                 200                 205

Leu Phe Gln Glu Met Asn Ile Glu Leu Val Pro Pro Tyr Met Ile Ala
    210                 215                 220

Ser Lys Glu Ala Val Arg Glu Gly Ser Pro Ala Asn Trp Lys Arg Lys
225                 230                 235                 240

Glu Lys Leu Pro Gln Val Thr Arg Ser Trp His Asn Tyr Met Cys Asn
                245                 250                 255

Cys Val Ile Gln Asp Phe Gln Ala Ser Val Leu Gln Val Ser Asp Ser
            260                 265                 270

Thr Tyr Asp Glu Gln Val Ala Ala Gln Met Pro Thr Val His Tyr Glu
        275                 280                 285

Phe Pro Asn Gly Tyr Asn Cys Asp Phe Gly Ala Glu Arg Leu Lys Ile
    290                 295                 300

Pro Glu Gly Leu Phe Asp Pro Ser Asn Val Lys Gly Leu Ser Gly Asn
305                 310                 315                 320

Thr Met Leu Gly Val Ser His Val Val Thr Thr Ser Val Gly Met Cys
                325                 330                 335

Asp Ile Asp Ile Arg Pro Gly Leu Tyr Gly Ser Val Ile Val Ala Gly
```

```
            340                 345                 350

Gly Asn Thr Leu Ile Gln Ser Phe Thr Asp Arg Leu Asn Arg Glu Leu
        355                 360                 365

Ser Gln Lys Thr Pro Pro Ser Met Arg Leu Lys Leu Ile Ala Asn Asn
    370                 375                 380

Thr Thr Val Glu Arg Arg Phe Ser Ser Trp Ile Gly Gly Ser Ile Leu
385                 390                 395                 400

Ala Ser Leu Gly Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr
                405                 410                 415

Glu Glu Gly Gly Lys Gln Cys Val Glu Arg Lys Cys Pro
            420                 425


<210> 1554
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 445; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL6A; "

<220>
<221> source
<223> /note="Gene Name:
      actin-like 6A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420153"

<400> 1554
Met Val Val Glu Arg Asp Asp Gly Ser Thr Leu Met Glu Ile Asp Gly
1               5                   10                  15

Asp Lys Gly Lys Gln Gly Gly Pro Thr Tyr Tyr Ile Asp Thr Asn Ala
            20                  25                  30

Leu Arg Val Pro Arg Glu Asn Met Glu Ala Ile Ser Pro Leu Lys Asn
        35                  40                  45
```

Gly Met
    50

<210> 1555
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 445; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL6A; "

<220>
<221> source
<223> /note="Gene Name:
      actin-like 6A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420694"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1555
Xaa Phe Ser Asp Glu Val Gly Ala Leu Val Phe Asp Ile Gly Ser Tyr
1   5   10   15

Thr Val Arg Ala Gly Tyr Ala Gly Glu Asp Cys Pro Lys Val Asp Phe
            20   25   30

Pro Thr Ala Ile Gly Met Val Val Glu Arg Asp Asp Gly Ser Thr Leu
        35   40   45

Met Glu Ile Asp Gly Asp Lys Gly Lys Gln Gly Gly Pro Thr Tyr Tyr
    50   55   60

Ile Asp Thr Asn Ala Leu Arg Val Pro Arg Glu Asn Met Glu Ala Ile
65   70   75   80

Ser Pro Leu Lys Asn Gly Met Val Glu Asp Trp Asp Ser Phe Gln Ala
                85   90   95

```
Ile Leu Asp His Thr Tyr Lys Met His Val Lys Ser Glu Ala Ser Leu
            100                 105                 110

His Pro Val Leu Met Ser Glu Ala Pro Trp Asn Thr Arg Ala Lys Arg
        115                 120                 125

Glu Lys Leu Thr Glu Leu Met Phe Glu His Tyr Asn Ile Pro Ala Phe
    130                 135                 140

Phe Leu Cys Lys Thr Ala Val Leu Thr Ala Phe Ile His His Leu Leu
145                 150                 155                 160

His
```

<210> 1556
<211> 426
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 446; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL6B; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 6B; "

<220>
<221> source
<223> /note="Uniprot ID: O94805; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000160382"

<400> 1556

```
Met Ser Gly Gly Val Tyr Gly Gly Asp Glu Val Gly Ala Leu Val Phe
1               5                   10                  15

Asp Ile Gly Ser Phe Ser Val Arg Ala Gly Tyr Ala Gly Glu Asp Cys
            20                  25                  30

Pro Lys Ala Asp Phe Pro Thr Thr Val Gly Leu Leu Ala Ala Glu Glu
```

```
        35                  40                  45

Gly Gly Gly Leu Glu Leu Glu Gly Asp Lys Glu Lys Lys Gly Lys Ile
    50                  55                  60

Phe His Ile Asp Thr Asn Ala Leu His Val Pro Arg Asp Gly Ala Glu
65                  70                  75                  80

Val Met Ser Pro Leu Lys Asn Gly Met Ile Glu Asp Trp Glu Cys Phe
                85                  90                  95

Arg Ala Ile Leu Asp His Thr Tyr Ser Lys His Val Lys Ser Glu Pro
            100                 105                 110

Asn Leu His Pro Val Leu Met Ser Glu Ala Pro Trp Asn Thr Arg Ala
        115                 120                 125

Lys Arg Glu Lys Leu Thr Glu Leu Met Phe Glu Gln Tyr Asn Ile Pro
    130                 135                 140

Ala Phe Phe Leu Cys Lys Thr Ala Val Leu Thr Ala Phe Ala Asn Gly
145                 150                 155                 160

Arg Ser Thr Gly Leu Val Leu Asp Ser Gly Ala Thr His Thr Thr Ala
                165                 170                 175

Ile Pro Val His Asp Gly Tyr Val Leu Gln Gln Gly Ile Val Lys Ser
            180                 185                 190

Pro Leu Ala Gly Asp Phe Ile Ser Met Gln Cys Arg Glu Leu Phe Gln
        195                 200                 205

Glu Met Ala Ile Asp Ile Ile Pro Pro Tyr Met Ile Ala Ala Lys Glu
    210                 215                 220

Pro Val Arg Glu Gly Ala Pro Pro Asn Trp Lys Lys Lys Glu Lys Leu
225                 230                 235                 240

Pro Gln Val Ser Lys Ser Trp His Asn Tyr Met Cys Asn Glu Val Ile
                245                 250                 255

Gln Asp Phe Gln Ala Ser Val Leu Gln Val Ser Asp Ser Pro Tyr Asp
            260                 265                 270
```

```
Glu Gln Val Ala Ala Gln Met Pro Thr Val His Tyr Glu Met Pro Asn
        275                 280                 285

Gly Tyr Asn Thr Asp Tyr Gly Ala Glu Arg Leu Arg Ile Pro Glu Gly
    290                 295                 300

Leu Phe Asp Pro Ser Asn Val Lys Gly Leu Ser Gly Asn Thr Met Leu
305                 310                 315                 320

Gly Val Gly His Val Val Thr Thr Ser Ile Gly Met Cys Asp Ile Asp
                325                 330                 335

Ile Arg Pro Gly Leu Tyr Gly Ser Val Ile Val Thr Gly Gly Asn Thr
            340                 345                 350

Leu Leu Gln Gly Phe Thr Asp Arg Leu Asn Arg Glu Leu Ser Gln Lys
        355                 360                 365

Thr Pro Pro Ser Met Arg Leu Lys Leu Ile Ala Ser Asn Ser Thr Met
    370                 375                 380

Glu Arg Lys Phe Ser Pro Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu
385                 390                 395                 400

Gly Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Glu Glu Gly
                405                 410                 415

Gly Lys Gln Cys Val Glu Arg Lys Cys Pro
            420                 425


<210> 1557
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 446; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL6B; "

<220>
<221> source
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<223> /note="Gene Name:
actin-like 6B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420151"

<400> 1557
Met Ser Pro Leu Lys Asn Gly Met Ile Glu Asp Trp Glu Cys Phe Arg
1 5 10 15

Ala Ile Leu Asp His Thr Tyr Ser Lys His Val Lys Ser Glu Pro Asn
20 25 30

Leu His Pro Val Leu Met Ser Glu Ala Pro Trp Asn Thr Arg Ala Lys
35 40 45

Arg Glu Lys Leu Thr Glu Leu Met Phe Glu Gln Tyr Asn Ile Pro Ala
50 55 60

Phe Phe
65

<210> 1558
<211> 435
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 447; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL7A; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 7A; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y615; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000334300"

<400> 1558
Met Trp Ala Pro Pro Ala Ala Ile Met Gly Asp Gly Pro Thr Lys Lys
1 5 10 15

```
Val Gly Asn Gln Ala Pro Leu Gln Thr Gln Ala Leu Gln Thr Ala Ser
            20                  25                  30

Leu Arg Asp Gly Pro Ala Lys Arg Ala Val Trp Val Arg His Thr Ser
        35                  40                  45

Ser Glu Pro Gln Glu Pro Thr Glu Ser Lys Ala Ala Lys Glu Arg Pro
    50                  55                  60

Lys Gln Glu Val Thr Lys Ala Val Val Val Asp Leu Gly Thr Gly Tyr
65                  70                  75                  80

Cys Lys Cys Gly Phe Ala Gly Leu Pro Arg Pro Thr His Lys Ile Ser
                85                  90                  95

Thr Thr Val Gly Lys Pro Tyr Met Glu Thr Ala Lys Thr Gly Asp Asn
            100                 105                 110

Arg Lys Glu Thr Phe Val Gly Gln Glu Leu Asn Asn Thr Asn Val His
        115                 120                 125

Leu Lys Leu Val Asn Pro Leu Arg His Gly Ile Ile Val Asp Trp Asp
    130                 135                 140

Thr Val Gln Asp Ile Trp Glu Tyr Leu Phe Arg Gln Glu Met Lys Ile
145                 150                 155                 160

Ala Pro Glu Glu His Ala Val Leu Val Ser Asp Pro Pro Leu Ser Pro
                165                 170                 175

His Thr Asn Arg Glu Lys Tyr Ala Glu Met Leu Phe Glu Ala Phe Asn
            180                 185                 190

Thr Pro Ala Met His Ile Ala Tyr Gln Ser Arg Leu Ser Met Tyr Ser
        195                 200                 205

Tyr Gly Arg Thr Ser Gly Leu Val Val Glu Val Gly His Gly Val Ser
    210                 215                 220

Tyr Val Val Pro Ile Tyr Glu Gly Tyr Pro Leu Pro Ser Ile Thr Gly
225                 230                 235                 240
```

```
Arg Leu Asp Tyr Ala Gly Ser Asp Leu Thr Ala Tyr Leu Leu Gly Leu
                245                 250                 255

Leu Asn Ser Ala Gly Asn Glu Phe Thr Gln Asp Gln Met Gly Ile Val
            260                 265                 270

Glu Asp Ile Lys Lys Lys Cys Cys Phe Val Ala Leu Asp Pro Ile Glu
        275                 280                 285

Glu Lys Lys Val Pro Leu Ser Glu His Thr Ile Arg Tyr Val Leu Pro
    290                 295                 300

Asp Gly Lys Glu Ile Gln Leu Cys Gln Glu Arg Phe Leu Cys Ser Glu
305                 310                 315                 320

Met Phe Phe Lys Pro Ser Leu Ile Lys Ser Met Gln Leu Gly Leu His
                325                 330                 335

Thr Gln Thr Val Ser Cys Leu Asn Lys Cys Asp Ile Ala Leu Lys Arg
            340                 345                 350

Asp Leu Met Gly Asn Ile Leu Leu Cys Gly Gly Ser Thr Met Leu Ser
        355                 360                 365

Gly Phe Pro Asn Arg Leu Gln Lys Glu Leu Ser Ser Met Cys Pro Asn
    370                 375                 380

Asp Thr Pro Gln Val Asn Val Leu Pro Glu Arg Asp Ser Ala Val Trp
385                 390                 395                 400

Thr Gly Gly Ser Ile Leu Ala Ser Leu Gln Gly Phe Gln Pro Leu Trp
                405                 410                 415

Val His Arg Phe Glu Tyr Glu Glu His Gly Pro Phe Phe Leu Tyr Arg
            420                 425                 430

Arg Cys Phe
        435
```

<210> 1559
<211> 415
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 448; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL7B; "

<220>
<221> source
<223> /note="Gene Name:
actin-like 7B; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y614; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000363799"

<400> 1559

```
Met Ala Thr Arg Asn Ser Pro Met Pro Leu Gly Thr Ala Gln Gly Asp
1               5                  10                  15

Pro Gly Glu Ala Gly Thr Arg Pro Gly Pro Asp Ala Ser Leu Arg Asp
            20                  25                  30

Thr Gly Ala Ala Thr Gln Leu Lys Met Lys Pro Arg Lys Val His Lys
        35                  40                  45

Ile Lys Ala Val Ile Ile Asp Leu Gly Ser Gln Tyr Cys Lys Cys Gly
    50                  55                  60

Tyr Ala Gly Glu Pro Arg Pro Thr Tyr Phe Ile Ser Ser Thr Val Gly
65                  70                  75                  80

Lys Arg Cys Pro Glu Ala Ala Asp Ala Gly Asp Thr Arg Lys Trp Thr
                85                  90                  95

Leu Val Gly His Glu Leu Leu Asn Thr Glu Ala Pro Leu Lys Leu Val
            100                 105                 110

Asn Pro Leu Lys His Gly Ile Val Val Asp Trp Asp Cys Val Gln Asp
        115                 120                 125

Ile Trp Glu Tyr Ile Phe Arg Thr Ala Met Lys Ile Leu Pro Glu Glu
    130                 135                 140
```

```
His Ala Val Leu Val Ser Asp Pro Pro Leu Ser Pro Ser Ser Asn Arg
145                 150                 155                 160

Glu Lys Tyr Ala Glu Leu Met Phe Glu Thr Phe Gly Ile Pro Ala Met
                165                 170                 175

His Val Thr Ser Gln Ser Leu Leu Ser Ile Tyr Ser Tyr Gly Lys Thr
            180                 185                 190

Ser Gly Leu Val Val Glu Ser Gly His Gly Val Ser His Val Val Pro
        195                 200                 205

Ile Ser Glu Gly Asp Val Leu Pro Gly Leu Thr Ser Arg Ala Asp Tyr
    210                 215                 220

Ala Gly Gly Asp Leu Thr Asn Tyr Leu Met Gln Leu Leu Asn Glu Ala
225                 230                 235                 240

Gly His Ala Phe Thr Asp Asp His Leu His Ile Ile Glu His Ile Lys
                245                 250                 255

Lys Lys Cys Cys Tyr Ala Ala Phe Leu Pro Glu Glu Glu Leu Gly Leu
            260                 265                 270

Val Pro Glu Glu Leu Arg Val Asp Tyr Glu Leu Pro Asp Gly Lys Leu
        275                 280                 285

Ile Thr Ile Gly Gln Glu Arg Phe Arg Cys Ser Glu Met Leu Phe Gln
    290                 295                 300

Pro Ser Leu Ala Gly Ser Thr Gln Pro Gly Leu Pro Glu Leu Thr Ala
305                 310                 315                 320

Ala Cys Leu Gly Arg Cys Gln Asp Thr Gly Phe Lys Glu Glu Met Ala
                325                 330                 335

Ala Asn Val Leu Leu Cys Gly Gly Cys Thr Met Leu Asp Gly Phe Pro
            340                 345                 350

Glu Arg Phe Gln Arg Glu Leu Ser Leu Leu Cys Pro Gly Asp Ser Pro
        355                 360                 365
```

```
Ala Val Ala Ala Ala Pro Glu Arg Lys Thr Ser Val Trp Thr Gly Gly
    370                 375                 380

Ser Ile Leu Ala Ser Leu Gln Ala Phe Gln Gln Leu Trp Val Ser Lys
385                 390                 395                 400

Glu Glu Phe Glu Glu Arg Gly Ser Val Ala Ile Tyr Ser Lys Cys
                405                 410                 415

<210> 1560
<211> 366
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 449; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL8; "

<220>
<221> source
<223> /note="Gene Name:
      actin-like 8; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H568; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000364555"

<400> 1560
Met Ala Ala Arg Thr Val Ile Ile Asp His Gly Ser Gly Phe Leu Lys
1               5                   10                  15

Ala Gly Thr Ala Gly Trp Asn Glu Pro Gln Met Val Phe Pro Asn Ile
            20                  25                  30

Val Asn Tyr Leu Pro Cys Lys Glu Asn Pro Gly Pro Ser Tyr Ala Arg
        35                  40                  45

Arg Arg Val Ser Leu Gly Ile Asp Ile Cys His Pro Asp Thr Phe Ser
    50                  55                  60

Tyr Pro Ile Glu Arg Gly Arg Ile Leu Asn Trp Glu Gly Val Gln Tyr
```

65 70 75 80

Leu Trp Ser Phe Val Leu Glu Asn His Arg Arg Glu Gln Glu Val Pro
85 90 95

Pro Val Ile Ile Thr Glu Thr Pro Leu Arg Glu Pro Ala Asp Arg Lys
100 105 110

Lys Met Leu Glu Ile Leu Phe Glu Leu Leu His Val Pro Ser Val Leu
115 120 125

Leu Ala Asp Gln Leu Gln Met Ser Leu Tyr Ala Ser Gly Leu Leu Thr
130 135 140

Gly Val Val Val Asp Ser Gly Tyr Gly Leu Thr Arg Val Gln Pro Phe
145 150 155 160

His Gln Gly Arg Pro Leu Pro Ala Ser Gly Lys Thr Leu Glu Phe Ala
165 170 175

Gly Gln Asp Leu Ser Ala Tyr Leu Leu Lys Ser Leu Phe Lys Glu Asp
180 185 190

Cys Asp Arg Arg Cys Leu Phe Gln Leu Glu Thr Val Ala Val Thr Gln
195 200 205

Met Asn Lys Cys Tyr Val Pro Gln Asn Leu Gly Glu Ala Leu Asp Phe
210 215 220

Arg Glu Arg Gln Gln Ser Ala Leu Asp Glu Ser Asn Thr Tyr Gln Leu
225 230 235 240

Pro Asp Gly Ser Arg Val Glu Leu Thr Pro Met Gln Arg Val Ala Pro
245 250 255

Glu Met Phe Phe Ser Pro Gln Val Phe Glu Gln Pro Gly Pro Ser Ile
260 265 270

Pro Arg Ala Ile Val Glu Ser Val Glu Ser Cys Glu Ile Ser Leu Arg
275 280 285

Pro Leu Leu Val Ser His Val Met Ala Cys Gly Gly Asn Thr Leu Tyr
290 295 300

```
Pro Gly Phe Thr Lys Arg Leu Phe Arg Glu Leu Met Gly Asp His Val
305                 310                 315                 320


Ser Ser Thr Lys Ala Thr Val Trp Glu Gly Ser Asn Arg Asn Phe Ser
                325                 330                 335


Val Trp Leu Gly Ala Ser Val Val Ala His Leu Ser Thr Tyr Gln Ser
            340                 345                 350


Glu Trp Met Ser Arg Glu Glu Tyr Gly Glu His Met Arg Met
        355                 360                 365


<210> 1561
<211> 366
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 449; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL8; "

<220>
<221> source
<223> /note="Gene Name:
      actin-like 8; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H568; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481590"

<400> 1561
Met Ala Ala Arg Thr Val Ile Ile Asp His Gly Ser Gly Phe Leu Lys
1               5                   10                  15


Ala Gly Thr Ala Gly Trp Asn Glu Pro Gln Met Val Phe Pro Asn Ile
            20                  25                  30


Val Asn Tyr Leu Pro Cys Lys Glu Asn Pro Gly Pro Ser Tyr Ala Arg
        35                  40                  45
```

```
Arg Arg Val Ser Leu Gly Ile Asp Ile Cys His Pro Asp Thr Phe Ser
    50                  55                  60

Tyr Pro Ile Glu Arg Gly Arg Ile Leu Asn Trp Glu Gly Val Gln Tyr
65                  70                  75                  80

Leu Trp Ser Phe Val Leu Glu Asn His Arg Arg Glu Gln Glu Val Pro
                85                  90                  95

Pro Val Ile Ile Thr Glu Thr Pro Leu Arg Glu Pro Ala Asp Arg Lys
            100                 105                 110

Lys Met Leu Glu Ile Leu Phe Glu Leu Leu His Val Pro Ser Val Leu
        115                 120                 125

Leu Ala Asp Gln Leu Gln Met Ser Leu Tyr Ala Ser Gly Leu Leu Thr
    130                 135                 140

Gly Val Val Val Asp Ser Gly Tyr Gly Leu Thr Arg Val Gln Pro Phe
145                 150                 155                 160

His Gln Gly Arg Pro Leu Pro Ala Ser Gly Lys Thr Leu Glu Phe Ala
                165                 170                 175

Gly Gln Asp Leu Ser Ala Tyr Leu Leu Lys Ser Leu Phe Lys Glu Asp
            180                 185                 190

Cys Asp Arg Arg Cys Leu Phe Gln Leu Glu Thr Val Ala Val Thr Gln
        195                 200                 205

Met Asn Lys Cys Tyr Val Pro Gln Asn Leu Gly Glu Ala Leu Asp Phe
    210                 215                 220

Arg Glu Arg Gln Gln Ser Ala Leu Asp Glu Ser Asn Thr Tyr Gln Leu
225                 230                 235                 240

Pro Asp Gly Ser Arg Val Glu Leu Thr Pro Met Gln Arg Val Ala Pro
                245                 250                 255

Glu Met Phe Phe Ser Pro Gln Val Phe Glu Gln Pro Gly Pro Ser Ile
            260                 265                 270

Pro Arg Ala Ile Val Glu Ser Val Glu Ser Cys Glu Ile Ser Leu Arg
```

```
        275                 280                 285

Pro Leu Leu Val Ser His Val Met Ala Cys Gly Gly Asn Thr Leu Tyr
    290                 295                 300

Pro Gly Phe Thr Lys Arg Leu Phe Arg Glu Leu Met Gly Asp His Val
305                 310                 315                 320

Ser Ser Thr Lys Ala Thr Val Trp Glu Gly Ser Asn Arg Asn Phe Ser
                325                 330                 335

Val Trp Leu Gly Ala Ser Val Val Ala His Leu Ser Thr Tyr Gln Ser
            340                 345                 350

Glu Trp Met Ser Arg Glu Glu Tyr Gly Glu His Met Arg Met
        355                 360                 365


<210> 1562
<211> 416
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 450; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL9; "

<220>
<221> source
<223> /note="Gene Name:
      actin-like 9; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TC94; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000316674"

<400> 1562
Met Asp Ala Ser Arg Pro Lys Ser Ser Glu Ser Gln Ser Ser Leu Glu
1               5                   10                  15

Ala Pro Arg Pro Gly Pro Asn Pro Ser Pro Asn Val Val Asn Lys Pro
            20                  25                  30
```

```
Leu Gln Arg Asp Ser Pro Gly Met Val Ala Asp Arg Leu Pro Pro Lys
        35                  40                  45

Thr Gly Ala Val Val Ile Asp Met Gly Thr Gly Thr Cys Lys Val Gly
    50                  55                  60

Phe Ala Gly Gln Ala Ser Pro Thr Tyr Thr Val Ala Thr Ile Leu Gly
65                  70                  75                  80

Cys Gln Pro Lys Lys Pro Ala Thr Ser Gly Gln Ser Gly Leu Gln Thr
                85                  90                  95

Phe Ile Gly Glu Ala Ala Arg Val Leu Pro Glu Leu Thr Leu Val Gln
            100                 105                 110

Pro Leu Arg Ser Gly Ile Val Val Asp Trp Asp Ala Ala Glu Leu Ile
        115                 120                 125

Trp Arg His Leu Leu Glu His Asp Leu Arg Val Ala Thr His Asp His
    130                 135                 140

Pro Leu Leu Phe Ser Asp Pro Pro Phe Ser Pro Ala Thr Asn Arg Glu
145                 150                 155                 160

Lys Leu Val Glu Val Ala Phe Glu Ser Leu Arg Ser Pro Ala Met Tyr
                165                 170                 175

Val Ala Ser Gln Ser Val Leu Ser Val Tyr Ala His Gly Arg Val Ser
            180                 185                 190

Gly Leu Val Val Asp Thr Gly His Gly Val Thr Tyr Thr Val Pro Val
        195                 200                 205

Phe Gln Gly Tyr Asn Leu Leu His Ala Thr Glu Arg Leu Asp Leu Ala
    210                 215                 220

Gly Asn Asn Leu Thr Ala Phe Leu Ala Glu Met Leu Leu Gln Ala Gly
225                 230                 235                 240

Leu Pro Leu Gly Gln Gln Asp Leu Asp Leu Val Glu Asn Ile Lys His
                245                 250                 255
```

```
His Tyr Cys Tyr Val Ala Ser Asp Phe Gln Lys Glu Gln Ala Arg Pro
            260                 265                 270

Glu Gln Glu Tyr Lys Arg Thr Leu Lys Leu Pro Asp Gly Arg Thr Val
        275                 280                 285

Thr Leu Gly Lys Glu Leu Phe Gln Cys Pro Glu Leu Leu Phe Asn Pro
    290                 295                 300

Pro Glu Val Pro Gly Leu Ser Pro Val Gly Leu Ser Thr Met Ala Lys
305                 310                 315                 320

Gln Ser Leu Arg Lys Leu Ser Leu Glu Met Arg Ala Asp Leu Ala Gln
                325                 330                 335

Asn Val Leu Leu Cys Gly Gly Ser Ser Leu Phe Thr Gly Phe Glu Gly
            340                 345                 350

Arg Phe Arg Ala Glu Leu Leu Arg Ala Leu Pro Ala Glu Thr His Val
        355                 360                 365

Val Val Ala Ala Gln Pro Thr Arg Asn Phe Ser Val Trp Ile Gly Gly
    370                 375                 380

Ser Ile Leu Ala Ser Leu Arg Ala Phe Gln Ser Cys Trp Val Leu Arg
385                 390                 395                 400

Glu Gln Tyr Glu Glu Gln Gly Pro Tyr Ile Val Tyr Arg Lys Cys Tyr
                405                 410                 415


<210> 1563
<211> 416
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 450; "

<220>
<221> source
<223> /note="Gene Symbol: ACTL9; "

<220>
<221> source
<223> /note="Gene Name:
      actin-like 9; "
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<220>
<221> source
<223> /note="Uniprot ID: Q8TC94; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482603"

<400> 1563
Met Asp Ala Ser Arg Pro Lys Ser Ser Glu Ser Gln Ser Ser Leu Glu
1   5   10   15

Ala Pro Arg Pro Gly Pro Asn Pro Ser Pro Asn Val Val Asn Lys Pro
            20   25   30

Leu Gln Arg Asp Ser Pro Gly Met Val Ala Asp Arg Leu Pro Pro Lys
        35   40   45

Thr Gly Ala Val Val Ile Asp Met Gly Thr Gly Thr Cys Lys Val Gly
    50   55   60

Phe Ala Gly Gln Ala Ser Pro Thr Tyr Thr Val Ala Thr Ile Leu Gly
65   70   75   80

Cys Gln Pro Lys Lys Pro Ala Thr Ser Gly Gln Ser Gly Leu Gln Thr
                85   90   95

Phe Ile Gly Glu Ala Ala Arg Val Leu Pro Glu Leu Thr Leu Val Gln
            100   105   110

Pro Leu Arg Ser Gly Ile Val Val Asp Trp Asp Ala Ala Glu Leu Ile
        115   120   125

Trp Arg His Leu Leu Glu His Asp Leu Arg Val Ala Thr His Asp His
    130   135   140

Pro Leu Leu Phe Ser Asp Pro Pro Phe Ser Pro Ala Thr Asn Arg Glu
145   150   155   160

Lys Leu Val Glu Val Ala Phe Glu Ser Leu Arg Ser Pro Ala Met Tyr
                165   170   175

Val Ala Ser Gln Ser Val Leu Ser Val Tyr Ala His Gly Arg Val Ser
            180   185   190

```
Gly Leu Val Val Asp Thr Gly His Gly Val Thr Tyr Thr Val Pro Val
        195                 200                 205

Phe Gln Gly Tyr Asn Leu Leu His Ala Thr Glu Arg Leu Asp Leu Ala
    210                 215                 220

Gly Asn Asn Leu Thr Ala Phe Leu Ala Glu Met Leu Leu Gln Ala Gly
225                 230                 235                 240

Leu Pro Leu Gly Gln Gln Asp Leu Asp Leu Val Glu Asn Ile Lys His
                245                 250                 255

His Tyr Cys Tyr Val Ala Ser Asp Phe Gln Lys Glu Gln Ala Arg Pro
            260                 265                 270

Glu Gln Glu Tyr Lys Arg Thr Leu Lys Leu Pro Asp Gly Arg Thr Val
        275                 280                 285

Thr Leu Gly Lys Glu Leu Phe Gln Cys Pro Glu Leu Leu Phe Asn Pro
    290                 295                 300

Pro Glu Val Pro Gly Leu Ser Pro Val Gly Leu Ser Thr Met Ala Lys
305                 310                 315                 320

Gln Ser Leu Arg Lys Leu Ser Leu Glu Met Arg Ala Asp Leu Ala Gln
                325                 330                 335

Asn Val Leu Leu Cys Gly Gly Ser Ser Leu Phe Thr Gly Phe Glu Gly
            340                 345                 350

Arg Phe Arg Ala Glu Leu Leu Arg Ala Leu Pro Ala Glu Thr His Val
        355                 360                 365

Val Val Ala Ala Gln Pro Thr Arg Asn Phe Ser Val Trp Ile Gly Gly
    370                 375                 380

Ser Ile Leu Ala Ser Leu Arg Ala Phe Gln Ser Cys Trp Val Leu Arg
385                 390                 395                 400

Glu Gln Tyr Glu Glu Gln Gly Pro Tyr Ile Val Tyr Arg Lys Cys Tyr
                405                 410                 415
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<210> 1564
<211> 417
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="Uniprot ID: Q9NZ32; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000254286"

<400> 1564
Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1   5   10   15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu
            20   25   30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
        35   40   45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
    50   55   60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
65   70   75   80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
                85   90   95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
            100   105   110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
        115   120   125

```
Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
    130                 135                 140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys
145                 150                 155                 160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu
                165                 170                 175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu
            180                 185                 190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu
        195                 200                 205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu
    210                 215                 220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro
225                 230                 235                 240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu
                245                 250                 255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu
            260                 265                 270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu
        275                 280                 285

Ile Gln Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala Glu Asn Leu Val
    290                 295                 300

Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu His Arg Leu Leu
305                 310                 315                 320

Ala Glu Ile Arg Tyr Leu Val Glu Lys Pro Lys Tyr Lys Lys Ala Leu
                325                 330                 335

Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala Lys Ala Asn Cys
            340                 345                 350
```

```
Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu Gln Asp Ile Leu
        355                 360                 365

Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Gln Thr Gly Arg Ile
    370                 375                 380

Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu Met Met Phe Asp
385                 390                 395                 400

Val Gly Lys Thr Gln Pro Pro Leu Met Lys Arg Ala Phe Ser Thr Glu
                405                 410                 415

Lys
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<210> 1565
<211> 185
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438183"

<400> 1565

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Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1               5                   10                  15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu
            20                  25                  30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
        35                  40                  45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
```

```
    50                  55                  60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
65                  70                  75                  80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
                85                  90                  95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
            100                 105                 110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
        115                 120                 125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
    130                 135                 140

Glu Ser Leu Val Leu Pro Ile Ser Phe Leu Asn Pro Ser Ser Lys Leu
145                 150                 155                 160

Leu Gly Ser Thr Thr Pro Arg Arg Lys Ser Ser Ser Gln Arg Val Gly
                165                 170                 175

Asn Ser Thr Ile Gly Thr Met Tyr Cys
            180                 185


<210> 1566
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
      actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450796"
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<400> 1566
Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1   5   10   15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu
            20   25   30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
        35   40   45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
    50   55   60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
65   70   75   80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
                85   90   95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
            100   105   110

Phe Glu Arg Val Gly Asn Ser Thr Ile Gly Thr Met Tyr Cys
        115   120   125

<210> 1567
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
      actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451289"

<220>

<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1567
Xaa Ser Asp Leu Lys Arg Gly Leu Lys Ile Gln Ala Ala Lys Phe Asn
1 5 10 15

Ile Asp Gly Asn Asn Glu Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala
20 25 30

Glu Asn Leu Val Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu
35 40 45

His Arg Leu Leu Ala Glu Ile Arg Tyr Leu Val Glu Lys Pro Lys Tyr
50 55 60

Lys Lys Ala Leu Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala
65 70 75 80

Lys Ala Asn Cys Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu
85 90 95

Gln Asp Ile Leu Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Gln
100 105 110

Thr Gly Arg Ile Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu
115 120 125

Met Met Phe Asp Val Gly Lys Thr Gln Pro Pro Leu Met Lys Arg Ala
130 135 140

Phe Ser Thr Glu Lys
145

<210> 1568
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451336"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1568
Xaa Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu Lys Ile Gln
1 5 10 15

Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Phe Ser Cys Gly
20 25 30

Asn Ser Phe
35

<210> 1569
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451863"

<400> 1569
Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1 5 10 15

Val Ile Asp Leu Gly Glu Ala Phe Thr Asn Leu Ser Glu Leu Phe Ser

20 25 30

Ile Ile Ser Ile Gln Lys Asn Tyr Ile Pro Thr
35 40

<210> 1570
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452135"

<400> 1570
Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1 5 10 15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu
20 25 30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
35 40 45

Pro Lys Val Leu Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly Thr Ile
50 55 60

Leu Ala His Cys Asn Leu Cys Leu Pro Ala Thr Ser Thr Ser Trp Val
65 70 75 80

Gln Ala Val Leu Pro Leu Gln Pro Pro Glu
85 90

<210> 1571
<211> 179
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452586"

<400> 1571
Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1 5 10 15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu
20 25 30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
35 40 45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
50 55 60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
65 70 75 80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
85 90 95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
100 105 110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
115 120 125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
130 135 140

Glu Ser Leu Val Asn Pro Ser Ser Lys Leu Leu Gly Ser Thr Thr Pro

145 150 155 160

Arg Arg Lys Ser Ser Ser Gln Arg Val Gly Asn Ser Thr Ile Gly Thr
165 170 175

Met Tyr Cys

<210> 1572
<211> 302
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 451; "

<220>
<221> source
<223> /note="Gene Symbol: ACTR10; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 10 homolog (S. cerevisiae); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000477173"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1572
Xaa Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val
1 5 10 15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu
20 25 30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
35 40 45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
50 55 60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu

65 70 75 80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
85 90 95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
100 105 110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
115 120 125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
130 135 140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys
145 150 155 160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu
165 170 175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu
180 185 190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu
195 200 205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu
210 215 220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro
225 230 235 240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu
245 250 255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu
260 265 270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu
275 280 285

Ile Gln Cys Cys Ser Cys Cys Pro Gly Trp Ser Ala Met Ala
290 295 300

<210> 1573
<211> 226
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 452; "

<220>
<221> source
<223> /note="Gene Symbol: ARPIN; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 2/3 complex inhibitor; "

<220>
<221> source
<223> /note="Uniprot ID: Q7Z6K5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000350075"

<400> 1573
Met Ser Arg Ile Tyr His Asp Gly Ala Leu Arg Asn Lys Ala Val Gln
1   5   10   15

Ser Val Arg Leu Pro Gly Ala Trp Asp Pro Ala Ala His Gln Gly Gly
            20   25   30

Asn Gly Val Leu Leu Glu Gly Glu Leu Ile Asp Val Ser Arg His Ser
        35   40   45

Ile Leu Asp Thr His Gly Arg Lys Glu Arg Tyr Tyr Val Leu Tyr Ile
    50   55   60

Arg Pro Ser His Ile His Arg Arg Lys Phe Asp Ala Lys Gly Asn Glu
65   70   75   80

Ile Glu Pro Asn Phe Ser Ala Thr Arg Lys Val Asn Thr Gly Phe Leu
                85   90   95

Met Ser Ser Tyr Lys Val Glu Ala Lys Gly Asp Thr Asp Arg Leu Thr
            100   105   110

```
Pro Glu Ala Leu Lys Gly Leu Val Asn Lys Pro Glu Leu Leu Ala Leu
        115                 120                 125

Thr Glu Ser Leu Thr Pro Asp His Thr Val Ala Phe Trp Met Pro Glu
    130                 135                 140

Ser Glu Met Glu Val Met Glu Leu Glu Leu Gly Ala Gly Val Arg Leu
145                 150                 155                 160

Lys Thr Arg Gly Asp Gly Pro Phe Leu Asp Ser Leu Ala Lys Leu Glu
                165                 170                 175

Ala Gly Thr Val Thr Lys Cys Asn Phe Thr Gly Asp Gly Lys Thr Gly
            180                 185                 190

Ala Ser Trp Thr Asp Asn Ile Met Ala Gln Lys Cys Ser Lys Gly Ala
        195                 200                 205

Ala Ala Glu Ile Arg Glu Gln Gly Asp Gly Ala Glu Asp Glu Glu Trp
    210                 215                 220

Asp Asp
225
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<210> 1574
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 452; "

<220>
<221> source
<223> /note="Gene Symbol: ARPIN; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 2/3 complex inhibitor; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453006"

<220>
<221> MOD_RES

<222> (1)..(1)
<223> Any amino acid

<400> 1574
Xaa Ala Leu Lys Gly Leu Val Asn Lys Pro Glu Leu Leu Ala Leu Thr
1 5 10 15

Glu Ser Leu Thr Pro Asp His Thr Val Ala Phe Trp Met Pro Glu Ser
20 25 30

Glu Met Glu Val Met Glu Leu Glu Leu Gly Ala Gly Val Arg Leu Lys
35 40 45

Thr Arg Gly Asp Gly Pro Phe Leu Asp Ser Leu Ala Lys Leu Glu Ala
50 55 60

Gly Thr Val Thr Lys Cys Asn Phe Thr Gly Asp Gly Lys Thr Gly Ala
65 70 75 80

Ser Trp Thr Asp Asn Ile Met Ala Gln Lys Cys Ser Lys Gly Ala Ala
85 90 95

Ala Glu Ile Arg Glu Gln Gly Asp Gly Ala Glu Asp Glu Glu Trp Val
100 105 110

Gly Thr Trp Cys Trp Cys Ser Cys Ile Ser Trp Gln Glu His Gly Thr
115 120 125

Tyr Trp Leu Arg Leu Trp Val Gly
130 135

<210> 1575
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 452; "

<220>
<221> source
<223> /note="Gene Symbol: ARPIN; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt 2/3 complex inhibitor; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453687"

<400> 1575
Met Ser Ser Tyr Lys Val Glu Ala Lys Gly Asp Thr Asp Arg Leu Thr
1   5   10   15

Pro Glu Ala Leu Lys Gly Leu Val Asn Lys Pro Glu Leu Leu Ala Leu
            20   25   30

Thr Glu Ser Leu Thr Pro Asp His Thr Val Ala Phe Trp Met Pro Glu
        35   40   45

Ser Glu Met Glu Val Met Glu Leu Glu Leu Gly Ala Gly Val Arg Leu
    50   55   60

Lys Thr Arg Gly Asp Gly Pro Phe Leu Asp Ser Leu Ala Lys Leu Glu
65   70   75   80

Ala Gly Thr Val Thr Lys Cys Asn Phe Thr Gly Asp Gly Lys Thr Gly
                85   90   95

Ala Ser Trp Thr Asp Asn Ile Met Ala Gln Lys Cys Ser Lys Gly Ala
            100   105   110

Ala Ala Glu Ile Arg Glu Gln Gly Asp Gly Ala Glu Asp Glu Glu Trp
        115   120   125

Asp Asp
    130

<210> 1576
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 453; "

<220>
<221> source
<223> /note="Gene Symbol: ACTRT1; "

<220>
<221> source

<223> /note="Gene Name:
actin-related prt T1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TDG2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000360165"

<400> 1576

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Met Phe Asn Pro His Ala Leu Asp Val Pro Ala Val Ile Phe Asp Asn
1               5                  10                  15

Gly Ser Gly Leu Cys Lys Ala Gly Leu Ser Gly Glu Ile Gly Pro Arg
            20                  25                  30

His Val Ile Ser Ser Val Leu Gly His Cys Lys Phe Asn Val Pro Leu
        35                  40                  45

Ala Arg Leu Asn Gln Lys Tyr Phe Val Gly Gln Glu Ala Leu Tyr Lys
    50                  55                  60

Tyr Glu Ala Leu His Leu His Tyr Pro Ile Glu Arg Gly Leu Val Thr
65                  70                  75                  80

Gly Trp Asp Asp Met Glu Lys Leu Trp Lys His Leu Phe Glu Arg Glu
                85                  90                  95

Leu Gly Val Lys Pro Ser Gln Gln Pro Val Leu Met Thr Glu Pro Ser
            100                 105                 110

Leu Asn Pro Arg Glu Ile Arg Glu Lys Leu Ala Glu Met Met Phe Glu
        115                 120                 125

Thr Phe Ser Val Pro Gly Phe Tyr Leu Ser Asn His Ala Val Ala Ala
    130                 135                 140

Leu Tyr Ala Ser Ala Cys Val Thr Gly Leu Val Val Asp Ser Gly Asp
145                 150                 155                 160

Gly Val Thr Cys Thr Val Pro Ile Phe Glu Gly Tyr Ser Leu Pro His
                165                 170                 175

Ala Val Thr Lys Leu Cys Met Ala Gly Arg Asp Ile Thr Glu His Leu
```

```
            180                 185                 190

Thr Arg Leu Leu Phe Ala Ser Gly Phe Asn Phe Pro Cys Ile Leu Asn
        195                 200                 205

Lys Ala Val Val Asn Asn Ile Lys Glu Lys Leu Cys Tyr Ile Ala Leu
    210                 215                 220

Glu Pro Glu Lys Glu Leu Arg Lys Ser Arg Gly Glu Val Leu Gly Ala
225                 230                 235                 240

Tyr Arg Leu Pro Asp Gly His Val Ile His Phe Gly Asp Glu Leu Tyr
                245                 250                 255

Gln Val Pro Glu Val Leu Phe Ala Pro Asp Gln Leu Gly Ile His Ser
            260                 265                 270

Pro Gly Leu Ser Lys Met Val Ser Ser Ser Ile Met Lys Cys Asp Thr
        275                 280                 285

Asp Ile Gln Asn Lys Leu Tyr Ala Asp Ile Val Leu Ser Gly Gly Thr
    290                 295                 300

Thr Leu Leu Pro Gly Leu Glu Glu Arg Leu Met Lys Glu Val Glu Gln
305                 310                 315                 320

Leu Ala Ser Lys Gly Thr Pro Ile Lys Ile Thr Ala Ser Pro Asp Arg
                325                 330                 335

Cys Phe Ser Ala Trp Ile Gly Ala Ser Ile Met Thr Ser Met Ser Ser
            340                 345                 350

Phe Lys Gln Met Trp Val Thr Ser Ala Asp Phe Lys Glu Tyr Gly Thr
        355                 360                 365

Ser Val Val Gln Arg Arg Cys Phe
    370                 375
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<210> 1577
<211> 377
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 454; "

<220>
<221> source
<223> /note="Gene Symbol: ACTRT2; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt T2; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TDY3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000367658"

<400> 1577

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Met Phe Asn Pro His Ala Leu Asp Ser Pro Ala Val Ile Phe Asp Asn
1               5                  10                  15


Gly Ser Gly Phe Cys Lys Ala Gly Leu Ser Gly Glu Phe Gly Pro Arg
            20                  25                  30


His Met Val Ser Ser Ile Val Gly His Leu Lys Phe Gln Ala Pro Ser
        35                  40                  45


Ala Glu Ala Asn Gln Lys Lys Tyr Phe Val Gly Glu Glu Ala Leu Tyr
    50                  55                  60


Lys Gln Glu Ala Leu Gln Leu His Ser Pro Phe Glu Arg Gly Leu Ile
65                  70                  75                  80


Thr Gly Trp Asp Asp Val Glu Arg Leu Trp Lys His Leu Phe Glu Trp
                85                  90                  95


Glu Leu Gly Val Lys Pro Ser Asp Gln Pro Leu Leu Ala Thr Glu Pro
            100                 105                 110


Ser Leu Asn Pro Arg Glu Asn Arg Glu Lys Met Ala Glu Val Met Phe
        115                 120                 125


Glu Asn Phe Gly Val Pro Ala Phe Tyr Leu Ser Asp Gln Ala Val Leu
    130                 135                 140
```

```
Ala Leu Tyr Ala Ser Ala Cys Val Thr Gly Leu Val Val Asp Ser Gly
145                 150                 155                 160

Asp Ala Val Thr Cys Thr Val Pro Ile Phe Glu Gly Tyr Ser Leu Pro
                165                 170                 175

His Ala Val Thr Lys Leu His Val Ala Gly Arg Asp Ile Thr Glu Leu
            180                 185                 190

Leu Met Gln Leu Leu Leu Ala Ser Gly His Thr Phe Pro Cys Gln Leu
        195                 200                 205

Asp Lys Gly Leu Val Asp Asp Ile Lys Lys Lys Leu Cys Tyr Val Ala
    210                 215                 220

Leu Glu Pro Glu Lys Glu Leu Ser Arg Arg Pro Glu Glu Val Leu Arg
225                 230                 235                 240

Glu Tyr Lys Leu Pro Asp Gly Asn Ile Ile Ser Leu Gly Asp Pro Leu
                245                 250                 255

His Gln Ala Pro Glu Ala Leu Phe Val Pro Gln Gln Leu Gly Ser Gln
            260                 265                 270

Ser Pro Gly Leu Ser Asn Met Val Ser Ser Ser Ile Thr Lys Cys Asp
        275                 280                 285

Thr Asp Ile Gln Lys Ile Leu Phe Gly Glu Ile Val Leu Ser Gly Gly
    290                 295                 300

Thr Thr Leu Phe His Gly Leu Asp Asp Arg Leu Leu Lys Glu Leu Glu
305                 310                 315                 320

Gln Leu Ala Ser Lys Asp Thr Pro Ile Lys Ile Thr Ala Pro Pro Asp
                325                 330                 335

Arg Trp Phe Ser Thr Trp Ile Gly Ala Ser Ile Val Thr Ser Leu Ser
            340                 345                 350

Ser Phe Lys Gln Met Trp Val Thr Ala Ala Asp Phe Lys Glu Phe Gly
        355                 360                 365

Thr Ser Val Val Gln Arg Arg Cys Phe
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370 375

<210> 1578
<211> 372
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 455; "

<220>
<221> source
<223> /note="Gene Symbol: ACTRT3; "

<220>
<221> source
<223> /note="Gene Name:
actin-related prt T3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BYD9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000333037"

<400> 1578
Met Asn His Cys Gln Leu Pro Val Val Ile Asp Asn Gly Ser Gly Met
1 5 10 15

Ile Lys Ala Gly Val Ala Gly Cys Arg Glu Pro Gln Phe Ile Tyr Pro
20 25 30

Asn Ile Ile Gly Arg Ala Lys Gly Gln Ser Arg Ala Ala Gln Gly Gly
35 40 45

Leu Glu Leu Cys Val Gly Asp Gln Ala Gln Asp Trp Arg Ser Ser Leu
50 55 60

Phe Ile Ser Tyr Pro Val Glu Arg Gly Leu Ile Thr Ser Trp Glu Asp
65 70 75 80

Met Glu Ile Met Trp Lys His Ile Tyr Asp Tyr Asn Leu Lys Leu Lys
85 90 95

Pro Cys Asp Gly Pro Val Leu Ile Thr Glu Pro Ala Leu Asn Pro Leu
100 105 110

```
Ala Asn Arg Gln Gln Ile Thr Glu Met Phe Phe Glu His Leu Gly Val
        115                 120                 125

Pro Ala Phe Tyr Met Ser Ile Gln Ala Val Leu Ala Leu Phe Ala Ala
    130                 135                 140

Gly Phe Thr Thr Gly Leu Val Leu Asn Ser Gly Ala Gly Val Thr Gln
145                 150                 155                 160

Ser Val Pro Ile Phe Glu Gly Tyr Cys Leu Pro His Gly Val Gln Gln
                165                 170                 175

Leu Asp Leu Ala Gly Leu Asp Leu Thr Asn Tyr Leu Met Val Leu Met
            180                 185                 190

Lys Asn His Gly Ile Met Leu Leu Ser Ala Ser Asp Arg Lys Ile Val
        195                 200                 205

Glu Asp Ile Lys Glu Ser Phe Cys Tyr Val Ala Met Asn Tyr Glu Glu
    210                 215                 220

Glu Met Ala Lys Lys Pro Asp Cys Leu Glu Lys Val Tyr Gln Leu Pro
225                 230                 235                 240

Asp Gly Lys Val Ile Gln Leu His Asp Gln Leu Phe Ser Cys Pro Glu
                245                 250                 255

Ala Leu Phe Ser Pro Cys His Met Asn Leu Glu Ala Pro Gly Ile Asp
            260                 265                 270

Lys Ile Cys Phe Ser Ser Ile Met Lys Cys Asp Thr Gly Leu Arg Asn
        275                 280                 285

Ser Phe Phe Ser Asn Ile Ile Leu Ala Gly Gly Ser Thr Ser Phe Pro
    290                 295                 300

Gly Leu Asp Lys Arg Leu Val Lys Asp Ile Ala Lys Val Ala Pro Ala
305                 310                 315                 320

Asn Thr Ala Val Gln Val Ile Ala Pro Pro Glu Arg Lys Ile Ser Val
                325                 330                 335
```

```
Trp Met Gly Gly Ser Ile Leu Ala Ser Leu Ser Ala Phe Gln Asp Met
            340                 345                 350

Trp Ile Thr Ala Ala Glu Phe Lys Glu Val Gly Pro Asn Ile Val His
        355                 360                 365

Gln Arg Cys Phe
    370
```

<210> 1579
<211> 583
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 456; "

<220>
<221> source
<223> /note="Gene Symbol: ALCAM; "

<220>
<221> source
<223> /note="Gene Name:
activated leukocyte cell adhesion
molecule; "

<220>
<221> source
<223> /note="Uniprot ID: Q13740; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000305988"

<400> 1579

```
Met Glu Ser Lys Gly Ala Ser Ser Cys Arg Leu Leu Phe Cys Leu Leu
1               5                  10                  15

Ile Ser Ala Thr Val Phe Arg Pro Gly Leu Gly Trp Tyr Thr Val Asn
            20                  25                  30

Ser Ala Tyr Gly Asp Thr Ile Ile Ile Pro Cys Arg Leu Asp Val Pro
        35                  40                  45

Gln Asn Leu Met Phe Gly Lys Trp Lys Tyr Glu Lys Pro Asp Gly Ser
    50                  55                  60

Pro Val Phe Ile Ala Phe Arg Ser Ser Thr Lys Lys Ser Val Gln Tyr
```

65 70 75 80

Asp Asp Val Pro Glu Tyr Lys Asp Arg Leu Asn Leu Ser Glu Asn Tyr
85 90 95

Thr Leu Ser Ile Ser Asn Ala Arg Ile Ser Asp Glu Lys Arg Phe Val
100 105 110

Cys Met Leu Val Thr Glu Asp Asn Val Phe Glu Ala Pro Thr Ile Val
115 120 125

Lys Val Phe Lys Gln Pro Ser Lys Pro Glu Ile Val Ser Lys Ala Leu
130 135 140

Phe Leu Glu Thr Glu Gln Leu Lys Lys Leu Gly Asp Cys Ile Ser Glu
145 150 155 160

Asp Ser Tyr Pro Asp Gly Asn Ile Thr Trp Tyr Arg Asn Gly Lys Val
165 170 175

Leu His Pro Leu Glu Gly Ala Val Val Ile Ile Phe Lys Lys Glu Met
180 185 190

Asp Pro Val Thr Gln Leu Tyr Thr Met Thr Ser Thr Leu Glu Tyr Lys
195 200 205

Thr Thr Lys Ala Asp Ile Gln Met Pro Phe Thr Cys Ser Val Thr Tyr
210 215 220

Tyr Gly Pro Ser Gly Gln Lys Thr Ile His Ser Glu Gln Ala Val Phe
225 230 235 240

Asp Ile Tyr Tyr Pro Thr Glu Gln Val Thr Ile Gln Val Leu Pro Pro
245 250 255

Lys Asn Ala Ile Lys Glu Gly Asp Asn Ile Thr Leu Lys Cys Leu Gly
260 265 270

Asn Gly Asn Pro Pro Pro Glu Glu Phe Leu Phe Tyr Leu Pro Gly Gln
275 280 285

Pro Glu Gly Ile Arg Ser Ser Asn Thr Tyr Thr Leu Thr Asp Val Arg
290 295 300

```
Arg Asn Ala Thr Gly Asp Tyr Lys Cys Ser Leu Ile Asp Lys Lys Ser
305                 310                 315                 320

Met Ile Ala Ser Thr Ala Ile Thr Val His Tyr Leu Asp Leu Ser Leu
                325                 330                 335

Asn Pro Ser Gly Glu Val Thr Arg Gln Ile Gly Asp Ala Leu Pro Val
            340                 345                 350

Ser Cys Thr Ile Ser Ala Ser Arg Asn Ala Thr Val Val Trp Met Lys
        355                 360                 365

Asp Asn Ile Arg Leu Arg Ser Ser Pro Ser Phe Ser Ser Leu His Tyr
    370                 375                 380

Gln Asp Ala Gly Asn Tyr Val Cys Glu Thr Ala Leu Gln Glu Val Glu
385                 390                 395                 400

Gly Leu Lys Lys Arg Glu Ser Leu Thr Leu Ile Val Glu Gly Lys Pro
                405                 410                 415

Gln Ile Lys Met Thr Lys Lys Thr Asp Pro Ser Gly Leu Ser Lys Thr
            420                 425                 430

Ile Ile Cys His Val Glu Gly Phe Pro Lys Pro Ala Ile Gln Trp Thr
        435                 440                 445

Ile Thr Gly Ser Gly Ser Val Ile Asn Gln Thr Glu Glu Ser Pro Tyr
    450                 455                 460

Ile Asn Gly Arg Tyr Tyr Ser Lys Ile Ile Ile Ser Pro Glu Glu Asn
465                 470                 475                 480

Val Thr Leu Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val Asn
                485                 490                 495

Ser Leu Asn Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp
            500                 505                 510

Glu Ile Ser Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu
        515                 520                 525
```

```
Ile Val Gly Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly
    530                 535                 540

Val Val Tyr Trp Leu Tyr Met Lys Lys Ser Lys Thr Ala Ser Lys His
545                 550                 555                 560

Val Asn Lys Asp Leu Gly Asn Met Glu Glu Asn Lys Lys Leu Glu Glu
                565                 570                 575

Asn Asn His Lys Thr Glu Ala
            580


<210> 1580
<211> 532
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 456; "

<220>
<221> source
<223> /note="Gene Symbol: ALCAM; "

<220>
<221> source
<223> /note="Gene Name:
      activated leukocyte cell adhesion
      molecule; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418213"

<400> 1580
Met Phe Gly Lys Trp Lys Tyr Glu Lys Pro Asp Gly Ser Pro Val Phe
1               5                   10                  15

Ile Ala Phe Arg Ser Ser Thr Lys Lys Ser Val Gln Tyr Asp Asp Val
            20                  25                  30

Pro Glu Tyr Lys Asp Arg Leu Asn Leu Ser Glu Asn Tyr Thr Leu Ser
        35                  40                  45

Ile Ser Asn Ala Arg Ile Ser Asp Glu Lys Arg Phe Val Cys Met Leu
    50                  55                  60
```

Val Thr Glu Asp Asn Val Phe Glu Ala Pro Thr Ile Val Lys Val Phe
65 70 75 80

Lys Gln Pro Ser Lys Pro Glu Ile Val Ser Lys Ala Leu Phe Leu Glu
85 90 95

Thr Glu Gln Leu Lys Lys Leu Gly Asp Cys Ile Ser Glu Asp Ser Tyr
100 105 110

Pro Asp Gly Asn Ile Thr Trp Tyr Arg Asn Gly Lys Val Leu His Pro
115 120 125

Leu Glu Gly Ala Val Val Ile Ile Phe Lys Lys Glu Met Asp Pro Val
130 135 140

Thr Gln Leu Tyr Thr Met Thr Ser Thr Leu Glu Tyr Lys Thr Thr Lys
145 150 155 160

Ala Asp Ile Gln Met Pro Phe Thr Cys Ser Val Thr Tyr Tyr Gly Pro
165 170 175

Ser Gly Gln Lys Thr Ile His Ser Glu Gln Ala Val Phe Asp Ile Tyr
180 185 190

Tyr Pro Thr Glu Gln Val Thr Ile Gln Val Leu Pro Pro Lys Asn Ala
195 200 205

Ile Lys Glu Gly Asp Asn Ile Thr Leu Lys Cys Leu Gly Asn Gly Asn
210 215 220

Pro Pro Pro Glu Glu Phe Leu Phe Tyr Leu Pro Gly Gln Pro Glu Gly
225 230 235 240

Ile Arg Ser Ser Asn Thr Tyr Thr Leu Thr Asp Val Arg Arg Asn Ala
245 250 255

Thr Gly Asp Tyr Lys Cys Ser Leu Ile Asp Lys Lys Ser Met Ile Ala
260 265 270

Ser Thr Ala Ile Thr Val His Tyr Leu Asp Leu Ser Leu Asn Pro Ser
275 280 285

Gly Glu Val Thr Arg Gln Ile Gly Asp Ala Leu Pro Val Ser Cys Thr

290 295 300

Ile Ser Ala Ser Arg Asn Ala Thr Val Val Trp Met Lys Asp Asn Ile
305 310 315 320

Arg Leu Arg Ser Ser Pro Ser Phe Ser Ser Leu His Tyr Gln Asp Ala
325 330 335

Gly Asn Tyr Val Cys Glu Thr Ala Leu Gln Glu Val Glu Gly Leu Lys
340 345 350

Lys Arg Glu Ser Leu Thr Leu Ile Val Glu Gly Lys Pro Gln Ile Lys
355 360 365

Met Thr Lys Lys Thr Asp Pro Ser Gly Leu Ser Lys Thr Ile Ile Cys
370 375 380

His Val Glu Gly Phe Pro Lys Pro Ala Ile Gln Trp Thr Ile Thr Gly
385 390 395 400

Ser Gly Ser Val Ile Asn Gln Thr Glu Glu Ser Pro Tyr Ile Asn Gly
405 410 415

Arg Tyr Tyr Ser Lys Ile Ile Ile Ser Pro Glu Glu Asn Val Thr Leu
420 425 430

Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn
435 440 445

Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser
450 455 460

Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile Val Gly
465 470 475 480

Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly Val Val Tyr
485 490 495

Trp Leu Tyr Met Lys Lys Ser Lys Thr Ala Ser Lys His Val Asn Lys
500 505 510

Asp Leu Gly Asn Met Glu Glu Asn Lys Lys Leu Glu Glu Asn Asn His
515 520 525

Lys Thr Glu Ala
530

<210> 1581
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 456; "

<220>
<221> source
<223> /note="Gene Symbol: ALCAM; "

<220>
<221> source
<223> /note="Gene Name:
activated leukocyte cell adhesion
molecule; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418937"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1581
Xaa Leu Gly Asp Cys Ile Ser Glu Asp Ser Tyr Pro Asp Gly Asn Ile
1 5 10 15

Thr Trp Tyr Arg Asn Gly Lys Val Leu His Pro Leu Glu Gly Ala Val
20 25 30

Val Ile Ile Phe Lys Lys Glu Met Asp Pro Val Thr Gln Leu Tyr Thr
35 40 45

Met Thr Ser Thr Leu Glu Tyr Lys Thr Thr Lys Ala Asp Ile Gln Met
50 55 60

Pro Phe Thr Cys Ser Val Thr Tyr Tyr Gly Pro Ser Gly Gln Lys Thr
65 70 75 80

Ile His Ser Glu Gln Ala Val Phe Asp Ile Tyr Tyr Leu Asp Leu Ser

```
                85                  90                  95

Leu Asn Pro Ser Gly Glu Val Thr Arg Gln Ile Gly Asp Ala Leu Pro
            100                 105                 110

Val Ser Cys Thr Ile Ser Ala Ser Arg Asn Ala Thr Val Val Trp Met
        115                 120                 125

Lys Asp Asn Ile Arg Leu Arg Ser Ser Pro Ser Phe Ser Ser Leu His
    130                 135                 140

Tyr Gln Asp Ala Gly Asn Tyr Val Cys Glu Thr Ala Leu Gln Glu Val
145                 150                 155                 160

Glu Gly Leu Lys Lys Arg Glu Ser Leu Thr Leu Ile Val Glu Gly Lys
                165                 170                 175

Pro Gln Ile Lys Met Thr Lys Lys Thr Asp Pro Ser Gly Leu Ser Lys
            180                 185                 190

Thr Ile Ile Cys His Val Glu Gly Phe Pro Lys Pro Ala Ile Gln Trp
        195                 200                 205

Thr Ile Thr Gly Ser Gly Ser Val Ile Asn Gln Thr Glu Glu Ser Pro
    210                 215                 220

Tyr Ile Asn Gly Arg Tyr Tyr Ser Lys Ile Ile Ile Ser Pro Glu Glu
225                 230                 235                 240

Asn Val Thr Leu Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val
                245                 250                 255

Asn Ser Leu Asn Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala
            260                 265                 270

Asp Glu Ile Ser Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys
        275                 280                 285

Leu Ile Val Gly Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala
    290                 295                 300

Gly Val Val Tyr Trp Leu Tyr Met Lys Lys Ser Lys Thr Ala Ser Lys
305                 310                 315                 320
```

```
His Val Asn Lys Asp Leu Gly Asn Met Glu Glu Asn Lys Lys Leu Glu
                325                 330                 335

Glu Asn Asn His Lys Thr Glu Ala
            340
```

<210> 1582
<211> 570
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 456; "

<220>
<221> source
<223> /note="Gene Symbol: ALCAM; "

<220>
<221> source
<223> /note="Gene Name:
activated leukocyte cell adhesion
molecule; "

<220>
<221> source
<223> /note="Uniprot ID: Q13740; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419236"

<400> 1582

```
Met Glu Ser Lys Gly Ala Ser Ser Cys Arg Leu Leu Phe Cys Leu Leu
1               5                  10                  15

Ile Ser Ala Thr Val Phe Arg Pro Gly Leu Gly Trp Tyr Thr Val Asn
            20                  25                  30

Ser Ala Tyr Gly Asp Thr Ile Ile Ile Pro Cys Arg Leu Asp Val Pro
        35                  40                  45

Gln Asn Leu Met Phe Gly Lys Trp Lys Tyr Glu Lys Pro Asp Gly Ser
    50                  55                  60

Pro Val Phe Ile Ala Phe Arg Ser Ser Thr Lys Lys Ser Val Gln Tyr
65                  70                  75                  80
```

```
Asp Asp Val Pro Glu Tyr Lys Asp Arg Leu Asn Leu Ser Glu Asn Tyr
                85                  90                  95

Thr Leu Ser Ile Ser Asn Ala Arg Ile Ser Asp Glu Lys Arg Phe Val
            100                 105                 110

Cys Met Leu Val Thr Glu Asp Asn Val Phe Glu Ala Pro Thr Ile Val
        115                 120                 125

Lys Val Phe Lys Gln Pro Ser Lys Pro Glu Ile Val Ser Lys Ala Leu
    130                 135                 140

Phe Leu Glu Thr Glu Gln Leu Lys Lys Leu Gly Asp Cys Ile Ser Glu
145                 150                 155                 160

Asp Ser Tyr Pro Asp Gly Asn Ile Thr Trp Tyr Arg Asn Gly Lys Val
                165                 170                 175

Leu His Pro Leu Glu Gly Ala Val Val Ile Ile Phe Lys Lys Glu Met
            180                 185                 190

Asp Pro Val Thr Gln Leu Tyr Thr Met Thr Ser Thr Leu Glu Tyr Lys
        195                 200                 205

Thr Thr Lys Ala Asp Ile Gln Met Pro Phe Thr Cys Ser Val Thr Tyr
    210                 215                 220

Tyr Gly Pro Ser Gly Gln Lys Thr Ile His Ser Glu Gln Ala Val Phe
225                 230                 235                 240

Asp Ile Tyr Tyr Pro Thr Glu Gln Val Thr Ile Gln Val Leu Pro Pro
                245                 250                 255

Lys Asn Ala Ile Lys Glu Gly Asp Asn Ile Thr Leu Lys Cys Leu Gly
            260                 265                 270

Asn Gly Asn Pro Pro Pro Glu Glu Phe Leu Phe Tyr Leu Pro Gly Gln
        275                 280                 285

Pro Glu Gly Ile Arg Ser Ser Asn Thr Tyr Thr Leu Thr Asp Val Arg
    290                 295                 300
```

```
Arg Asn Ala Thr Gly Asp Tyr Lys Cys Ser Leu Ile Asp Lys Lys Ser
305                 310                 315                 320

Met Ile Ala Ser Thr Ala Ile Thr Val His Tyr Leu Asp Leu Ser Leu
                325                 330                 335

Asn Pro Ser Gly Glu Val Thr Arg Gln Ile Gly Asp Ala Leu Pro Val
            340                 345                 350

Ser Cys Thr Ile Ser Ala Ser Arg Asn Ala Thr Val Val Trp Met Lys
        355                 360                 365

Asp Asn Ile Arg Leu Arg Ser Ser Pro Ser Phe Ser Ser Leu His Tyr
    370                 375                 380

Gln Asp Ala Gly Asn Tyr Val Cys Glu Thr Ala Leu Gln Glu Val Glu
385                 390                 395                 400

Gly Leu Lys Lys Arg Glu Ser Leu Thr Leu Ile Val Glu Gly Lys Pro
                405                 410                 415

Gln Ile Lys Met Thr Lys Lys Thr Asp Pro Ser Gly Leu Ser Lys Thr
            420                 425                 430

Ile Ile Cys His Val Glu Gly Phe Pro Lys Pro Ala Ile Gln Trp Thr
        435                 440                 445

Ile Thr Gly Ser Gly Ser Val Ile Asn Gln Thr Glu Glu Ser Pro Tyr
    450                 455                 460

Ile Asn Gly Arg Tyr Tyr Ser Lys Ile Ile Ile Ser Pro Glu Glu Asn
465                 470                 475                 480

Val Thr Leu Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val Asn
                485                 490                 495

Ser Leu Asn Val Ser Ala Asn Glu Asn Arg Glu Lys Val Asn Asp Gln
            500                 505                 510

Ala Lys Leu Ile Val Gly Ile Val Val Gly Leu Leu Leu Ala Ala Leu
        515                 520                 525

Val Ala Gly Val Val Tyr Trp Leu Tyr Met Lys Lys Ser Lys Thr Ala
```

```
    530                 535                 540

Ser Lys His Val Asn Lys Asp Leu Gly Asn Met Glu Glu Asn Lys Lys
545                 550                 555                 560

Leu Glu Glu Asn Asn His Lys Thr Glu Ala
                565                 570


<210> 1583
<211> 357
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N9N2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000320461"

<400> 1583
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1               5                   10                  15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20                  25                  30

Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
        35                  40                  45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
    50                  55                  60

Ala Pro Ser Leu Leu Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr
65                  70                  75                  80
```

```
Arg Lys Lys Ile Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys
                85                  90                  95

Pro Gly Gln Asp Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly
            100                 105                 110

Val Ile Ser Ala Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg
        115                 120                 125

Arg Lys Gln Pro Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val
    130                 135                 140

Glu Val Gln Glu Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys
145                 150                 155                 160

Cys Ser Met Asp His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys
                165                 170                 175

Lys Leu His Leu Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu
            180                 185                 190

Ile Gln Gln Thr Cys Glu Met Leu Gln Gln Cys Lys Glu Glu Phe Ile
        195                 200                 205

Asn Asp Ile Ser Gly Gly Lys Pro Leu Glu Val Glu Met Ala Gly Ile
    210                 215                 220

Glu Tyr Met Asn Asp Asp Pro Gly Met Val Asp Val Leu Tyr Ala Lys
225                 230                 235                 240

Val His Met Lys Asp Gly Ser Asn Arg Leu Gln Glu Leu Val Asp Arg
                245                 250                 255

Val Leu Glu Arg Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp Asn
            260                 265                 270

Ser Val Lys Leu His Ala Thr Val Met Asn Thr Leu Phe Arg Lys Asp
        275                 280                 285

Pro Asn Ala Glu Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys Tyr
    290                 295                 300
```

```
Ile Phe Lys Glu Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys Leu
305                 310                 315                 320


Phe Glu Asn Phe Tyr Phe Gly Ser Leu Lys Leu Asn Ser Ile His Ile
                325                 330                 335


Ser Gln Arg Phe Thr Val Asp Ser Phe Gly Asn Tyr Ala Ser Cys Gly
            340                 345                 350


Gln Ile Asp Phe Ser
        355


<210> 1584
<211> 357
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N9N2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000320810"

<400> 1584
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1               5                   10                  15


Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20                  25                  30


Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
        35                  40                  45
```

```
Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
    50                  55                  60

Ala Pro Ser Leu Leu Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr
65                  70                  75                  80

Arg Lys Lys Ile Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys
                85                  90                  95

Pro Gly Gln Asp Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly
            100                 105                 110

Val Ile Ser Ala Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg
        115                 120                 125

Arg Lys Gln Pro Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val
    130                 135                 140

Glu Val Gln Glu Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys
145                 150                 155                 160

Cys Ser Met Asp His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys
                165                 170                 175

Lys Leu His Leu Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu
            180                 185                 190

Ile Gln Gln Thr Cys Glu Met Leu Gln Gln Cys Lys Glu Glu Phe Ile
        195                 200                 205

Asn Asp Ile Ser Gly Gly Lys Pro Leu Glu Val Glu Met Ala Gly Ile
    210                 215                 220

Glu Tyr Met Asn Asp Asp Pro Gly Met Val Asp Val Leu Tyr Ala Lys
225                 230                 235                 240

Val His Met Lys Asp Gly Ser Asn Arg Leu Gln Glu Leu Val Asp Arg
                245                 250                 255

Val Leu Glu Arg Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp Asn
            260                 265                 270

Ser Val Lys Leu His Ala Thr Val Met Asn Thr Leu Phe Arg Lys Asp
```

```
        275                 280                 285

Pro Asn Ala Glu Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys Tyr
    290                 295                 300

Ile Phe Lys Glu Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys Leu
305                 310                 315                 320

Phe Glu Asn Phe Tyr Phe Gly Ser Leu Lys Leu Asn Ser Ile His Ile
                325                 330                 335

Ser Gln Arg Phe Thr Val Asp Ser Phe Gly Asn Tyr Ala Ser Cys Gly
            340                 345                 350

Gln Ile Asp Phe Ser
        355


<210> 1585
<211> 400
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N9N2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000339404"

<400> 1585
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1               5                   10                  15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20                  25                  30
```

```
Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
        35                  40                  45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
    50                  55                  60

Ala Pro Ser Leu Leu Tyr Asn Leu Ile His Leu Asn Thr Ser Asn Asp
65                  70                  75                  80

Cys Gly Phe Gln Lys Ile Thr Leu Asp Cys Gln Asn Ile Tyr Thr Trp
                85                  90                  95

Lys Ser Arg His Ile Val Gly Lys Arg Gly Asp Thr Arg Lys Lys Ile
            100                 105                 110

Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys Pro Gly Gln Asp
        115                 120                 125

Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly Val Ile Ser Ala
    130                 135                 140

Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg Arg Lys Gln Pro
145                 150                 155                 160

Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val Glu Val Gln Glu
                165                 170                 175

Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys Cys Ser Met Asp
            180                 185                 190

His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys Lys Leu His Leu
        195                 200                 205

Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu Ile Gln Gln Thr
    210                 215                 220

Cys Glu Met Leu Gln Gln Cys Lys Glu Glu Phe Ile Asn Asp Ile Ser
225                 230                 235                 240

Gly Gly Lys Pro Leu Glu Val Glu Met Ala Gly Ile Glu Tyr Met Asn
                245                 250                 255
```

```
Asp Asp Pro Gly Met Val Asp Val Leu Tyr Ala Lys Val His Met Lys
            260                 265                 270

Asp Gly Ser Asn Arg Leu Gln Glu Leu Val Asp Arg Val Leu Glu Arg
        275                 280                 285

Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp Asn Ser Val Lys Leu
    290                 295                 300

His Ala Thr Val Met Asn Thr Leu Phe Arg Lys Asp Pro Asn Ala Glu
305                 310                 315                 320

Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys Tyr Ile Phe Lys Glu
                325                 330                 335

Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys Ser Phe Ala Leu Leu
            340                 345                 350

Pro Arg Leu Glu Tyr Asn Asp Ala Ile Ser Ala His Cys Asn Leu Cys
        355                 360                 365

Leu Pro Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser Gln Val Ala Gly
    370                 375                 380

Ile Thr Gly Val Ser Asp Ala Tyr Ser Gln Ser Leu Pro Gly Lys Ser
385                 390                 395                 400
```

<210> 1586
<211> 400
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>

<221> source
<223> /note="Uniprot ID: Q8N9N2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378373"

<400> 1586
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1   5   10   15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20   25   30

Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
        35   40   45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
    50   55   60

Ala Pro Ser Leu Leu Tyr Asn Leu Ile His Leu Asn Thr Ser Asn Asp
65   70   75   80

Cys Gly Phe Gln Lys Ile Thr Leu Asp Cys Gln Asn Ile Tyr Thr Trp
                85   90   95

Lys Ser Arg His Ile Val Gly Lys Arg Gly Asp Thr Arg Lys Lys Ile
            100   105   110

Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys Pro Gly Gln Asp
        115   120   125

Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly Val Ile Ser Ala
    130   135   140

Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg Arg Lys Gln Pro
145   150   155   160

Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val Glu Val Gln Glu
                165   170   175

Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys Cys Ser Met Asp
            180   185   190

His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys Lys Leu His Leu

```
        195                 200                 205

Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu Ile Gln Gln Thr
    210                 215                 220

Cys Glu Met Leu Gln Gln Cys Lys Glu Glu Phe Ile Asn Asp Ile Ser
225                 230                 235                 240

Gly Gly Lys Pro Leu Glu Val Glu Met Ala Gly Ile Glu Tyr Met Asn
                245                 250                 255

Asp Asp Pro Gly Met Val Asp Val Leu Tyr Ala Lys Val His Met Lys
            260                 265                 270

Asp Gly Ser Asn Arg Leu Gln Glu Leu Val Asp Arg Val Leu Glu Arg
        275                 280                 285

Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp Asn Ser Val Lys Leu
    290                 295                 300

His Ala Thr Val Met Asn Thr Leu Phe Arg Lys Asp Pro Asn Ala Glu
305                 310                 315                 320

Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys Tyr Ile Phe Lys Glu
                325                 330                 335

Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys Ser Phe Ala Leu Leu
            340                 345                 350

Pro Arg Leu Glu Tyr Asn Asp Ala Ile Ser Ala His Cys Asn Leu Cys
        355                 360                 365

Leu Pro Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser Gln Val Ala Gly
    370                 375                 380

Ile Thr Gly Val Ser Asp Ala Tyr Ser Gln Ser Leu Pro Gly Lys Ser
385                 390                 395                 400
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<210> 1587
<211> 357
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N9N2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378377"

<400> 1587

```
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1               5                  10                  15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20                  25                  30

Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
        35                  40                  45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
    50                  55                  60

Ala Pro Ser Leu Leu Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr
65                  70                  75                  80

Arg Lys Lys Ile Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys
                85                  90                  95

Pro Gly Gln Asp Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly
            100                 105                 110

Val Ile Ser Ala Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg
        115                 120                 125

Arg Lys Gln Pro Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val
    130                 135                 140
```

```
Glu Val Gln Glu Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys
145                 150                 155                 160

Cys Ser Met Asp His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys
                165                 170                 175

Lys Leu His Leu Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu
            180                 185                 190

Ile Gln Gln Thr Cys Glu Met Leu Gln Gln Cys Lys Glu Glu Phe Ile
        195                 200                 205

Asn Asp Ile Ser Gly Gly Lys Pro Leu Glu Val Glu Met Ala Gly Ile
    210                 215                 220

Glu Tyr Met Asn Asp Asp Pro Gly Met Val Asp Val Leu Tyr Ala Lys
225                 230                 235                 240

Val His Met Lys Asp Gly Ser Asn Arg Leu Gln Glu Leu Val Asp Arg
                245                 250                 255

Val Leu Glu Arg Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp Asn
            260                 265                 270

Ser Val Lys Leu His Ala Thr Val Met Asn Thr Leu Phe Arg Lys Asp
        275                 280                 285

Pro Asn Ala Glu Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys Tyr
    290                 295                 300

Ile Phe Lys Glu Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys Leu
305                 310                 315                 320

Phe Glu Asn Phe Tyr Phe Gly Ser Leu Lys Leu Asn Ser Ile His Ile
                325                 330                 335

Ser Gln Arg Phe Thr Val Asp Ser Phe Gly Asn Tyr Ala Ser Cys Gly
            340                 345                 350

Gln Ile Asp Phe Ser
        355
```

<210> 1588
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431255"

<400> 1588
Met Glu Cys Ala Asp Glu Pro Cys Asp Ala Tyr Glu Val Glu Gln Thr
1 5 10 15

Pro Gln Gly Phe Arg Ser Thr Leu Arg Ala Pro Ser Leu Leu Tyr Lys
20 25 30

His Ile Val Gly Lys Arg Gly Asp Thr Arg Lys Lys Ile Glu Met Glu
35 40 45

Thr Lys Thr Ser Ile Ser Ile Pro Lys Pro Gly Gln Asp Gly Glu Ile
50 55 60

Val Ile Thr Gly Gln His Arg Asn Gly Val Ile Ser Ala Arg Thr Arg
65 70 75 80

Ile Asp Val Leu Leu Asp Thr Phe Arg Arg Lys Gln Pro Phe Thr His
85 90 95

Phe Leu Ala Phe Phe Leu Asn Glu Val Glu Val Gln Glu Gly Phe Leu
100 105 110

Arg Phe Gln Glu Glu Val Leu Ala Lys Cys Ser Met
115 120

<210> 1589

<211> 292
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431299"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1589
Xaa Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr Arg Lys Lys Ile
1 5 10 15

Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys Pro Gly Gln Asp
20 25 30

Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly Val Ile Ser Ala
35 40 45

Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg Arg Lys Gln Pro
50 55 60

Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val Glu Val Gln Glu
65 70 75 80

Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys Cys Ser Met Asp
85 90 95

His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys Lys Leu His Leu
100 105 110

```
Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu Ile Gln Gln Thr
        115                 120                 125

Cys Glu Met Leu Gln Gln Cys Lys Glu Glu Phe Ile Asn Asp Ile Ser
    130                 135                 140

Gly Gly Lys Pro Leu Glu Val Glu Met Ala Gly Ile Glu Tyr Met Asn
145                 150                 155                 160

Asp Asp Pro Gly Met Val Asp Val Leu Tyr Ala Lys Val His Met Lys
                165                 170                 175

Asp Gly Ser Asn Arg Leu Gln Glu Leu Val Asp Arg Val Leu Glu Arg
            180                 185                 190

Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp Asn Ser Val Lys Leu
        195                 200                 205

His Ala Thr Val Met Asn Thr Leu Phe Arg Lys Asp Pro Asn Ala Glu
    210                 215                 220

Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys Tyr Ile Phe Lys Glu
225                 230                 235                 240

Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys Ser Phe Ala Leu Leu
                245                 250                 255

Pro Arg Leu Glu Tyr Asn Asp Ala Ile Ser Ala His Cys Asn Leu Cys
            260                 265                 270

Leu Pro Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser Gln Val Ala Gly
        275                 280                 285

Ile Thr Val Val
    290


<210> 1590
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "
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<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431419"

<400> 1590
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1 5 10 15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
20 25 30

Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
35 40 45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
50 55 60

Ala Pro Ser Leu Leu Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr
65 70 75 80

Arg Lys Lys Ile Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys
85 90 95

Pro Gly Gln Asp Gly Glu Ile
100

<210> 1591
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>

<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431573"

<400> 1591
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1 5 10 15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
20 25 30

Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
35 40 45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
50 55 60

Ala Pro Ser Leu Leu Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr
65 70 75 80

Arg Lys Lys Ile Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys
85 90 95

Pro Gly Gln Asp Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly
100 105 110

Val Ile Ser Ala Arg Thr Arg Ile Asp Val Leu
115 120

<210> 1592
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source

<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431746"

<400> 1592
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1 5 10 15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
20 25 30

Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
35 40 45

Ala Tyr Glu Val Glu Gln Thr Pro
50 55

<210> 1593
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432418"

<400> 1593
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1 5 10 15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
20 25 30

```
Glu Asp Phe Tyr Gln Gly Ser Met Glu Cys Ala Asp Glu Pro Cys Asp
        35                  40                  45

Ala Tyr Glu Val Glu Gln Thr Pro Gln Gly Phe Arg Ser Thr Leu Arg
    50                  55                  60

Ala Pro Ser Leu Leu Tyr Lys His Ile Val Gly Lys Arg Gly Asp Thr
65                  70                  75                  80

Arg Lys Lys Ile Glu Met Glu Thr Lys Thr Ser Ile Ser Ile Pro Lys
                85                  90                  95

Pro Gly Gln Asp Gly Glu Ile Val Ile Thr Gly Gln His Arg Asn Gly
            100                 105                 110

Val Ile Ser Ala Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg
        115                 120                 125

Arg Lys Gln Pro Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val
    130                 135                 140

Glu Val Gln Glu Gly Phe Leu Arg
145                 150


<210> 1594
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434468"

<400> 1594
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
```

```
1               5                   10                  15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20                  25                  30

Glu Asp Phe Tyr Gln Gly Trp Ser Ala Val Ala
        35                  40


<210> 1595
<211> 176
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435147"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1595
Xaa Ile Thr Gly Gln His Arg Asn Gly Val Ile Ser Ala Arg Thr Arg
1               5                   10                  15

Ile Asp Val Leu Leu Asp Thr Phe Arg Arg Lys Gln Pro Phe Thr His
            20                  25                  30

Phe Leu Ala Phe Phe Leu Asn Glu Val Glu Val Gln Glu Gly Phe Leu
        35                  40                  45

Arg Phe Gln Glu Glu Val Leu Ala Lys Cys Ser Met Asp His Gly Val
    50                  55                  60
```

```
Asp Ser Ser Ile Phe Gln Asn Pro Lys Lys Leu His Leu Thr Ile Gly
65                  70                  75                  80

Met Leu Val Leu Leu Ser Glu Glu Glu Ile Gln Gln Thr Cys Glu Met
                85                  90                  95

Leu Gln Gln Cys Lys Glu Glu Phe Ile Lys Leu Gln Glu Leu Val Asp
            100                 105                 110

Arg Val Leu Glu Arg Phe Gln Ala Ser Gly Leu Ile Val Lys Glu Trp
        115                 120                 125

Asn Ser Val Lys Leu His Ala Thr Val Met Asn Thr Leu Phe Arg Lys
    130                 135                 140

Asp Pro Asn Ala Glu Gly Arg Tyr Asn Leu Tyr Thr Ala Glu Gly Lys
145                 150                 155                 160

Tyr Ile Phe Lys Glu Arg Glu Ser Phe Asp Gly Arg Asn Ile Leu Lys
                165                 170                 175
```

<210> 1596
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435191"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1596
Xaa Leu Ile His Leu Asn Thr Ser Asn Asp Cys Gly Phe Gln Lys Ile
1   5   10   15

Thr Leu Asp Cys Gln Asn Ile Tyr Thr Trp Lys Ser Arg His Ile Val
            20   25   30

Gly Lys Arg Gly Asp Thr Arg Lys Lys Ile Glu Met Glu Thr Lys Thr
        35   40   45

Ser Ile Ser Ile Pro Lys Pro Gly Gln Asp Gly Glu Ile Glu Lys Ser
    50   55   60

Glu Lys Glu Met Ile Trp
65   70

<210> 1597
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436098"

<400> 1597
Met Glu Val Leu Arg Pro Gln Leu Ile Arg Ile Asp Gly Arg Asn Tyr
1   5   10   15

Arg Lys Asn Pro Val Gln Glu Gln Thr Tyr Gln His Glu Glu Asp Glu
            20   25   30

Glu Asp Phe Tyr Gln Val Ile Thr Gly Gln His Arg Asn Gly Val Ile
        35   40   45

```
Ser Ala Arg Thr Arg Ile Asp Val Leu Leu Asp Thr Phe Arg Arg Lys
    50                  55                  60

Gln Pro Phe Thr His Phe Leu Ala Phe Phe Leu Asn Glu Val Glu Val
65                  70                  75                  80

Gln Glu Gly Phe Leu Arg Phe Gln Glu Glu Val Leu Ala Lys Cys Ser
                85                  90                  95

Met Asp His Gly Val Asp Ser Ser Ile Phe Gln Asn Pro Lys Lys Leu
            100                 105                 110

His Leu Thr Ile Gly Met Leu Val Leu Leu Ser Glu Glu Glu Ile Gln
        115                 120                 125

Gln Thr Cys Glu Met Leu Gln Gln Cys Lys Glu
    130                 135


<210> 1598
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 457; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC1; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436409"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1598
Xaa Lys Glu Glu Phe Ile Asn Asp Ile Ser Gly Gly Lys Pro Leu Glu
1               5                   10                  15
```

```
Val Glu Met Ala Gly Ile Glu Tyr Met Asn Asp Asp Pro Gly Met Val
            20                  25                  30

Asp Val Leu Tyr Ala Lys Val His Met Lys Asp Gly Ser Asn Arg Leu
        35                  40                  45

Gln Glu Leu Val Asp Arg Val Leu Glu Arg Phe Gln Ala Ser Gly Leu
    50                  55                  60

Ile Val Lys Glu Trp Asn Ser Val Lys Leu His Ala Thr Val Met Asn
65                  70                  75                  80

Thr Leu Phe Arg Lys Asp Pro Asn Ala Glu Gly Arg Tyr Asn Leu Tyr
                85                  90                  95

Thr Ala Glu Gly Lys Tyr Ile Phe Lys Glu Arg Glu Ser Phe Asp Gly
            100                 105                 110

Arg Asn Ile Leu Lys Val Ser Leu Met His Ile Leu Arg Ala Tyr Gln
        115                 120                 125

Glu Asn Pro Arg Ile Glu Lys Gly Leu Gly His Arg Glu Leu Val Val
    130                 135                 140

Val
145


<210> 1599
<211> 757
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 2; "

<220>
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<221> source
<223> /note="Uniprot ID: Q9H1I8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000305502"

<400> 1599
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1   5   10   15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu His Pro Glu Gln Lys
            20   25   30

Ala Asp Arg Tyr Phe Val Leu Tyr Lys Pro Pro Pro Lys Asp Asn Ile
        35   40   45

Pro Ala Leu Val Glu Glu Tyr Leu Glu Arg Ala Thr Phe Val Ala Asn
    50   55   60

Asp Leu Asp Trp Leu Leu Ala Leu Pro His Asp Lys Phe Trp Cys Gln
65   70   75   80

Val Ile Phe Asp Glu Thr Leu Gln Lys Cys Leu Asp Ser Tyr Leu Arg
                85   90   95

Tyr Val Pro Arg Lys Phe Asp Glu Gly Val Ala Ser Ala Pro Glu Val
            100   105   110

Val Asp Met Gln Lys Arg Leu His Arg Ser Val Phe Leu Thr Phe Leu
        115   120   125

Arg Met Ser Thr His Lys Glu Ser Lys Asp His Phe Ile Ser Pro Ser
    130   135   140

Ala Phe Gly Glu Ile Leu Tyr Asn Asn Phe Leu Phe Asp Ile Pro Lys
145   150   155   160

Ile Leu Asp Leu Cys Val Leu Phe Gly Lys Gly Asn Ser Pro Leu Leu
                165   170   175

Gln Lys Met Ile Gly Asn Ile Phe Thr Gln Gln Pro Ser Tyr Tyr Ser
            180   185   190

Asp Leu Asp Glu Thr Leu Pro Thr Ile Leu Gln Val Phe Ser Asn Ile

```
        195                 200                 205

Leu Gln His Cys Gly Leu Gln Gly Asp Gly Ala Asn Thr Thr Pro Gln
    210                 215                 220

Lys Leu Glu Glu Arg Gly Arg Leu Thr Pro Ser Asp Met Pro Leu Leu
225                 230                 235                 240

Glu Leu Lys Asp Ile Val Leu Tyr Leu Cys Asp Thr Cys Thr Thr Leu
                245                 250                 255

Trp Ala Phe Leu Asp Ile Phe Pro Leu Ala Cys Gln Thr Phe Gln Lys
            260                 265                 270

His Asp Phe Cys Tyr Arg Leu Ala Ser Phe Tyr Glu Ala Ala Ile Pro
        275                 280                 285

Glu Met Glu Ser Ala Ile Lys Lys Arg Arg Leu Glu Asp Ser Lys Leu
    290                 295                 300

Leu Gly Asp Leu Trp Gln Arg Leu Ser His Ser Arg Lys Lys Leu Met
305                 310                 315                 320

Glu Ile Phe His Ile Ile Leu Asn Gln Ile Cys Leu Leu Pro Ile Leu
                325                 330                 335

Glu Ser Ser Cys Asp Asn Ile Gln Gly Phe Ile Glu Glu Phe Leu Gln
            340                 345                 350

Ile Phe Ser Ser Leu Leu Gln Glu Lys Arg Phe Leu Arg Asp Tyr Asp
        355                 360                 365

Ala Leu Phe Pro Val Ala Glu Asp Ile Ser Leu Leu Gln Gln Ala Ser
    370                 375                 380

Ser Val Leu Asp Glu Thr Arg Thr Ala Tyr Ile Leu Gln Ala Val Glu
385                 390                 395                 400

Ser Ala Trp Glu Gly Val Asp Arg Arg Lys Ala Thr Asp Ala Lys Asp
                405                 410                 415

Pro Ser Val Ile Glu Glu Pro Asn Gly Glu Pro Asn Gly Val Thr Val
            420                 425                 430
```

```
Thr Ala Glu Ala Val Ser Gln Ala Ser Ser His Pro Glu Asn Ser Glu
        435                 440                 445

Glu Glu Glu Cys Met Gly Ala Ala Ala Ala Val Gly Pro Ala Met Cys
    450                 455                 460

Gly Val Glu Leu Asp Ser Leu Ile Ser Gln Val Lys Asp Leu Leu Pro
465                 470                 475                 480

Asp Leu Gly Glu Gly Phe Ile Leu Ala Cys Leu Glu Tyr Tyr His Tyr
                485                 490                 495

Asp Pro Glu Gln Val Ile Asn Asn Ile Leu Glu Glu Arg Leu Ala Pro
            500                 505                 510

Thr Leu Ser Gln Leu Asp Arg Asn Leu Asp Arg Glu Met Lys Pro Asp
        515                 520                 525

Pro Thr Pro Leu Leu Thr Ser Arg His Asn Val Phe Gln Asn Asp Glu
    530                 535                 540

Phe Asp Val Phe Ser Arg Asp Ser Val Asp Leu Ser Arg Val His Lys
545                 550                 555                 560

Gly Lys Ser Thr Arg Lys Glu Glu Asn Thr Arg Ser Leu Leu Asn Asp
                565                 570                 575

Lys Arg Ala Val Ala Ala Gln Arg Gln Arg Tyr Glu Gln Tyr Ser Val
            580                 585                 590

Val Val Glu Glu Val Pro Leu Gln Pro Gly Glu Ser Leu Pro Tyr His
        595                 600                 605

Ser Val Tyr Tyr Glu Asp Glu Tyr Asp Asp Thr Tyr Asp Gly Asn Gln
    610                 615                 620

Val Gly Ala Asn Asp Ala Asp Ser Asp Asp Glu Leu Ile Ser Arg Arg
625                 630                 635                 640

Pro Phe Thr Ile Pro Gln Val Leu Arg Thr Lys Val Pro Arg Glu Gly
                645                 650                 655
```

```
Gln Glu Glu Asp Asp Asp Asp Glu Glu Asp Asp Ala Asp Glu Glu Ala
            660                 665                 670

Pro Lys Pro Asp His Phe Val Gln Asp Pro Ala Val Leu Arg Glu Lys
        675                 680                 685

Ala Glu Ala Arg Arg Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His
    690                 695                 700

Asp Ser Ser Thr Ala Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser
705                 710                 715                 720

Arg Glu Thr Thr Gln Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr
                725                 730                 735

Arg Ala Asn His Asn Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys
            740                 745                 750

Gly Met Ile Pro Ser
        755


<210> 1600
<211> 757
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9H1I8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000380877"

<400> 1600
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```
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1               5                  10                  15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu His Pro Glu Gln Lys
            20                  25                  30

Ala Asp Arg Tyr Phe Val Leu Tyr Lys Pro Pro Pro Lys Asp Asn Ile
        35                  40                  45

Pro Ala Leu Val Glu Glu Tyr Leu Glu Arg Ala Thr Phe Val Ala Asn
    50                  55                  60

Asp Leu Asp Trp Leu Leu Ala Leu Pro His Asp Lys Phe Trp Cys Gln
65                  70                  75                  80

Val Ile Phe Asp Glu Thr Leu Gln Lys Cys Leu Asp Ser Tyr Leu Arg
                85                  90                  95

Tyr Val Pro Arg Lys Phe Asp Glu Gly Val Ala Ser Ala Pro Glu Val
            100                 105                 110

Val Asp Met Gln Lys Arg Leu His Arg Ser Val Phe Leu Thr Phe Leu
        115                 120                 125

Arg Met Ser Thr His Lys Glu Ser Lys Asp His Phe Ile Ser Pro Ser
    130                 135                 140

Ala Phe Gly Glu Ile Leu Tyr Asn Asn Phe Leu Phe Asp Ile Pro Lys
145                 150                 155                 160

Ile Leu Asp Leu Cys Val Leu Phe Gly Lys Gly Asn Ser Pro Leu Leu
                165                 170                 175

Gln Lys Met Ile Gly Asn Ile Phe Thr Gln Gln Pro Ser Tyr Tyr Ser
            180                 185                 190

Asp Leu Asp Glu Thr Leu Pro Thr Ile Leu Gln Val Phe Ser Asn Ile
        195                 200                 205

Leu Gln His Cys Gly Leu Gln Gly Asp Gly Ala Asn Thr Thr Pro Gln
    210                 215                 220

Lys Leu Glu Glu Arg Gly Arg Leu Thr Pro Ser Asp Met Pro Leu Leu
```

225 230 235 240

Glu Leu Lys Asp Ile Val Leu Tyr Leu Cys Asp Thr Cys Thr Thr Leu
245 250 255

Trp Ala Phe Leu Asp Ile Phe Pro Leu Ala Cys Gln Thr Phe Gln Lys
260 265 270

His Asp Phe Cys Tyr Arg Leu Ala Ser Phe Tyr Glu Ala Ala Ile Pro
275 280 285

Glu Met Glu Ser Ala Ile Lys Lys Arg Arg Leu Glu Asp Ser Lys Leu
290 295 300

Leu Gly Asp Leu Trp Gln Arg Leu Ser His Ser Arg Lys Lys Leu Met
305 310 315 320

Glu Ile Phe His Ile Ile Leu Asn Gln Ile Cys Leu Leu Pro Ile Leu
325 330 335

Glu Ser Ser Cys Asp Asn Ile Gln Gly Phe Ile Glu Glu Phe Leu Gln
340 345 350

Ile Phe Ser Ser Leu Leu Gln Glu Lys Arg Phe Leu Arg Asp Tyr Asp
355 360 365

Ala Leu Phe Pro Val Ala Glu Asp Ile Ser Leu Leu Gln Gln Ala Ser
370 375 380

Ser Val Leu Asp Glu Thr Arg Thr Ala Tyr Ile Leu Gln Ala Val Glu
385 390 395 400

Ser Ala Trp Glu Gly Val Asp Arg Arg Lys Ala Thr Asp Ala Lys Asp
405 410 415

Pro Ser Val Ile Glu Glu Pro Asn Gly Glu Pro Asn Gly Val Thr Val
420 425 430

Thr Ala Glu Ala Val Ser Gln Ala Ser Ser His Pro Glu Asn Ser Glu
435 440 445

Glu Glu Glu Cys Met Gly Ala Ala Ala Ala Val Gly Pro Ala Met Cys
450 455 460

```
Gly Val Glu Leu Asp Ser Leu Ile Ser Gln Val Lys Asp Leu Leu Pro
465                 470                 475                 480

Asp Leu Gly Glu Gly Phe Ile Leu Ala Cys Leu Glu Tyr Tyr His Tyr
                485                 490                 495

Asp Pro Glu Gln Val Ile Asn Asn Ile Leu Glu Glu Arg Leu Ala Pro
            500                 505                 510

Thr Leu Ser Gln Leu Asp Arg Asn Leu Asp Arg Glu Met Lys Pro Asp
        515                 520                 525

Pro Thr Pro Leu Leu Thr Ser Arg His Asn Val Phe Gln Asn Asp Glu
    530                 535                 540

Phe Asp Val Phe Ser Arg Asp Ser Val Asp Leu Ser Arg Val His Lys
545                 550                 555                 560

Gly Lys Ser Thr Arg Lys Glu Glu Asn Thr Arg Ser Leu Leu Asn Asp
                565                 570                 575

Lys Arg Ala Val Ala Ala Gln Arg Gln Arg Tyr Glu Gln Tyr Ser Val
            580                 585                 590

Val Val Glu Glu Val Pro Leu Gln Pro Gly Glu Ser Leu Pro Tyr His
        595                 600                 605

Ser Val Tyr Tyr Glu Asp Glu Tyr Asp Asp Thr Tyr Asp Gly Asn Gln
    610                 615                 620

Val Gly Ala Asn Asp Ala Asp Ser Asp Asp Glu Leu Ile Ser Arg Arg
625                 630                 635                 640

Pro Phe Thr Ile Pro Gln Val Leu Arg Thr Lys Val Pro Arg Glu Gly
                645                 650                 655

Gln Glu Glu Asp Asp Asp Asp Glu Glu Asp Asp Ala Asp Glu Glu Ala
            660                 665                 670

Pro Lys Pro Asp His Phe Val Gln Asp Pro Ala Val Leu Arg Glu Lys
        675                 680                 685
```

```
Ala Glu Ala Arg Arg Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His
    690                 695                 700

Asp Ser Ser Thr Ala Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser
705                 710                 715                 720

Arg Glu Thr Thr Gln Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr
                725                 730                 735

Arg Ala Asn His Asn Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys
            740                 745                 750

Gly Met Ile Pro Ser
        755


<210> 1601
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397077"

<400> 1601
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1               5                   10                  15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu Glu Thr Ser Leu His
            20                  25                  30

Ser Ser Gln Val Thr Thr Val Thr Trp Met Lys Pro Cys Leu Pro Ser
        35                  40                  45
```

Phe Arg Ser Ser Ala Ile Ser Ser Ser Thr Val Val Cys Lys Gly Thr
    50   55   60

Gly Pro Ile Pro His Pro Arg Ser Leu Arg Arg Gly Ala Asp
65   70   75

<210> 1602
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403031"

<400> 1602
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1   5   10   15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu Ile Cys Thr Cys Asn
            20   25   30

Ser Met Ile Gln Ile
        35

<210> 1603
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000408930"

<400> 1603
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1 5 10 15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu Ile Cys Thr Cys Asn
20 25 30

Ser Met Ile Gln Ile
35

<210> 1604
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410531"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1604
Xaa Ser Ala Gly Ala Gln Gly Ala Val Thr Val Val Gly Gly Gly Gly
1 5 10 15

Gly Gly Gly Gly Thr Glu Pro Val Val Glu Pro Pro Arg Pro Pro Arg
            20   25   30

Val Cys Arg Asp His Val Cys Leu Ile Cys Trp Asp Pro Arg Ala Gly
        35   40   45

Thr Gly Gln Val Ile Leu
    50

<210> 1605
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412382"

<400> 1605
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1   5   10   15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu His Pro Glu Gln Lys
            20   25   30

Ala Asp Arg Tyr Phe Val Leu Tyr Lys Pro Pro Pro Lys Asp Asn Ile
        35   40   45

Pro Ala Leu Val Glu Glu Tyr Leu Glu Arg Ala Thr Phe Val Ala Asn
    50   55   60

Asp Leu Asp Trp Leu Leu Ala Leu Pro His Asp Lys Phe Trp Cys Gln
65   70   75   80

Val Ile Phe Asp Glu Thr Leu Gln Lys Cys Leu Asp Ser Tyr Leu Arg

```
                85                  90                  95

Tyr Val Pro Arg Lys Phe Asp Glu Gly Val Ala Ser Ala Pro Glu Val
            100                 105                 110

Val Asp Met Gln Lys Arg Leu His Arg Ser Val Phe Leu Thr Phe Leu
        115                 120                 125

Arg Met Ser Thr His Lys Glu Ser Lys Asp His Phe Ile Ser Pro Ser
    130                 135                 140

Ala Phe Gly Glu Ile Leu Tyr Asn Asn Phe Leu Phe Asp Ile Pro Lys
145                 150                 155                 160

Ile Leu Asp Leu Cys Val Leu Phe Gly Lys Gly Asn Ser Pro Leu Leu
                165                 170                 175

Gln Lys Met Ile Gly Asn Ile Phe Thr Gln Gln Pro Ser Tyr Tyr Ser
            180                 185                 190

Asp Leu Asp Glu Thr Leu Pro Thr Ile Leu Gln Val Phe Ser Asn Ile
        195                 200                 205

Leu Gln His Cys Gly Leu Gln Gly Asp Gly Ala Asn Thr Thr Pro Gln
    210                 215                 220

Lys Leu Glu Glu Arg Gly Arg Leu Thr Pro Ser Asp Met Pro Leu Leu
225                 230                 235                 240
```

<210> 1606
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414545"

<400> 1606
Ser Trp Pro Ala Trp Ser Thr Thr Thr Thr Thr Gln Ser Arg Glu Met
1   5   10   15

Lys Pro Asp Pro Thr Pro Leu Leu Thr Ser Arg His Asn Val Phe Gln
            20   25   30

Asn Asp Glu Phe Asp Val Phe Ser Arg Asp Ser Val Asp Leu Ser Arg
        35   40   45

Val His Lys Gly Lys Ser Thr Arg Lys Glu Glu Asn Thr Arg Ser Leu
    50   55   60

Leu Asn Asp Lys Arg Ala Val Ala Ala Gln Arg Gln Arg Tyr Glu Gln
65   70   75   80

Tyr Ser Val Val Val Glu Glu
                85

<210> 1607
<211> 681
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 458; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC2; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H1I8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437570"

<400> 1607
Met Pro Ala Leu Pro Leu Asp Gln Leu Gln Ile Thr His Lys Asp Pro
1 5 10 15

Lys Thr Gly Lys Leu Arg Thr Ser Pro Ala Leu Val Ile Phe Asp Glu
20 25 30

Thr Leu Gln Lys Cys Leu Asp Ser Tyr Leu Arg Tyr Val Pro Arg Lys
35 40 45

Phe Asp Glu Gly Val Ala Ser Ala Pro Glu Val Val Asp Met Gln Lys
50 55 60

Arg Leu His Arg Ser Val Phe Leu Thr Phe Leu Arg Met Ser Thr His
65 70 75 80

Lys Glu Ser Lys Ile Leu Asp Leu Cys Val Leu Phe Gly Lys Gly Asn
85 90 95

Ser Pro Leu Leu Gln Lys Met Ile Gly Asn Ile Phe Thr Gln Gln Pro
100 105 110

Ser Tyr Tyr Ser Asp Leu Asp Glu Thr Leu Pro Thr Ile Leu Gln Val
115 120 125

Phe Ser Asn Ile Leu Gln His Cys Gly Leu Gln Gly Asp Gly Ala Asn
130 135 140

Thr Thr Pro Gln Lys Leu Glu Glu Arg Gly Arg Leu Thr Pro Ser Asp
145 150 155 160

Met Pro Leu Leu Glu Leu Lys Asp Ile Val Leu Tyr Leu Cys Asp Thr
165 170 175

Cys Thr Thr Leu Trp Ala Phe Leu Asp Ile Phe Pro Leu Ala Cys Gln
180 185 190

Thr Phe Gln Lys His Asp Phe Cys Tyr Arg Leu Ala Ser Phe Tyr Glu
195 200 205

Ala Ala Ile Pro Glu Met Glu Ser Ala Ile Lys Lys Arg Arg Leu Glu
210 215 220

```
Asp Ser Lys Leu Leu Gly Asp Leu Trp Gln Arg Leu Ser His Ser Arg
225                 230                 235                 240

Lys Lys Leu Met Glu Ile Phe His Ile Ile Leu Asn Gln Ile Cys Leu
                245                 250                 255

Leu Pro Ile Leu Glu Ser Ser Cys Asp Asn Ile Gln Gly Phe Ile Glu
            260                 265                 270

Glu Phe Leu Gln Ile Phe Ser Ser Leu Leu Gln Glu Lys Arg Phe Leu
        275                 280                 285

Arg Asp Tyr Asp Ala Leu Phe Pro Val Ala Glu Asp Ile Ser Leu Leu
    290                 295                 300

Gln Gln Ala Ser Ser Val Leu Asp Glu Thr Arg Thr Ala Tyr Ile Leu
305                 310                 315                 320

Gln Ala Val Glu Ser Ala Trp Glu Gly Val Asp Arg Arg Lys Ala Thr
                325                 330                 335

Asp Ala Lys Asp Pro Ser Val Ile Glu Glu Pro Asn Gly Glu Pro Asn
            340                 345                 350

Gly Val Thr Val Thr Ala Glu Ala Val Ser Gln Ala Ser Ser His Pro
        355                 360                 365

Glu Asn Ser Glu Glu Glu Glu Cys Met Gly Ala Ala Ala Ala Val Gly
    370                 375                 380

Pro Ala Met Cys Gly Val Glu Leu Asp Ser Leu Ile Ser Gln Val Lys
385                 390                 395                 400

Asp Leu Leu Pro Asp Leu Gly Glu Gly Phe Ile Leu Ala Cys Leu Glu
                405                 410                 415

Tyr Tyr His Tyr Asp Pro Glu Gln Val Ile Asn Asn Ile Leu Glu Glu
            420                 425                 430

Arg Leu Ala Pro Thr Leu Ser Gln Leu Asp Arg Asn Leu Asp Arg Glu
        435                 440                 445

Met Lys Pro Asp Pro Thr Pro Leu Leu Thr Ser Arg His Asn Val Phe
```

```
    450                 455                 460

Gln Asn Asp Glu Phe Asp Val Phe Ser Arg Asp Ser Val Asp Leu Ser
465                 470                 475                 480

Arg Val His Lys Gly Lys Ser Thr Arg Lys Glu Glu Asn Thr Arg Ser
                485                 490                 495

Leu Leu Asn Asp Lys Arg Ala Val Ala Ala Gln Arg Gln Arg Tyr Glu
            500                 505                 510

Gln Tyr Ser Val Val Val Glu Glu Val Pro Leu Gln Pro Gly Glu Ser
        515                 520                 525

Leu Pro Tyr His Ser Val Tyr Tyr Glu Asp Glu Tyr Asp Asp Thr Tyr
    530                 535                 540

Asp Gly Asn Gln Val Gly Ala Asn Asp Ala Asp Ser Asp Asp Glu Leu
545                 550                 555                 560

Ile Ser Arg Arg Pro Phe Thr Ile Pro Gln Val Leu Arg Thr Lys Val
                565                 570                 575

Pro Arg Glu Gly Gln Glu Glu Asp Asp Asp Asp Glu Glu Asp Asp Ala
            580                 585                 590

Asp Glu Glu Ala Pro Lys Pro Asp His Phe Val Gln Asp Pro Ala Val
        595                 600                 605

Leu Arg Glu Lys Ala Glu Ala Arg Arg Met Ala Phe Leu Ala Lys Lys
    610                 615                 620

Gly Tyr Arg His Asp Ser Ser Thr Ala Val Ala Gly Ser Pro Arg Gly
625                 630                 635                 640

His Gly Gln Ser Arg Glu Thr Thr Gln Glu Arg Arg Lys Lys Glu Ala
                645                 650                 655

Asn Lys Ala Thr Arg Ala Asn His Asn Arg Arg Thr Met Ala Asp Arg
            660                 665                 670

Lys Arg Ser Lys Gly Met Ile Pro Ser
        675                 680
```

<210> 1608
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 459; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC3; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000320252"

<400> 1608
Met Ala Leu Pro Arg Leu Thr Gly Ala Leu Arg Ser Phe Ser Asn Val
1 5 10 15

Thr Lys Gln Asp Asn Tyr Asn Glu Glu Val Ala Asp Leu Lys Leu Glu
20 25 30

Leu Ile Met Gly Glu Lys Gln Leu Lys Val Gly Leu His Phe Ser Ser
35 40 45

<210> 1609
<211> 176
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 459; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC3; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000320777"

<400> 1609
Met Ala Leu Pro Arg Leu Thr Gly Ala Leu Arg Ser Phe Ser Asn Val
1   5   10   15

Thr Lys Gln Asp Asn Tyr Asn Glu Glu Val Ala Asp Leu Lys Ile Lys
            20   25   30

Arg Ser Lys Leu His Glu Gln Val Leu Asp Leu Gly Leu Thr Trp Lys
        35   40   45

Lys Ile Ile Lys Phe Leu Asn Glu Lys Leu Glu Lys Ser Lys Met Gln
    50   55   60

Ser Ile Asn Glu Asp Leu Lys Asp Ile Leu His Ala Ala Lys Gln Ile
65   70   75   80

Val Gly Thr Asp Asn Gly Arg Glu Ala Ile Glu Ser Gly Ala Ala Phe
                85   90   95

Leu Phe Met Thr Phe His Leu Lys Asp Ser Val Gly His Lys Glu Thr
            100   105   110

Lys Ala Ile Lys Gln Met Phe Gly Pro Phe Pro Ser Ser Ser Ala Thr
        115   120   125

Ala Ala Cys Asn Ala Thr Asn Arg Ile Ile Ser His Phe Ser Gln Asp
    130   135   140

Asp Leu Thr Ala Leu Val Gln Met Thr Glu Lys Glu His Gly Asp Arg
145   150   155   160

Val Phe Phe Gly Lys Asn Leu Ala Phe Ser Phe Asp Met His Asp Leu
                165   170   175

<210> 1610
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 459; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC3; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N3C0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358139"

<400> 1610
Met Ala Leu Pro Arg Leu Thr Gly Ala Leu Arg Ser Phe Ser Asn Val
1   5   10   15

Thr Lys Gln Asp Asn Tyr Asn Glu Glu Val Ala Asp Leu Lys Ile Lys
            20   25   30

Arg Ser Lys Leu His Glu Gln Val Leu Asp Leu Gly Leu Thr Trp Lys
        35   40   45

Lys Ile Ile Lys Phe Leu Asn Glu Lys Leu Glu Lys Ser Lys Met Gln
    50   55   60

Ser Ile Asn Glu Asp Leu Lys Asp Ile Leu His Ala Ala Lys Gln Ile
65   70   75   80

Glu Val Asn Cys Pro Phe Gln Lys Arg Arg Leu Asp Gly Lys Glu Glu
                85   90   95

Asp Glu Lys Met Ser Arg Ala Ser Asp Arg Phe Arg Gly Leu Arg
            100   105   110

<210> 1611
<211> 2202
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 459; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC3; "

<220>
<221> source
<223> /note="Gene Name:
activating signal cointegrator 1 complex
subunit 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N3C0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358159"

<400> 1611
Met Ala Leu Pro Arg Leu Thr Gly Ala Leu Arg Ser Phe Ser Asn Val
1 5 10 15

Thr Lys Gln Asp Asn Tyr Asn Glu Glu Val Ala Asp Leu Lys Ile Lys
            20 25 30

Arg Ser Lys Leu His Glu Gln Val Leu Asp Leu Gly Leu Thr Trp Lys
        35 40 45

Lys Ile Ile Lys Phe Leu Asn Glu Lys Leu Glu Lys Ser Lys Met Gln
    50 55 60

Ser Ile Asn Glu Asp Leu Lys Asp Ile Leu His Ala Ala Lys Gln Ile
65 70 75 80

Val Gly Thr Asp Asn Gly Arg Glu Ala Ile Glu Ser Gly Ala Ala Phe
                85 90 95

Leu Phe Met Thr Phe His Leu Lys Asp Ser Val Gly His Lys Glu Thr
            100 105 110

Lys Ala Ile Lys Gln Met Phe Gly Pro Phe Pro Ser Ser Ser Ala Thr
        115 120 125

Ala Ala Cys Asn Ala Thr Asn Arg Ile Ile Ser His Phe Ser Gln Asp
    130 135 140

Asp Leu Thr Ala Leu Val Gln Met Thr Glu Lys Glu His Gly Asp Arg
145 150 155 160

```
Val Phe Phe Gly Lys Asn Leu Ala Phe Ser Phe Asp Met His Asp Leu
                165                 170                 175

Asp His Phe Asp Glu Leu Pro Ile Asn Gly Glu Thr Gln Lys Thr Ile
            180                 185                 190

Ser Leu Asp Tyr Lys Lys Phe Leu Asn Glu His Leu Gln Glu Ala Cys
        195                 200                 205

Thr Pro Glu Leu Lys Pro Val Glu Lys Thr Asn Gly Ser Phe Leu Trp
    210                 215                 220

Cys Glu Val Glu Lys Tyr Leu Asn Ser Thr Leu Lys Glu Met Thr Glu
225                 230                 235                 240

Val Pro Arg Val Glu Asp Leu Cys Cys Thr Leu Tyr Asp Met Leu Ala
                245                 250                 255

Ser Ile Lys Ser Gly Asp Glu Leu Gln Asp Glu Leu Phe Glu Leu Leu
            260                 265                 270

Gly Pro Glu Gly Leu Glu Leu Ile Glu Lys Leu Leu Gln Asn Arg Ile
        275                 280                 285

Thr Ile Val Asp Arg Phe Leu Asn Ser Ser Asn Asp His Arg Phe Gln
    290                 295                 300

Ala Leu Gln Asp Asn Cys Lys Lys Ile Leu Gly Glu Asn Ala Lys Pro
305                 310                 315                 320

Asn Tyr Gly Cys Gln Val Thr Ile Gln Ser Glu Gln Glu Lys Gln Leu
                325                 330                 335

Met Lys Gln Tyr Arg Arg Glu Glu Lys Arg Ile Ala Arg Arg Glu Lys
            340                 345                 350

Lys Ala Gly Glu Asp Leu Glu Val Ser Glu Gly Leu Met Cys Phe Asp
        355                 360                 365

Pro Lys Glu Leu Arg Ile Gln Arg Glu Gln Ala Leu Leu Asn Ala Arg
    370                 375                 380
```

```
Ser Val Pro Ile Leu Ser Arg Gln Arg Asp Ala Asp Val Glu Lys Ile
385                 390                 395                 400

His Tyr Pro His Val Tyr Asp Ser Gln Ala Glu Ala Met Lys Thr Ser
                405                 410                 415

Ala Phe Ile Ala Gly Ala Lys Met Ile Leu Pro Glu Gly Ile Gln Arg
            420                 425                 430

Glu Asn Asn Lys Leu Tyr Glu Glu Val Arg Ile Pro Tyr Ser Glu Pro
        435                 440                 445

Met Pro Leu Ser Phe Glu Glu Lys Pro Val Tyr Ile Gln Asp Leu Asp
    450                 455                 460

Glu Ile Gly Gln Leu Ala Phe Lys Gly Met Lys Arg Leu Asn Arg Ile
465                 470                 475                 480

Gln Ser Ile Val Phe Glu Thr Ala Tyr Asn Thr Asn Glu Asn Met Leu
                485                 490                 495

Ile Cys Ala Pro Thr Gly Ala Gly Lys Thr Asn Ile Ala Met Leu Thr
            500                 505                 510

Val Leu His Glu Ile Arg Gln His Phe Gln Gln Gly Val Ile Lys Lys
        515                 520                 525

Asn Glu Phe Lys Ile Val Tyr Val Ala Pro Met Lys Ala Leu Ala Ala
    530                 535                 540

Glu Met Thr Asp Tyr Phe Ser Arg Arg Leu Glu Pro Leu Gly Ile Ile
545                 550                 555                 560

Val Lys Glu Leu Thr Gly Asp Met Gln Leu Ser Lys Ser Glu Ile Leu
                565                 570                 575

Arg Thr Gln Met Leu Val Thr Thr Pro Glu Lys Trp Asp Val Val Thr
            580                 585                 590

Arg Lys Ser Val Gly Asp Val Ala Leu Ser Gln Ile Val Arg Leu Leu
        595                 600                 605
```

```
Ile Leu Asp Glu Val His Leu Leu His Glu Asp Arg Gly Pro Val Leu
    610                 615                 620

Glu Ser Ile Val Ala Arg Thr Leu Arg Gln Val Glu Ser Thr Gln Ser
625                 630                 635                 640

Met Ile Arg Ile Leu Gly Leu Ser Ala Thr Leu Pro Asn Tyr Leu Asp
                645                 650                 655

Val Ala Thr Phe Leu His Val Asn Pro Tyr Ile Gly Leu Phe Phe Phe
            660                 665                 670

Asp Gly Arg Phe Arg Pro Val Pro Leu Gly Gln Thr Phe Leu Gly Ile
        675                 680                 685

Lys Cys Ala Asn Lys Met Gln Gln Leu Asn Asn Met Asp Glu Val Cys
    690                 695                 700

Tyr Glu Asn Val Leu Lys Gln Val Lys Ala Gly His Gln Val Met Val
705                 710                 715                 720

Phe Val His Ala Arg Asn Ala Thr Val Arg Thr Ala Met Ser Leu Ile
                725                 730                 735

Glu Arg Ala Lys Asn Cys Gly His Ile Pro Phe Phe Phe Pro Thr Gln
            740                 745                 750

Gly His Asp Tyr Val Leu Ala Glu Lys Gln Val Gln Arg Ser Arg Asn
        755                 760                 765

Lys Gln Val Arg Glu Leu Phe Pro Asp Gly Phe Ser Ile His His Ala
    770                 775                 780

Gly Met Leu Arg Gln Asp Arg Asn Leu Val Glu Asn Leu Phe Ser Asn
785                 790                 795                 800

Gly His Ile Lys Val Leu Val Cys Thr Ala Thr Leu Ala Trp Gly Val
                805                 810                 815

Asn Leu Pro Ala His Ala Val Ile Ile Lys Gly Thr Gln Ile Tyr Ala
            820                 825                 830

Ala Lys Arg Gly Ser Phe Val Asp Leu Gly Ile Leu Asp Val Met Gln
```

```
        835                 840                 845

Ile Phe Gly Arg Ala Gly Arg Pro Gln Phe Asp Lys Phe Gly Glu Gly
    850                 855                 860

Ile Ile Ile Thr Thr His Asp Lys Leu Ser His Tyr Leu Thr Leu Leu
865                 870                 875                 880

Thr Gln Arg Asn Pro Ile Glu Ser Gln Phe Leu Glu Ser Leu Ala Asp
                885                 890                 895

Asn Leu Asn Ala Glu Ile Ala Leu Gly Thr Val Thr Asn Val Glu Glu
            900                 905                 910

Ala Val Lys Trp Ile Ser Tyr Thr Tyr Leu Tyr Val Arg Met Arg Ala
        915                 920                 925

Asn Pro Leu Ala Tyr Gly Ile Ser His Lys Ala Tyr Gln Ile Asp Pro
    930                 935                 940

Thr Leu Arg Lys His Arg Glu Gln Leu Val Ile Glu Val Gly Arg Lys
945                 950                 955                 960

Leu Asp Lys Ala Gln Met Ile Arg Phe Glu Glu Arg Thr Gly Tyr Phe
                965                 970                 975

Ser Ser Thr Asp Leu Gly Arg Thr Ala Ser His Tyr Tyr Ile Lys Tyr
            980                 985                 990

Asn Thr Ile Glu Thr Phe Asn Glu  Leu Phe Asp Ala His  Lys Thr
Glu
        995                 1000                1005

Gly Asp  Ile Phe Ala Ile Val  Ser Lys Ala Glu Glu  Phe Asp Gln
    1010                1015                1020

Ile Lys  Val Arg Glu Glu Glu  Ile Glu Glu Leu Asp  Thr Leu Leu
    1025                1030                1035

Ser Asn  Phe Cys Glu Leu Ser  Thr Pro Gly Gly Val  Glu Asn Ser
    1040                1045                1050

Tyr Gly  Lys Ile Asn Ile Leu  Leu Gln Thr Tyr Ile  Ser Arg Gly
```

1055 1060 1065

Glu Met Asp Ser Phe Ser Leu Ile Ser Asp Ser Ala Tyr Val Ala
1070 1075 1080

Gln Asn Ala Ala Arg Ile Val Arg Ala Leu Phe Glu Ile Ala Leu
1085 1090 1095

Arg Lys Arg Trp Pro Thr Met Thr Tyr Arg Leu Leu Asn Leu Ser
1100 1105 1110

Lys Val Ile Asp Lys Arg Leu Trp Gly Trp Ala Ser Pro Leu Arg
1115 1120 1125

Gln Phe Ser Ile Leu Pro Pro His Ile Leu Thr Arg Leu Glu Glu
1130 1135 1140

Lys Lys Leu Thr Val Asp Lys Leu Lys Asp Met Arg Lys Asp Glu
1145 1150 1155

Ile Gly His Ile Leu His His Val Asn Ile Gly Leu Lys Val Lys
1160 1165 1170

Gln Cys Val His Gln Ile Pro Ser Val Met Met Glu Ala Ser Ile
1175 1180 1185

Gln Pro Ile Thr Arg Thr Val Leu Arg Val Thr Leu Ser Ile Tyr
1190 1195 1200

Ala Asp Phe Thr Trp Asn Asp Gln Val His Gly Thr Val Gly Glu
1205 1210 1215

Pro Trp Trp Ile Trp Val Glu Asp Pro Thr Asn Asp His Ile Tyr
1220 1225 1230

His Ser Glu Tyr Phe Leu Ala Leu Lys Lys Gln Val Ile Ser Lys
1235 1240 1245

Glu Ala Gln Leu Leu Val Phe Thr Ile Pro Ile Phe Glu Pro Leu
1250 1255 1260

Pro Ser Gln Tyr Tyr Ile Arg Ala Val Ser Asp Arg Trp Leu Gly
1265 1270 1275

```
Ala Glu  Ala Val Cys Ile Ile  Asn Phe Gln His Leu  Ile Leu Pro
    1280                1285                1290

Glu Arg  His Pro Pro His Thr  Glu Leu Leu Asp Leu  Gln Pro Leu
    1295                1300                1305

Pro Ile  Thr Ala Leu Gly Cys  Lys Ala Tyr Glu Ala  Leu Tyr Asn
    1310                1315                1320

Phe Ser  His Phe Asn Pro Val  Gln Thr Gln Ile Phe  His Thr Leu
    1325                1330                1335

Tyr His  Thr Asp Cys Asn Val  Leu Leu Gly Ala Pro  Thr Gly Ser
    1340                1345                1350

Gly Lys  Thr Val Ala Ala Glu  Leu Ala Ile Phe Arg  Val Phe Asn
    1355                1360                1365

Lys Tyr  Pro Thr Ser Lys Ala  Val Tyr Ile Ala Pro  Leu Lys Ala
    1370                1375                1380

Leu Val  Arg Glu Arg Met Asp  Asp Trp Lys Val Arg  Ile Glu Glu
    1385                1390                1395

Lys Leu  Gly Lys Lys Val Ile  Glu Leu Thr Gly Asp  Val Thr Pro
    1400                1405                1410

Asp Met  Lys Ser Ile Ala Lys  Ala Asp Leu Ile Val  Thr Thr Pro
    1415                1420                1425

Glu Lys  Trp Asp Gly Val Ser  Arg Ser Trp Gln Asn  Arg Asn Tyr
    1430                1435                1440

Val Gln  Gln Val Thr Ile Leu  Ile Ile Asp Glu Ile  His Leu Leu
    1445                1450                1455

Gly Glu  Glu Arg Gly Pro Val  Leu Glu Val Ile Val  Ser Arg Thr
    1460                1465                1470

Asn Phe  Ile Ser Ser His Thr  Glu Lys Pro Val Arg  Ile Val Gly
    1475                1480                1485
```

```
Leu Ser  Thr Ala Leu Ala Asn  Ala Arg Asp Leu Ala  Asp Trp Leu
    1490                1495                1500

Asn Ile  Lys Gln Met Gly Leu  Phe Asn Phe Arg Pro  Ser Val Arg
    1505                1510                1515

Pro Val  Pro Leu Glu Val His  Ile Gln Gly Phe Pro  Gly Gln His
    1520                1525                1530

Tyr Cys  Pro Arg Met Ala Ser  Met Asn Lys Pro Ala  Phe Gln Ala
    1535                1540                1545

Ile Arg  Ser His Ser Pro Ala  Lys Pro Val Leu Ile  Phe Val Ser
    1550                1555                1560

Ser Arg  Arg Gln Thr Arg Leu  Thr Ala Leu Glu Leu  Ile Ala Phe
    1565                1570                1575

Leu Ala  Thr Glu Glu Asp Pro  Lys Gln Trp Leu Asn  Met Asp Glu
    1580                1585                1590

Arg Glu  Met Glu Asn Ile Ile  Ala Thr Val Arg Asp  Ser Asn Leu
    1595                1600                1605

Lys Leu  Thr Leu Ala Phe Gly  Ile Gly Met His His  Ala Gly Leu
    1610                1615                1620

His Glu  Arg Asp Arg Lys Thr  Val Glu Glu Leu Phe  Val Asn Cys
    1625                1630                1635

Lys Val  Gln Val Leu Ile Ala  Thr Ser Thr Leu Ala  Trp Gly Val
    1640                1645                1650

Asn Phe  Pro Ala His Leu Val  Ile Ile Lys Gly Thr  Glu Tyr Tyr
    1655                1660                1665

Asp Gly  Lys Thr Arg Arg Tyr  Val Asp Phe Pro Ile  Thr Asp Val
    1670                1675                1680

Leu Gln  Met Met Gly Arg Ala  Gly Arg Pro Gln Phe  Asp Asp Gln
    1685                1690                1695
```

Gly Lys Ala Val Ile Leu Val His Asp Ile Lys Lys Asp Phe Tyr
1700 1705 1710

Lys Lys Phe Leu Tyr Glu Pro Phe Pro Val Glu Ser Ser Leu Leu
1715 1720 1725

Gly Val Leu Ser Asp His Leu Asn Ala Glu Ile Ala Gly Gly Thr
1730 1735 1740

Ile Thr Ser Lys Gln Asp Ala Leu Asp Tyr Ile Thr Trp Thr Tyr
1745 1750 1755

Phe Phe Arg Arg Leu Ile Met Asn Pro Ser Tyr Tyr Asn Leu Gly
1760 1765 1770

Asp Val Ser His Asp Ser Val Asn Lys Phe Leu Ser His Leu Ile
1775 1780 1785

Glu Lys Ser Leu Ile Glu Leu Glu Leu Ser Tyr Cys Ile Glu Ile
1790 1795 1800

Gly Glu Asp Asn Arg Ser Ile Glu Pro Leu Thr Tyr Gly Arg Ile
1805 1810 1815

Ala Ser Tyr Tyr Tyr Leu Lys His Gln Thr Val Lys Met Phe Lys
1820 1825 1830

Asp Arg Leu Lys Pro Glu Cys Ser Thr Glu Glu Leu Leu Ser Ile
1835 1840 1845

Leu Ser Asp Ala Glu Glu Tyr Thr Asp Leu Pro Val Arg His Asn
1850 1855 1860

Glu Asp His Met Asn Ser Glu Leu Ala Lys Cys Leu Pro Ile Glu
1865 1870 1875

Ser Asn Pro His Ser Phe Asp Ser Pro His Thr Lys Ala His Leu
1880 1885 1890

Leu Leu Gln Ala His Leu Ser Arg Ala Met Leu Pro Cys Pro Asp
1895 1900 1905

Tyr Asp Thr Asp Thr Lys Thr Val Leu Asp Gln Ala Leu Arg Val

1910 1915 1920

Cys Gln Ala Met Leu Asp Val Ala Ala Asn Gln Gly Trp Leu Val
1925 1930 1935

Thr Val Leu Asn Ile Thr Asn Leu Ile Gln Met Val Ile Gln Gly
1940 1945 1950

Arg Trp Leu Lys Asp Ser Ser Leu Leu Thr Leu Pro Asn Ile Glu
1955 1960 1965

Asn His His Leu His Leu Phe Lys Lys Trp Lys Pro Ile Met Lys
1970 1975 1980

Gly Pro His Ala Arg Gly Arg Thr Ser Ile Glu Ser Leu Pro Glu
1985 1990 1995

Leu Ile His Ala Cys Gly Gly Lys Asp His Val Phe Ser Ser Met
2000 2005 2010

Val Glu Ser Glu Leu His Ala Ala Lys Thr Lys Gln Ala Trp Asn
2015 2020 2025

Phe Leu Ser His Leu Pro Val Ile Asn Val Gly Ile Ser Val Lys
2030 2035 2040

Gly Ser Trp Asp Asp Leu Val Glu Gly His Asn Glu Leu Ser Val
2045 2050 2055

Ser Thr Leu Thr Ala Asp Lys Arg Asp Asp Asn Lys Trp Ile Lys
2060 2065 2070

Leu His Ala Asp Gln Glu Tyr Val Leu Gln Val Ser Leu Gln Arg
2075 2080 2085

Val His Phe Gly Phe His Lys Gly Lys Pro Glu Ser Cys Ala Val
2090 2095 2100

Thr Pro Arg Phe Pro Lys Ser Lys Asp Glu Gly Trp Phe Leu Ile
2105 2110 2115

Leu Gly Glu Val Asp Lys Arg Glu Leu Ile Ala Leu Lys Arg Val
2120 2125 2130

```
Gly Tyr  Ile Arg Asn His His  Val Ala Ser Leu Ser  Phe Tyr Thr
    2135                2140                2145


Pro Glu  Ile Pro Gly Arg Tyr  Ile Tyr Thr Leu Tyr  Phe Met Ser
    2150                2155                2160


Asp Cys  Tyr Leu Gly Leu Asp  Gln Gln Tyr Asp Ile  Tyr Leu Asn
    2165                2170                2175


Val Thr  Gln Ala Ser Leu Ser  Ala Gln Val Asn Thr  Lys Val Ser
    2180                2185                2190


Asp Ser  Leu Thr Asp Leu Ala  Leu Lys
    2195                2200


<210> 1612
<211> 731
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 459; "

<220>
<221> source
<223> /note="Gene Symbol: ASCC3; "

<220>
<221> source
<223> /note="Gene Name:
      activating signal cointegrator 1 complex
      subunit 3; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N3C0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430769"

<400> 1612
Met Ala Leu Pro Arg Leu Thr Gly Ala Leu Arg Ser Phe Ser Asn Val
1               5                  10                  15


Thr Lys Gln Asp Asn Tyr Asn Glu Glu Val Ala Asp Leu Lys Ile Lys
            20                  25                  30
```

```
Arg Ser Lys Leu His Glu Gln Val Leu Asp Leu Gly Leu Thr Trp Lys
        35                  40                  45

Lys Ile Ile Lys Phe Leu Asn Glu Lys Leu Glu Lys Ser Lys Met Gln
    50                  55                  60

Ser Ile Asn Glu Asp Leu Lys Asp Ile Leu His Ala Ala Lys Gln Ile
65                  70                  75                  80

Val Gly Thr Asp Asn Gly Arg Glu Ala Ile Glu Ser Gly Ala Ala Phe
                85                  90                  95

Leu Phe Met Thr Phe His Leu Lys Asp Ser Val Gly His Lys Glu Thr
            100                 105                 110

Lys Ala Ile Lys Gln Met Phe Gly Pro Phe Pro Ser Ser Ser Ala Thr
        115                 120                 125

Ala Ala Cys Asn Ala Thr Asn Arg Ile Ile Ser His Phe Ser Gln Asp
    130                 135                 140

Asp Leu Thr Ala Leu Val Gln Met Thr Glu Lys Glu His Gly Asp Arg
145                 150                 155                 160

Val Phe Phe Gly Lys Asn Leu Ala Phe Ser Phe Asp Met His Asp Leu
                165                 170                 175

Asp His Phe Asp Glu Leu Pro Ile Asn Gly Glu Thr Gln Lys Thr Ile
            180                 185                 190

Ser Leu Asp Tyr Lys Lys Phe Leu Asn Glu His Leu Gln Glu Ala Cys
        195                 200                 205

Thr Pro Glu Leu Lys Pro Val Glu Lys Thr Asn Gly Ser Phe Leu Trp
    210                 215                 220

Cys Glu Val Glu Lys Tyr Leu Asn Ser Thr Leu Lys Glu Met Thr Glu
225                 230                 235                 240

Val Pro Arg Val Glu Asp Leu Cys Cys Thr Leu Tyr Asp Met Leu Ala
                245                 250                 255
```

```
Ser Ile Lys Ser Gly Asp Glu Leu Gln Asp Glu Leu Phe Glu Leu Leu
            260                 265                 270

Gly Pro Glu Gly Leu Glu Leu Ile Glu Lys Leu Leu Gln Asn Arg Ile
        275                 280                 285

Thr Ile Val Asp Arg Phe Leu Asn Ser Ser Asn Asp His Arg Phe Gln
    290                 295                 300

Ala Leu Gln Asp Asn Cys Lys Lys Ile Leu Gly Glu Asn Ala Lys Pro
305                 310                 315                 320

Asn Tyr Gly Cys Gln Val Thr Ile Gln Ser Glu Gln Glu Lys Gln Leu
                325                 330                 335

Met Lys Gln Tyr Arg Arg Glu Glu Lys Arg Ile Ala Arg Arg Glu Lys
            340                 345                 350

Lys Ala Gly Glu Asp Leu Glu Val Ser Glu Gly Leu Met Cys Phe Asp
        355                 360                 365

Pro Lys Glu Leu Arg Ile Gln Arg Glu Gln Ala Leu Leu Asn Ala Arg
    370                 375                 380

Ser Val Pro Ile Leu Ser Arg Gln Arg Asp Ala Asp Val Glu Lys Ile
385                 390                 395                 400

His Tyr Pro His Val Tyr Asp Ser Gln Ala Glu Ala Met Lys Thr Ser
                405                 410                 415

Ala Phe Ile Ala Gly Ala Lys Met Ile Leu Pro Glu Gly Ile Gln Arg
            420                 425                 430

Glu Asn Asn Lys Leu Tyr Glu Glu Val Arg Ile Pro Tyr Ser Glu Pro
        435                 440                 445

Met Pro Leu Ser Phe Glu Glu Lys Pro Val Tyr Ile Gln Asp Leu Asp
    450                 455                 460

Glu Ile Gly Gln Leu Ala Phe Lys Gly Met Lys Arg Leu Asn Arg Ile
465                 470                 475                 480

Gln Ser Ile Val Phe Glu Thr Ala Tyr Asn Thr Asn Glu Asn Met Leu
```

485 490 495

Ile Cys Ala Pro Thr Gly Ala Gly Lys Thr Asn Ile Ala Met Leu Thr
500 505 510

Val Leu His Glu Ile Arg Gln His Phe Gln Gln Gly Val Ile Lys Lys
515 520 525

Asn Glu Phe Lys Ile Val Tyr Val Ala Pro Met Lys Ala Leu Ala Ala
530 535 540

Glu Met Thr Asp Tyr Phe Ser Arg Arg Leu Glu Pro Leu Gly Ile Ile
545 550 555 560

Val Lys Glu Leu Thr Gly Asp Met Gln Leu Ser Lys Ser Glu Ile Leu
565 570 575

Arg Thr Gln Met Leu Val Thr Thr Pro Glu Lys Trp Asp Val Val Thr
580 585 590

Arg Lys Ser Val Gly Asp Val Ala Leu Ser Gln Ile Val Arg Leu Leu
595 600 605

Ile Leu Asp Glu Val His Leu Leu His Glu Asp Arg Gly Pro Val Leu
610 615 620

Glu Ser Ile Val Ala Arg Thr Leu Arg Gln Val Glu Ser Thr Gln Ser
625 630 635 640

Met Ile Arg Ile Leu Gly Leu Ser Ala Thr Leu Pro Asn Tyr Leu Asp
645 650 655

Val Ala Thr Phe Leu His Val Asn Pro Tyr Ile Gly Leu Phe Phe Phe
660 665 670

Asp Gly Arg Phe Arg Pro Val Pro Leu Gly Gln Thr Phe Leu Gly Ile
675 680 685

Lys Cys Ala Asn Lys Met Gln Gln Leu Asn Asn Met Asp Glu Val Cys
690 695 700

Tyr Glu Asn Val Leu Lys Gln Val Lys Ala Gly His Gln Val His Leu
705 710 715 720

```
Phe Tyr Leu Leu Leu His Leu Phe Ile Cys Phe
                725                 730


<210> 1613
<211> 271
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 460; "

<220>
<221> source
<223> /note="Gene Symbol: ATF1; "

<220>
<221> source
<223> /note="Gene Name:
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      factor
      1; "

<220>
<221> source
<223> /note="Uniprot ID:  P18846; "

<220>
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<223> /note="ENSP ID: ENSP00000262053"

<400> 1613
Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
1               5                   10                  15


Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Val
            20                  25                  30


Ser Ser Leu Ser Glu Ser Glu Glu Ser Gln Asp Ser Ser Asp Ser Ile
        35                  40                  45


Gly Ser Ser Gln Lys Ala His Gly Ile Leu Ala Arg Arg Pro Ser Tyr
    50                  55                  60


Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu Asp Thr Arg Gly Arg Lys
65                  70                  75                  80


Gly Asp Gly Glu Asn Ser Gly Val Ser Ala Ala Val Thr Ser Met Ser
                85                  90                  95
```

```
Val Pro Thr Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile
            100                 105                 110

Ala Pro Asn Gly Ala Leu Gln Leu Ala Ser Pro Gly Thr Asp Gly Val
        115                 120                 125

Gln Gly Leu Gln Thr Leu Thr Met Thr Asn Ser Gly Ser Thr Gln Gln
    130                 135                 140

Gly Thr Thr Ile Leu Gln Tyr Ala Gln Thr Ser Asp Gly Gln Gln Ile
145                 150                 155                 160

Leu Val Pro Ser Asn Gln Val Val Val Gln Thr Ala Ser Gly Asp Met
                165                 170                 175

Gln Thr Tyr Gln Ile Arg Thr Thr Pro Ser Ala Thr Ser Leu Pro Gln
            180                 185                 190

Thr Val Val Met Thr Ser Pro Val Thr Leu Thr Ser Gln Thr Thr Lys
        195                 200                 205

Thr Asp Asp Pro Gln Leu Lys Arg Glu Ile Arg Leu Met Lys Asn Arg
    210                 215                 220

Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys
225                 230                 235                 240

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
                245                 250                 255

Glu Glu Leu Lys Thr Leu Lys Asp Leu Tyr Ser Asn Lys Ser Val
            260                 265                 270


<210> 1614
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 460; "

<220>
<221> source
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<223> /note="Gene Symbol: ATF1; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448421"

<400> 1614
Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
1 5 10 15

Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Gly
20 25 30

Leu Thr Leu Ser Pro Arg Leu Val Cys Ser Ser Val Asn Ile Ala His
35 40 45

Cys Ser Leu Asp Leu Leu Cys Ser Ser Asn Pro Pro Ala Ser Ala Pro
50 55 60

Gln Val Ala Gly Thr Thr Gly Ile Ile Phe Ile Arg Lys
65 70 75

<210> 1615
<211> 170
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 460; "

<220>
<221> source
<223> /note="Gene Symbol: ATF1; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448592"

<400> 1615
Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
1 5 10 15

Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Val
20 25 30

Ser Ser Leu Ser Glu Ser Glu Glu Ser Gln Asp Ser Ser Asp Ser Ile
35 40 45

Gly Ser Ser Gln Lys Ala His Gly Ile Leu Ala Arg Arg Pro Ser Tyr
50 55 60

Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu Asp Thr Arg Gly Arg Lys
65 70 75 80

Gly Asp Gly Glu Asn Ser Gly Val Ser Ala Ala Val Thr Ser Met Ser
85 90 95

Val Pro Thr Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile
100 105 110

Ala Pro Asn Gly Ala Leu Gln Leu Ala Ser Pro Gly Thr Asp Gly Val
115 120 125

Gln Gly Leu Gln Thr Leu Thr Met Thr Asn Ser Gly Ser Thr Gln Gln
130 135 140

Gly Thr Thr Ile Leu Gln Tyr Ala Gln Thr Ser Asp Gly Gln Gln Ile
145 150 155 160

Leu Val Pro Ser Asn Gln Val Val Val Gln
165 170

<210> 1616
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 460; "

<220>
<221> source

<223> /note="Gene Symbol: ATF1; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448921"

<400> 1616

```
Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
1               5                  10                  15

Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Val
            20                  25                  30

Ser Ser Leu Ser Glu Ser Glu Glu Ser Gln Asp Ser Ser Asp Ser Ile
        35                  40                  45

Gly Ser Ser Gln Lys Ala His Gly Ile Leu Ala Arg Arg Pro Ser Tyr
    50                  55                  60

Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu Asp Thr Arg Gly Arg Lys
65                  70                  75                  80

Gly Asp Gly Glu Asn Ser Gly Val Ser Ala Ala Val Thr Ser Met Ser
                85                  90                  95

Val Pro Thr Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile
            100                 105                 110

Ala Pro Asn Gly Ala Leu Gln Leu Ala Ser Pro Gly Thr Asp Gly Val
        115                 120                 125

Gln Gly Leu Gln Thr Leu Thr Met Thr Asn Ser Gly Ser Thr Gln Gln
    130                 135                 140

Gly Thr Thr Ile Leu Gln Tyr Ala Gln Thr Ser Asp Gly Gln Gln Ile
145                 150                 155                 160

Leu Val Pro Ser Asn Gln Val Val Val Gln Thr Ala Ser Gly Asp Met
                165                 170                 175
```

```
Gln Thr Tyr Gln Ile Arg Thr Thr Pro Ser Ala Thr Ser Leu Pro Gln
            180                 185                 190


Thr Val Val Met Thr Ser Pro Val
        195                 200


<210> 1617
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 460; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
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      factor
      1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448987"

<400> 1617
Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
1               5                   10                  15


Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Leu
            20                  25                  30


Pro Leu Pro Gln Met Glu Pro Tyr Ser Trp Gln Val Gln Ala Gln Met
        35                  40                  45


Glu Tyr Arg Asp Phe Arg His
    50                  55


<210> 1618
<211> 505
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 461; "

<220>
<221> source
<223> /note="Gene Symbol: ATF2; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
2; "

<220>
<221> source
<223> /note="Uniprot ID: P15336; "

<220>
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<223> /note="ENSP ID: ENSP00000264110"

<400> 1618

```
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1               5                   10                  15


Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
            20                  25                  30


Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
        35                  40                  45


His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
    50                  55                  60


Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu
65                  70                  75                  80


Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
                85                  90                  95


Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
            100                 105                 110


Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
        115                 120                 125


Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
    130                 135                 140
```

```
Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145                 150                 155                 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
                165                 170                 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
            180                 185                 190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
        195                 200                 205

Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly
    210                 215                 220

Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val
225                 230                 235                 240

His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro
                245                 250                 255

Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser
            260                 265                 270

Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro
        275                 280                 285

Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg
    290                 295                 300

Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr
305                 310                 315                 320

Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr
                325                 330                 335

Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp
            340                 345                 350

Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg
        355                 360                 365
```

```
Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala
    370                 375                 380

Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln Ser Glu Val Thr Leu
385                 390                 395                 400

Leu Arg Asn Glu Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys
                405                 410                 415

Asp Cys Pro Val Thr Ala Met Gln Lys Lys Ser Gly Tyr His Thr Ala
            420                 425                 430

Asp Lys Asp Asp Ser Ser Glu Asp Ile Ser Val Pro Ser Ser Pro His
        435                 440                 445

Thr Glu Ala Ile Gln His Ser Ser Val Ser Thr Ser Asn Gly Val Ser
    450                 455                 460

Ser Thr Ser Lys Ala Glu Ala Val Ala Thr Ser Val Leu Thr Gln Met
465                 470                 475                 480

Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser Gln Ile Val Met Ala Pro
                485                 490                 495

Ser Ser Gln Ser Gln Pro Ser Gly Ser
            500                 505


<210> 1619
<211> 447
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<221> source
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<400> 1619

```
Met Tyr Cys Ala Trp Met Trp Pro Asp Gln Thr Pro Thr Pro Thr Arg
1               5                  10                  15

Phe Leu Lys Asn Cys Glu Glu Val Gly Leu Phe Asn Glu Leu Ala Ser
            20                  25                  30

Pro Phe Glu Asn Glu Phe Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys
        35                  40                  45

Met Pro Leu Asp Leu Ser Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys
    50                  55                  60

Ile Glu Glu Pro Ser Val Val Glu Thr Thr His Gln Asp Ser Pro Leu
65                  70                  75                  80

Pro His Pro Glu Ser Thr Thr Ser Asp Glu Lys Glu Val Pro Leu Ala
                85                  90                  95

Gln Thr Ala Gln Pro Thr Ser Ala Ile Val Arg Pro Ala Ser Leu Gln
            100                 105                 110

Val Pro Asn Val Leu Leu Thr Ser Ser Asp Ser Ser Val Ile Ile Gln
        115                 120                 125

Gln Ala Val Pro Ser Pro Thr Ser Ser Thr Val Ile Thr Gln Ala Pro
    130                 135                 140

Ser Ser Asn Arg Pro Ile Val Pro Val Pro Gly Pro Phe Pro Leu Leu
145                 150                 155                 160

Leu His Leu Pro Asn Gly Gln Thr Met Pro Val Ala Ile Pro Ala Ser
                165                 170                 175

Ile Thr Ser Ser Asn Val His Val Pro Ala Ala Val Pro Leu Val Arg
            180                 185                 190

Pro Val Thr Met Val Pro Ser Val Pro Gly Ile Pro Gly Pro Ser Ser
```

```
        195                 200                 205

Pro Gln Pro Val Gln Ser Glu Ala Lys Met Arg Leu Lys Ala Ala Leu
    210                 215                 220

Thr Gln Gln His Pro Pro Val Thr Asn Gly Asp Thr Val Lys Gly His
225                 230                 235                 240

Gly Ser Gly Leu Val Arg Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser
                245                 250                 255

Leu Gln Gln Pro Ala Thr Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala
            260                 265                 270

His Thr Thr Pro Gln Thr Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala
        275                 280                 285

Ala Asn Glu Asp Pro Asp Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn
    290                 295                 300

Arg Ala Ala Ala Ser Arg Cys Arg Gln Lys Arg Lys Val Trp Val Gln
305                 310                 315                 320

Ser Leu Glu Lys Lys Ala Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu
                325                 330                 335

Gln Ser Glu Val Thr Leu Leu Arg Asn Glu Val Ala Gln Leu Lys Gln
            340                 345                 350

Leu Leu Leu Ala His Lys Asp Cys Pro Val Thr Ala Met Gln Lys Lys
        355                 360                 365

Ser Gly Tyr His Thr Ala Asp Lys Asp Asp Ser Ser Glu Asp Ile Ser
    370                 375                 380

Val Pro Ser Ser Pro His Thr Glu Ala Ile Gln His Ser Ser Val Ser
385                 390                 395                 400

Thr Ser Asn Gly Val Ser Ser Thr Ser Lys Ala Glu Ala Val Ala Thr
                405                 410                 415

Ser Val Leu Thr Gln Met Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser
            420                 425                 430
```

```
Gln Ile Val Met Ala Pro Ser Ser Gln Ser Gln Pro Ser Gly Ser
        435                 440                 445


<210> 1620
<211> 505
<212> PRT
<213> Homo sapiens

<220>
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      2; "

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<400> 1620
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1               5                   10                  15


Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
            20                  25                  30


Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
        35                  40                  45


His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
    50                  55                  60


Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu
65                  70                  75                  80


Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
                85                  90                  95
```

```
Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
            100                 105                 110

Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
        115                 120                 125

Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
    130                 135                 140

Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145                 150                 155                 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
                165                 170                 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
            180                 185                 190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
        195                 200                 205

Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly
    210                 215                 220

Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val
225                 230                 235                 240

His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro
                245                 250                 255

Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser
            260                 265                 270

Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro
        275                 280                 285

Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg
    290                 295                 300

Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr
305                 310                 315                 320
```

```
Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr
                325                 330                 335

Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp
            340                 345                 350

Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg
        355                 360                 365

Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala
    370                 375                 380

Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln Ser Glu Val Thr Leu
385                 390                 395                 400

Leu Arg Asn Glu Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys
                405                 410                 415

Asp Cys Pro Val Thr Ala Met Gln Lys Lys Ser Gly Tyr His Thr Ala
            420                 425                 430

Asp Lys Asp Asp Ser Ser Glu Asp Ile Ser Val Pro Ser Ser Pro His
        435                 440                 445

Thr Glu Ala Ile Gln His Ser Ser Val Ser Thr Ser Asn Gly Val Ser
    450                 455                 460

Ser Thr Ser Lys Ala Glu Ala Val Ala Thr Ser Val Leu Thr Gln Met
465                 470                 475                 480

Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser Gln Ile Val Met Ala Pro
                485                 490                 495

Ser Ser Gln Ser Gln Pro Ser Gly Ser
            500                 505


<210> 1621
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<400> 1621

```
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1               5                  10                  15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
            20                  25                  30

Gly Gln Ser Glu Val Thr Leu Leu Arg Asn Glu Val Ala Gln Leu Lys
        35                  40                  45

Gln Leu Leu Leu Ala His Lys Asp Cys Pro Val Thr Ala Met Gln Lys
    50                  55                  60

Lys Ser Gly Tyr His Thr Ala Asp Lys Asp Asp Ser Ser Glu Asp Ile
65                  70                  75                  80

Ser Val Pro Ser Ser Pro His Thr Glu Ala Ile Gln His Ser Ser Val
                85                  90                  95

Ser Thr Ser Asn Gly Val Ser Ser Thr Ser Lys Ala Glu Ala Val Ala
            100                 105                 110

Thr Ser Val Leu Thr Gln Met Ala Asp Gln Ser Thr Glu Pro Ala Leu
        115                 120                 125

Ser Gln Ile Val Met Ala Pro Ser Ser Gln Ser Gln Pro Ser Gly Ser
    130                 135                 140
```

<210> 1622
<211> 389
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<400> 1622
Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys Gly Gln
1 5 10 15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
20 25 30

Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile Val Ala
35 40 45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
50 55 60

Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe Lys Lys
65 70 75 80

Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser Pro Leu
85 90 95

Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val Val Glu
100 105 110

Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr Thr Ser
115 120 125

```
Asp Glu Lys Leu Val Arg Pro Val Thr Met Val Pro Ser Val Pro Gly
    130                 135                 140

Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser Glu Ala Lys Met
145                 150                 155                 160

Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro Val Thr Asn Gly
                165                 170                 175

Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg Thr Gln Ser Glu
            180                 185                 190

Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr Ser Thr Thr Glu
        195                 200                 205

Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr Gln Ser Thr Ser
    210                 215                 220

Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp Glu Lys Arg Arg
225                 230                 235                 240

Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg Cys Arg Gln Lys
                245                 250                 255

Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala Glu Asp Leu Ser
            260                 265                 270

Ser Leu Asn Gly Gln Leu Gln Ser Glu Val Thr Leu Leu Arg Asn Glu
        275                 280                 285

Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys Asp Cys Pro Val
    290                 295                 300

Thr Ala Met Gln Lys Lys Ser Gly Tyr His Thr Ala Asp Lys Asp Asp
305                 310                 315                 320

Ser Ser Glu Asp Ile Ser Val Pro Ser Ser Pro His Thr Glu Ala Ile
                325                 330                 335

Gln His Ser Ser Val Ser Thr Ser Asn Gly Val Ser Ser Thr Ser Lys
            340                 345                 350

Ala Glu Ala Val Ala Thr Ser Val Leu Thr Gln Met Ala Asp Gln Ser
```

355 360 365

Thr Glu Pro Ala Leu Ser Gln Ile Val Met Ala Pro Ser Ser Gln Ser
370 375 380

Gln Pro Ser Gly Ser
385

<210> 1623
<211> 209
<212> PRT
<213> Homo sapiens

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<223> /note="Gene Name:
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<223> /note="Uniprot ID: P15336; "

<220>
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<400> 1623
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1 5 10 15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
20 25 30

Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
35 40 45

His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
50 55 60

Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu

65 70 75 80

Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
85 90 95

Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
100 105 110

Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
115 120 125

Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
130 135 140

Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145 150 155 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
165 170 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
180 185 190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
195 200 205

Val

<210> 1624
<211> 447
<212> PRT
<213> Homo sapiens

<220>
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activating transcription
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<220>
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<223> /note="Uniprot ID: P15336; "

<220>
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<400> 1624
Met Tyr Cys Ala Trp Met Trp Pro Asp Gln Thr Pro Thr Pro Thr Arg
1   5   10   15

Phe Leu Lys Asn Cys Glu Glu Val Gly Leu Phe Asn Glu Leu Ala Ser
            20   25   30

Pro Phe Glu Asn Glu Phe Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys
        35   40   45

Met Pro Leu Asp Leu Ser Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys
    50   55   60

Ile Glu Glu Pro Ser Val Val Glu Thr Thr His Gln Asp Ser Pro Leu
65   70   75   80

Pro His Pro Glu Ser Thr Thr Ser Asp Glu Lys Glu Val Pro Leu Ala
                85   90   95

Gln Thr Ala Gln Pro Thr Ser Ala Ile Val Arg Pro Ala Ser Leu Gln
            100   105   110

Val Pro Asn Val Leu Leu Thr Ser Ser Asp Ser Ser Val Ile Ile Gln
        115   120   125

Gln Ala Val Pro Ser Pro Thr Ser Ser Thr Val Ile Thr Gln Ala Pro
    130   135   140

Ser Ser Asn Arg Pro Ile Val Pro Val Pro Gly Pro Phe Pro Leu Leu
145   150   155   160

Leu His Leu Pro Asn Gly Gln Thr Met Pro Val Ala Ile Pro Ala Ser
                165   170   175

Ile Thr Ser Ser Asn Val His Val Pro Ala Ala Val Pro Leu Val Arg
            180   185   190

```
Pro Val Thr Met Val Pro Ser Val Pro Gly Ile Pro Gly Pro Ser Ser
        195                 200                 205

Pro Gln Pro Val Gln Ser Glu Ala Lys Met Arg Leu Lys Ala Ala Leu
    210                 215                 220

Thr Gln Gln His Pro Pro Val Thr Asn Gly Asp Thr Val Lys Gly His
225                 230                 235                 240

Gly Ser Gly Leu Val Arg Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser
                245                 250                 255

Leu Gln Gln Pro Ala Thr Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala
            260                 265                 270

His Thr Thr Pro Gln Thr Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala
        275                 280                 285

Ala Asn Glu Asp Pro Asp Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn
    290                 295                 300

Arg Ala Ala Ala Ser Arg Cys Arg Gln Lys Arg Lys Val Trp Val Gln
305                 310                 315                 320

Ser Leu Glu Lys Lys Ala Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu
                325                 330                 335

Gln Ser Glu Val Thr Leu Leu Arg Asn Glu Val Ala Gln Leu Lys Gln
            340                 345                 350

Leu Leu Leu Ala His Lys Asp Cys Pro Val Thr Ala Met Gln Lys Lys
        355                 360                 365

Ser Gly Tyr His Thr Ala Asp Lys Asp Asp Ser Ser Glu Asp Ile Ser
    370                 375                 380

Val Pro Ser Ser Pro His Thr Glu Ala Ile Gln His Ser Ser Val Ser
385                 390                 395                 400

Thr Ser Asn Gly Val Ser Ser Thr Ser Lys Ala Glu Ala Val Ala Thr
                405                 410                 415
```

```
Ser Val Leu Thr Gln Met Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser
            420                 425                 430


Gln Ile Val Met Ala Pro Ser Ser Gln Ser Gln Pro Ser Gly Ser
        435                 440                 445


<210> 1625
<211> 395
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000389504"

<400> 1625
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1               5                   10                  15


Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
            20                  25                  30


Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
        35                  40                  45


His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
    50                  55                  60


Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu
65                  70                  75                  80


Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
                85                  90                  95
```

```
Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
            100                 105                 110

Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
        115                 120                 125

Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
    130                 135                 140

Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145                 150                 155                 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
                165                 170                 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
            180                 185                 190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
        195                 200                 205

Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly
    210                 215                 220

Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val
225                 230                 235                 240

His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro
                245                 250                 255

Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser
            260                 265                 270

Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro
        275                 280                 285

Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg
    290                 295                 300

Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr
305                 310                 315                 320
```

```
Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr
                325                 330                 335

Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp
            340                 345                 350

Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg
        355                 360                 365

Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala
    370                 375                 380

Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln
385                 390                 395


<210> 1626
<211> 43
<212> PRT
<213> Homo sapiens

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<223> /note="Gene Name:
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      factor
      2; "

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<223> /note="ENSP ID: ENSP00000402190"

<400> 1626
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1               5                   10                  15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
            20                  25                  30

Gly Gln Ile Arg Pro Gln His Gln Gln Asp Ser
        35                  40
```

<210> 1627
<211> 395
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
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factor
2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402229"

<400> 1627
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1 5 10 15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
20 25 30

Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
35 40 45

His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
50 55 60

Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu
65 70 75 80

Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
85 90 95

Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
100 105 110

Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
115 120 125

```
Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
    130                 135                 140

Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145                 150                 155                 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
                165                 170                 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
            180                 185                 190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
        195                 200                 205

Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly
    210                 215                 220

Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val
225                 230                 235                 240

His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro
                245                 250                 255

Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser
            260                 265                 270

Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro
        275                 280                 285

Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg
    290                 295                 300

Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr
305                 310                 315                 320

Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr
                325                 330                 335

Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp
            340                 345                 350

Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg
```

```
        355                 360                 365

Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala
    370                 375                 380

Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln
385                 390                 395


<210> 1628
<211> 265
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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      2; "

<220>
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 1628
Xaa Tyr Lys Asp Leu Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys
1               5                   10                  15

Thr Ala Pro Gly Cys Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala
            20                  25                  30

Val His Lys His Lys His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg
        35                  40                  45

Asn Asp Ser Val Ile Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe
    50                  55                  60
```

```
Leu Lys Asn Cys Glu Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro
65                  70                  75                  80

Phe Glu Asn Glu Phe Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met
                85                  90                  95

Pro Leu Asp Leu Ser Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile
            100                 105                 110

Glu Glu Pro Ser Val Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro
        115                 120                 125

His Pro Glu Ser Thr Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln
    130                 135                 140

Thr Ala Gln Pro Thr Ser Ala Ile Val Arg Pro Ala Ser Pro Ala His
145                 150                 155                 160

Thr Thr Pro Gln Thr Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala
                165                 170                 175

Asn Glu Asp Pro Asp Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg
            180                 185                 190

Ala Ala Ala Ser Arg Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser
        195                 200                 205

Leu Glu Lys Lys Ala Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln
    210                 215                 220

Leu Leu Ile Lys Met Ile Val Gln Lys Thr Phe Gln Cys Arg Val Val
225                 230                 235                 240

His Ile Gln Lys Leu Tyr Ser Ile Val Arg Ser Ala His Pro Met Glu
                245                 250                 255

Ser Val Gln Pro Pro Arg Gln Lys Leu
            260                 265
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<210> 1629
<211> 487
<212> PRT
<213> Homo sapiens

<220>
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<400> 1629
Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys Gly Gln
1   5   10   15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
            20   25   30

Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile Val Ala
        35   40   45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
    50   55   60

Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe Lys Lys
65   70   75   80

Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser Pro Leu
                85   90   95

Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val Val Glu
            100   105   110

Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr Thr Ser
        115   120   125

```
Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr Ser Ala
    130                 135                 140

Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu Thr Ser
145                 150                 155                 160

Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro Thr Ser
                165                 170                 175

Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile Val Pro
            180                 185                 190

Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly Gln Thr
        195                 200                 205

Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val His Val
    210                 215                 220

Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro Ser Val
225                 230                 235                 240

Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser Glu Ala
                245                 250                 255

Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro Val Thr
            260                 265                 270

Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg Thr Gln
        275                 280                 285

Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr Ser Thr
    290                 295                 300

Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr Gln Ser
305                 310                 315                 320

Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp Glu Lys
                325                 330                 335

Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg Cys Arg
            340                 345                 350

Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala Glu Asp
```

```
        355                 360                 365

Leu Ser Ser Leu Asn Gly Gln Leu Gln Ser Glu Val Thr Leu Leu Arg
    370                 375                 380

Asn Glu Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys Asp Cys
385                 390                 395                 400

Pro Val Thr Ala Met Gln Lys Lys Ser Gly Tyr His Thr Ala Asp Lys
                405                 410                 415

Asp Asp Ser Ser Glu Asp Ile Ser Val Pro Ser Ser Pro His Thr Glu
            420                 425                 430

Ala Ile Gln His Ser Ser Val Ser Thr Ser Asn Gly Val Ser Ser Thr
        435                 440                 445

Ser Lys Ala Glu Ala Val Ala Thr Ser Val Leu Thr Gln Met Ala Asp
    450                 455                 460

Gln Ser Thr Glu Pro Ala Leu Ser Gln Ile Val Met Ala Pro Ser Ser
465                 470                 475                 480

Gln Ser Gln Pro Ser Gly Ser
                485


<210> 1630
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<220>
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      2; "

<220>
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<223> /note="ENSP ID: ENSP00000410086"

<400> 1630
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1 5 10 15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
20 25 30

Gly Gln Ile Arg Pro Gln His Gln Gln Asp Ser
35 40

<210> 1631
<211> 237
<212> PRT
<213> Homo sapiens

<220>
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<220>
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factor
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<220>
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<400> 1631
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1 5 10 15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
20 25 30

Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
35 40 45

His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
50 55 60

Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu

```
65                  70                  75                  80

Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
                85                  90                  95

Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
            100                 105                 110

Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
        115                 120                 125

Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
    130                 135                 140

Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145                 150                 155                 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
                165                 170                 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
            180                 185                 190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
        195                 200                 205

Val Ser Phe Asp Gln Ser Pro Trp Cys Leu Val Phe Gln Glu Ser Gln
    210                 215                 220

Val Leu Pro Leu Pro Asn Gln Tyr Ser Gln Lys Gln Lys
225                 230                 235


<210> 1632
<211> 395
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<221> source
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factor
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<220>
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<400> 1632

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Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1               5                  10                  15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
            20                  25                  30

Gly Gln Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys
        35                  40                  45

His Glu Met Thr Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile
    50                  55                  60

Val Ala Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu
65                  70                  75                  80

Glu Val Gly Leu Phe Asn Glu Leu Ala Ser Pro Phe Glu Asn Glu Phe
                85                  90                  95

Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp Leu Ser
            100                 105                 110

Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro Ser Val
        115                 120                 125

Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu Ser Thr
    130                 135                 140

Thr Ser Asp Glu Lys Glu Val Pro Leu Ala Gln Thr Ala Gln Pro Thr
145                 150                 155                 160

Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val Leu Leu
                165                 170                 175

Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
            180                 185                 190
```

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
195 200 205

Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly
210 215 220

Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val
225 230 235 240

His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro
245 250 255

Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser
260 265 270

Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro
275 280 285

Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg
290 295 300

Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr
305 310 315 320

Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr
325 330 335

Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp
340 345 350

Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg
355 360 365

Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala
370 375 380

Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln
385 390 395

<210> 1633
<211> 43
<212> PRT

<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000414171"

<400> 1633
Met Lys Phe Lys Leu His Val Asn Ser Ala Arg Gln Tyr Lys Asp Leu
1 5 10 15

Trp Asn Met Ser Asp Asp Lys Pro Phe Leu Cys Thr Ala Pro Gly Cys
20 25 30

Gly Gln Ile Arg Pro Gln His Gln Gln Asp Ser
35 40

<210> 1634
<211> 189
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
activating transcription
factor
2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416854"

<400> 1634
Met Tyr Cys Ala Trp Met Trp Pro Asp Gln Thr Pro Thr Pro Thr Arg
1 5 10 15

Phe Leu Lys Asn Cys Glu Glu Val Gly Leu Phe Asn Glu Leu Ala Ser
20 25 30

Pro Phe Glu Asn Glu Phe Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys
35 40 45

Met Pro Leu Asp Leu Ser Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys
50 55 60

Ile Glu Glu Pro Ser Val Val Glu Thr Thr His Gln Asp Ser Pro Leu
65 70 75 80

Pro His Pro Glu Ser Thr Thr Ser Asp Glu Lys Glu Val Pro Leu Ala
85 90 95

Gln Thr Ala Gln Pro Thr Ser Ala Ile Val Arg Pro Ala Ser Leu Gln
100 105 110

Val Pro Asn Val Leu Leu Thr Ser Ser Asp Ser Ser Val Ile Ile Gln
115 120 125

Gln Ala Val Pro Ser Pro Thr Ser Ser Thr Val Ile Thr Gln Ala Pro
130 135 140

Ser Ser Asn Arg Pro Ile Val Pro Val Pro Gly Pro Phe Pro Leu Leu
145 150 155 160

Leu His Leu Pro Asn Gly Gln Thr Met Pro Val Ala Ile Pro Ala Ser
165 170 175

Ile Thr Ser Ser Asn Val His Val Pro Ala Ala Val Pro
180 185

<210> 1635
<211> 329
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 461; "

<220>
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<220>
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factor
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<220>
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<223> /note="ENSP ID: ENSP00000437952"

<400> 1635

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Met Ala Ala Tyr Lys Phe Gln Ile Ile Gln Gln Ala Val Pro Ser Pro
1               5                  10                  15

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
            20                  25                  30

Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro Asn Gly
        35                  40                  45

Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser Asn Val
    50                  55                  60

His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met Val Pro
65                  70                  75                  80

Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val Gln Ser
                85                  90                  95

Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His Pro Pro
            100                 105                 110

Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu Val Arg
        115                 120                 125

Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro Ala Thr
    130                 135                 140

Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro Gln Thr
145                 150                 155                 160
```

```
Gln Ser Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp Pro Asp
                165                 170                 175

Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg
            180                 185                 190

Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys Lys Ala
        195                 200                 205

Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln Ser Glu Val Thr Leu
    210                 215                 220

Leu Arg Asn Glu Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys
225                 230                 235                 240

Asp Cys Pro Val Thr Ala Met Gln Lys Lys Ser Gly Tyr His Thr Ala
                245                 250                 255

Asp Lys Asp Asp Ser Ser Glu Asp Ile Ser Val Pro Ser Ser Pro His
            260                 265                 270

Thr Glu Ala Ile Gln His Ser Ser Val Ser Thr Ser Asn Gly Val Ser
        275                 280                 285

Ser Thr Ser Lys Ala Glu Ala Val Ala Thr Ser Val Leu Thr Gln Met
    290                 295                 300

Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser Gln Ile Val Met Ala Pro
305                 310                 315                 320

Ser Ser Gln Ser Gln Pro Ser Gly Ser
                325


<210> 1636
<211> 106
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
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<220>
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<223> /note="Uniprot ID: P18847; "

<220>
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<223> /note="ENSP ID: ENSP00000336908"

<400> 1636
Met Met Leu Gln His Pro Gly Gln Val Ser Ala Ser Glu Glu Glu Leu
1   5   10   15

Arg Phe Ala Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser Ala
            20   25   30

Leu Glu Ser Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile Thr
        35   40   45

Lys Ala Glu Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg Arg
    50   55   60

Glu Arg Asn Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys Glu
65   70   75   80

Lys Thr Glu Cys Leu Gln Lys Leu Pro Arg Pro Phe Trp Val Gln Lys
                85   90   95

Thr Cys Ile Trp Ala Val Asp Ser Cys Lys
            100   105

<210> 1637
<211> 181
<212> PRT
<213> Homo sapiens

<220>
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<220>
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factor
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<220>
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<223> /note="Uniprot ID: P18847; "

<220>
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<223> /note="ENSP ID: ENSP00000344352"

<400> 1637
Met Met Leu Gln His Pro Gly Gln Val Ser Ala Ser Glu Val Ser Ala
1   5   10   15

Ser Ala Ile Val Pro Cys Leu Ser Pro Pro Gly Ser Leu Val Phe Glu
            20   25   30

Asp Phe Ala Asn Leu Thr Pro Phe Val Lys Glu Glu Leu Arg Phe Ala
        35   40   45

Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser Ala Leu Glu Ser
    50   55   60

Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile Thr Lys Ala Glu
65   70   75   80

Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg Arg Glu Arg Asn
                85   90   95

Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys Glu Lys Thr Glu
            100   105   110

Cys Leu Gln Lys Glu Ser Glu Lys Leu Glu Ser Val Asn Ala Glu Leu
        115   120   125

Lys Ala Gln Ile Glu Glu Leu Lys Asn Glu Lys Gln His Leu Ile Tyr
    130   135   140

Met Leu Asn Leu His Arg Pro Thr Cys Ile Val Arg Ala Gln Asn Gly
145   150   155   160

Arg Thr Pro Glu Asp Glu Arg Asn Leu Phe Ile Gln Gln Ile Lys Glu
165 170 175

Gly Thr Leu Gln Ser
180

<210> 1638
<211> 175
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 462; "

<220>
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<223> /note="Gene Symbol: ATF3; "

<220>
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<223> /note="Gene Name:
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factor
3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355948"

<400> 1638
Met Met Leu Gln His Pro Gly Gln Val Ser Ala Ser Glu Val Ser Ala
1 5 10 15

Ser Ala Ile Val Pro Cys Leu Ser Pro Pro Gly Ser Leu Val Phe Glu
20 25 30

Asp Phe Ala Asn Leu Thr Pro Phe Val Lys Glu Glu Leu Arg Phe Ala
35 40 45

Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser Ala Leu Glu Ser
50 55 60

Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile Thr Lys Ala Glu
65 70 75 80

Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg Arg Glu Arg Asn
85 90 95

```
Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys Glu Lys Thr Glu
            100                 105                 110

Cys Leu Gln Lys Glu Ser Glu Lys Leu Glu Ser Val Asn Ala Glu Leu
        115                 120                 125

Lys Ala Gln Ile Glu Glu Leu Lys Asn Glu Lys Gln His Leu Ile Tyr
    130                 135                 140

Met Leu Asn Leu His Arg Pro Thr Cys Ile Val Arg Ala Gln Asn Gly
145                 150                 155                 160

Arg Thr Pro Glu Asp Glu Arg Asn Leu Phe Ile Gln Gln Ile Lys
                165                 170                 175


<210> 1639
<211> 135
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  P18847; "

<220>
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<223> /note="ENSP ID: ENSP00000355950"

<400> 1639
Met Met Leu Gln His Pro Gly Gln Val Ser Ala Ser Glu Val Ser Ala
1               5                   10                  15

Ser Ala Ile Val Pro Cys Leu Ser Pro Pro Gly Ser Leu Val Phe Glu
            20                  25                  30
```

```
Asp Phe Ala Asn Leu Thr Pro Phe Val Lys Glu Glu Leu Arg Phe Ala
        35                  40                  45

Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser Ala Leu Glu Ser
    50                  55                  60

Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile Thr Lys Ala Glu
65                  70                  75                  80

Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg Arg Glu Arg Asn
                85                  90                  95

Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys Glu Lys Thr Glu
            100                 105                 110

Cys Leu Gln Lys Leu Pro Arg Pro Phe Trp Val Gln Lys Thr Cys Ile
        115                 120                 125

Trp Ala Val Asp Ser Cys Lys
    130                 135


<210> 1640
<211> 153
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 462; "

<220>
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      3; "

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<222> (1)..(1)
<223> Any amino acid
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<400> 1640
Xaa Glu Arg Ser Leu Glu Gln Asn Asp Ala Ser Thr Pro Arg Pro Glu
1 5 10 15

Leu Arg Phe Ala Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser
20 25 30

Ala Leu Glu Ser Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile
35 40 45

Thr Lys Ala Glu Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg
50 55 60

Arg Glu Arg Asn Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys
65 70 75 80

Glu Lys Thr Glu Cys Leu Gln Lys Glu Ser Glu Lys Leu Glu Ser Val
85 90 95

Asn Ala Glu Leu Lys Ala Gln Ile Glu Glu Leu Lys Asn Glu Lys Gln
100 105 110

His Leu Ile Tyr Met Leu Asn Leu His Arg Pro Thr Cys Ile Val Arg
115 120 125

Ala Gln Asn Gly Arg Thr Pro Glu Asp Glu Arg Asn Leu Phe Ile Gln
130 135 140

Gln Ile Lys Glu Gly Thr Leu Gln Ser
145 150

<210> 1641
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 462; "

<220>
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<223> /note="Gene Symbol: ATF3; "

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000355954"

<400> 1641

```
Met Met Leu Gln His Pro Gly Gln Val Ser Ala Ser Glu Val Ser Ala
1               5                   10                  15

Ser Ala Ile Val Pro Cys Leu Ser Pro Pro Gly Ser Leu Val Phe Glu
            20                  25                  30

Asp Phe Ala Asn Leu Thr Pro Phe Val Lys Glu Glu Leu Arg Phe Ala
        35                  40                  45

Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser Ala Leu Glu Ser
    50                  55                  60

Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile Thr Lys Ala Glu
65                  70                  75                  80

Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg Arg Glu Arg Asn
                85                  90                  95

Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys Glu Lys Thr Glu
            100                 105                 110

Cys Leu Gln Lys Glu Ser Glu Lys Leu Glu Ser Val Asn Ala Glu Leu
        115                 120                 125

Lys Ala Gln Ile Glu Glu Leu Lys Asn Glu Lys Gln His Leu Ile Tyr
    130                 135                 140

Met Leu Asn Leu His Arg Pro Thr Cys Ile Val Arg Ala Gln Asn Gly
145                 150                 155                 160

Arg Thr Pro Glu Asp Glu Arg Asn Leu Phe Ile Gln Gln Ile Lys Glu
                165                 170                 175
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Gly Thr Leu Gln Ser
180

<210> 1642
<211> 135
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Uniprot ID: P18847; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432208"

<400> 1642
Met Met Leu Gln His Pro Gly Gln Val Ser Ala Ser Glu Val Ser Ala
1 5 10 15

Ser Ala Ile Val Pro Cys Leu Ser Pro Pro Gly Ser Leu Val Phe Glu
20 25 30

Asp Phe Ala Asn Leu Thr Pro Phe Val Lys Glu Glu Leu Arg Phe Ala
35 40 45

Ile Gln Asn Lys His Leu Cys His Arg Met Ser Ser Ala Leu Glu Ser
50 55 60

Val Thr Val Ser Asp Arg Pro Leu Gly Val Ser Ile Thr Lys Ala Glu
65 70 75 80

Val Ala Pro Glu Glu Asp Glu Arg Lys Lys Arg Arg Arg Glu Arg Asn
85 90 95

```
Lys Ile Ala Ala Ala Lys Cys Arg Asn Lys Lys Lys Glu Lys Thr Glu
            100                 105                 110

Cys Leu Gln Lys Leu Pro Arg Pro Phe Trp Val Gln Lys Thr Cys Ile
        115                 120                 125

Trp Ala Val Asp Ser Cys Lys
    130                 135


<210> 1643
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 462; "

<220>
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<223> /note="Gene Name:
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      factor
      3; "

<220>
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<223> /note="Uniprot ID:  P18847; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480606"

<400> 1643
Met Ser Ser Ala Leu Glu Ser Val Thr Val Ser Asp Arg Pro Leu Gly
1               5                   10                  15

Val Ser Ile Thr Lys Ala Glu Val Ala Pro Glu Glu Asp Glu Arg Lys
            20                  25                  30

Lys Arg Arg Arg Glu Arg Asn Lys Ile Ala Ala Ala Lys Cys Arg Asn
        35                  40                  45

Lys Lys Lys Glu Lys Thr Glu Cys Leu Gln Lys Glu Ser Glu Lys Leu
    50                  55                  60
```

```
Glu Ser Val Asn Ala Glu Leu Lys Ala Gln Ile Glu Glu Leu Lys Asn
65                  70                  75                  80


Glu Lys Gln His Leu Ile Tyr Met Leu Asn Leu His Arg Pro Thr Cys
                85                  90                  95


Ile Val Arg Ala Gln Asn Gly Arg Thr Pro Glu Asp Glu Arg Asn Leu
            100                 105                 110


Phe Ile Gln Gln Ile Lys Glu Gly Thr Leu Gln Ser
        115                 120


<210> 1644
<211> 124
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 462; "

<220>
<221> source
<223> /note="Gene Symbol: ATF3; "

<220>
<221> source
<223> /note="Gene Name:
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      factor
      3; "

<220>
<221> source
<223> /note="Uniprot ID:  P18847; "

<220>
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<223> /note="ENSP ID: ENSP00000483576"

<400> 1644
Met Ser Ser Ala Leu Glu Ser Val Thr Val Ser Asp Arg Pro Leu Gly
1               5                   10                  15


Val Ser Ile Thr Lys Ala Glu Val Ala Pro Glu Glu Asp Glu Arg Lys
            20                  25                  30


Lys Arg Arg Arg Glu Arg Asn Lys Ile Ala Ala Ala Lys Cys Arg Asn
        35                  40                  45
```

```
Lys Lys Lys Glu Lys Thr Glu Cys Leu Gln Lys Glu Ser Glu Lys Leu
    50                  55                  60

Glu Ser Val Asn Ala Glu Leu Lys Ala Gln Ile Glu Glu Leu Lys Asn
65                  70                  75                  80

Glu Lys Gln His Leu Ile Tyr Met Leu Asn Leu His Arg Pro Thr Cys
                85                  90                  95

Ile Val Arg Ala Gln Asn Gly Arg Thr Pro Glu Asp Glu Arg Asn Leu
            100                 105                 110

Phe Ile Gln Gln Ile Lys Glu Gly Thr Leu Gln Ser
        115                 120


<210> 1645
<211> 351
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 463; "

<220>
<221> source
<223> /note="Gene Symbol: ATF4; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      4; "

<220>
<221> source
<223> /note="Uniprot ID:  P18848; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000336790"

<400> 1645
Met Thr Glu Met Ser Phe Leu Ser Ser Glu Val Leu Val Gly Asp Leu
1               5                   10                  15

Met Ser Pro Phe Asp Gln Ser Gly Leu Gly Ala Glu Glu Ser Leu Gly
            20                  25                  30
```

```
Leu Leu Asp Asp Tyr Leu Glu Val Ala Lys His Phe Lys Pro His Gly
        35                  40                  45

Phe Ser Ser Asp Lys Ala Lys Ala Gly Ser Ser Glu Trp Leu Ala Val
    50                  55                  60

Asp Gly Leu Val Ser Pro Ser Asn Asn Ser Lys Glu Asp Ala Phe Ser
65                  70                  75                  80

Gly Thr Asp Trp Met Leu Glu Lys Met Asp Leu Lys Glu Phe Asp Leu
                85                  90                  95

Asp Ala Leu Leu Gly Ile Asp Asp Leu Glu Thr Met Pro Asp Asp Leu
            100                 105                 110

Leu Thr Thr Leu Asp Asp Thr Cys Asp Leu Phe Ala Pro Leu Val Gln
        115                 120                 125

Glu Thr Asn Lys Gln Pro Pro Gln Thr Val Asn Pro Ile Gly His Leu
    130                 135                 140

Pro Glu Ser Leu Thr Lys Pro Asp Gln Val Ala Pro Phe Thr Phe Leu
145                 150                 155                 160

Gln Pro Leu Pro Leu Ser Pro Gly Val Leu Ser Ser Thr Pro Asp His
                165                 170                 175

Ser Phe Ser Leu Glu Leu Gly Ser Glu Val Asp Ile Thr Glu Gly Asp
            180                 185                 190

Arg Lys Pro Asp Tyr Thr Ala Tyr Val Ala Met Ile Pro Gln Cys Ile
        195                 200                 205

Lys Glu Glu Asp Thr Pro Ser Asp Asn Asp Ser Gly Ile Cys Met Ser
    210                 215                 220

Pro Glu Ser Tyr Leu Gly Ser Pro Gln His Ser Pro Ser Thr Arg Gly
225                 230                 235                 240

Ser Pro Asn Arg Ser Leu Pro Ser Pro Gly Val Leu Cys Gly Ser Ala
                245                 250                 255
```

```
Arg Pro Lys Pro Tyr Asp Pro Pro Gly Glu Lys Met Val Ala Ala Lys
            260                 265                 270

Val Lys Gly Glu Lys Leu Asp Lys Lys Leu Lys Lys Met Glu Gln Asn
        275                 280                 285

Lys Thr Ala Ala Thr Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu
    290                 295                 300

Ala Leu Thr Gly Glu Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu
305                 310                 315                 320

Lys Glu Arg Ala Asp Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp
                325                 330                 335

Leu Ile Glu Glu Val Arg Lys Ala Arg Gly Lys Lys Arg Val Pro
            340                 345                 350


<210> 1646
<211> 351
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 463; "

<220>
<221> source
<223> /note="Gene Symbol: ATF4; "

<220>
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<223> /note="Gene Name:
      activating transcription
      factor
      4; "

<220>
<221> source
<223> /note="Uniprot ID:  P18848; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000379912"

<400> 1646
Met Thr Glu Met Ser Phe Leu Ser Ser Glu Val Leu Val Gly Asp Leu
1               5                   10                  15
```

```
Met Ser Pro Phe Asp Gln Ser Gly Leu Gly Ala Glu Glu Ser Leu Gly
            20                  25                  30

Leu Leu Asp Asp Tyr Leu Glu Val Ala Lys His Phe Lys Pro His Gly
        35                  40                  45

Phe Ser Ser Asp Lys Ala Lys Ala Gly Ser Ser Glu Trp Leu Ala Val
    50                  55                  60

Asp Gly Leu Val Ser Pro Ser Asn Asn Ser Lys Glu Asp Ala Phe Ser
65                  70                  75                  80

Gly Thr Asp Trp Met Leu Glu Lys Met Asp Leu Lys Glu Phe Asp Leu
                85                  90                  95

Asp Ala Leu Leu Gly Ile Asp Asp Leu Glu Thr Met Pro Asp Asp Leu
            100                 105                 110

Leu Thr Thr Leu Asp Asp Thr Cys Asp Leu Phe Ala Pro Leu Val Gln
        115                 120                 125

Glu Thr Asn Lys Gln Pro Pro Gln Thr Val Asn Pro Ile Gly His Leu
    130                 135                 140

Pro Glu Ser Leu Thr Lys Pro Asp Gln Val Ala Pro Phe Thr Phe Leu
145                 150                 155                 160

Gln Pro Leu Pro Leu Ser Pro Gly Val Leu Ser Ser Thr Pro Asp His
                165                 170                 175

Ser Phe Ser Leu Glu Leu Gly Ser Glu Val Asp Ile Thr Glu Gly Asp
            180                 185                 190

Arg Lys Pro Asp Tyr Thr Ala Tyr Val Ala Met Ile Pro Gln Cys Ile
        195                 200                 205

Lys Glu Glu Asp Thr Pro Ser Asp Asn Asp Ser Gly Ile Cys Met Ser
    210                 215                 220

Pro Glu Ser Tyr Leu Gly Ser Pro Gln His Ser Pro Ser Thr Arg Gly
225                 230                 235                 240

Ser Pro Asn Arg Ser Leu Pro Ser Pro Gly Val Leu Cys Gly Ser Ala
```

```
                245                 250                 255

Arg Pro Lys Pro Tyr Asp Pro Pro Gly Glu Lys Met Val Ala Ala Lys
            260                 265                 270

Val Lys Gly Glu Lys Leu Asp Lys Lys Leu Lys Lys Met Glu Gln Asn
        275                 280                 285

Lys Thr Ala Ala Thr Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu
    290                 295                 300

Ala Leu Thr Gly Glu Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu
305                 310                 315                 320

Lys Glu Arg Ala Asp Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp
                325                 330                 335

Leu Ile Glu Glu Val Arg Lys Ala Arg Gly Lys Lys Arg Val Pro
            340                 345                 350


<210> 1647
<211> 351
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 463; "

<220>
<221> source
<223> /note="Gene Symbol: ATF4; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      4; "

<220>
<221> source
<223> /note="Uniprot ID:  P18848; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384587"

<400> 1647
Met Thr Glu Met Ser Phe Leu Ser Ser Glu Val Leu Val Gly Asp Leu
```

```
1               5                   10                  15

Met Ser Pro Phe Asp Gln Ser Gly Leu Gly Ala Glu Glu Ser Leu Gly
            20                  25                  30

Leu Leu Asp Asp Tyr Leu Glu Val Ala Lys His Phe Lys Pro His Gly
        35                  40                  45

Phe Ser Ser Asp Lys Ala Lys Ala Gly Ser Ser Glu Trp Leu Ala Val
    50                  55                  60

Asp Gly Leu Val Ser Pro Ser Asn Asn Ser Lys Glu Asp Ala Phe Ser
65                  70                  75                  80

Gly Thr Asp Trp Met Leu Glu Lys Met Asp Leu Lys Glu Phe Asp Leu
                85                  90                  95

Asp Ala Leu Leu Gly Ile Asp Asp Leu Glu Thr Met Pro Asp Asp Leu
            100                 105                 110

Leu Thr Thr Leu Asp Asp Thr Cys Asp Leu Phe Ala Pro Leu Val Gln
        115                 120                 125

Glu Thr Asn Lys Gln Pro Pro Gln Thr Val Asn Pro Ile Gly His Leu
    130                 135                 140

Pro Glu Ser Leu Thr Lys Pro Asp Gln Val Ala Pro Phe Thr Phe Leu
145                 150                 155                 160

Gln Pro Leu Pro Leu Ser Pro Gly Val Leu Ser Ser Thr Pro Asp His
                165                 170                 175

Ser Phe Ser Leu Glu Leu Gly Ser Glu Val Asp Ile Thr Glu Gly Asp
            180                 185                 190

Arg Lys Pro Asp Tyr Thr Ala Tyr Val Ala Met Ile Pro Gln Cys Ile
        195                 200                 205

Lys Glu Glu Asp Thr Pro Ser Asp Asn Asp Ser Gly Ile Cys Met Ser
    210                 215                 220

Pro Glu Ser Tyr Leu Gly Ser Pro Gln His Ser Pro Ser Thr Arg Gly
225                 230                 235                 240
```

```
Ser Pro Asn Arg Ser Leu Pro Ser Pro Gly Val Leu Cys Gly Ser Ala
                245                 250                 255

Arg Pro Lys Pro Tyr Asp Pro Pro Gly Glu Lys Met Val Ala Ala Lys
            260                 265                 270

Val Lys Gly Glu Lys Leu Asp Lys Lys Leu Lys Lys Met Glu Gln Asn
        275                 280                 285

Lys Thr Ala Ala Thr Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu
    290                 295                 300

Ala Leu Thr Gly Glu Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu
305                 310                 315                 320

Lys Glu Arg Ala Asp Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp
                325                 330                 335

Leu Ile Glu Glu Val Arg Lys Ala Arg Gly Lys Lys Arg Val Pro
            340                 345                 350
```

<210> 1648
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 464; "

<220>
<221> source
<223> /note="Gene Symbol: ATF5; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
5; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y2D1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000396954"

<400> 1648
Met Ser Leu Leu Ala Thr Leu Gly Leu Glu Leu Asp Arg Ala Leu Leu
1 5 10 15

Pro Ala Ser Gly Leu Gly Trp Leu Val Asp Tyr Gly Lys Leu Pro Pro
20 25 30

Ala Pro Ala Pro Leu Ala Pro Tyr Glu Val Leu Gly Gly Ala Leu Glu
35 40 45

Gly Gly Leu Pro Val Gly Gly Glu Pro Leu Ala Gly Asp Gly Phe Ser
50 55 60

Asp Trp Met Thr Glu Arg Val Asp Phe Thr Ala Leu Leu Pro Leu Glu
65 70 75 80

Pro Pro Leu Pro Pro Gly Thr Leu Pro Gln Pro Ser Pro Thr Pro Pro
85 90 95

Asp Leu Glu Ala Met Ala Ser Leu Leu Lys Lys Glu Leu Glu Gln Met
100 105 110

Glu Asp Phe Phe Leu Asp Ala Pro Pro Leu Pro Pro Pro Ser Pro Pro
115 120 125

Pro Leu Pro Pro Pro Pro Leu Pro Pro Ala Pro Ser Leu Pro Leu Ser
130 135 140

Leu Pro Ser Phe Asp Leu Pro Gln Pro Pro Val Leu Asp Thr Leu Asp
145 150 155 160

Leu Leu Ala Ile Tyr Cys Arg Asn Glu Ala Gly Gln Glu Glu Val Gly
165 170 175

Met Pro Pro Leu Pro Pro Pro Gln Gln Pro Pro Pro Pro Ser Pro Pro
180 185 190

Gln Pro Ser Arg Leu Ala Pro Tyr Pro His Pro Ala Thr Thr Arg Gly
195 200 205

Asp Arg Lys Gln Lys Lys Arg Asp Gln Asn Lys Ser Ala Ala Leu Arg
210 215 220

```
Tyr Arg Gln Arg Lys Arg Ala Glu Gly Glu Ala Leu Glu Gly Glu Cys
225                 230                 235                 240


Gln Gly Leu Glu Ala Arg Asn Arg Glu Leu Lys Glu Arg Ala Glu Ser
                245                 250                 255


Val Glu Arg Glu Ile Gln Tyr Val Lys Asp Leu Leu Ile Glu Val Tyr
            260                 265                 270


Lys Ala Arg Ser Gln Arg Thr Arg Ser Cys
        275                 280


<210> 1649
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 464; "

<220>
<221> source
<223> /note="Gene Symbol: ATF5; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470464"

<400> 1649
Met Ser Leu Leu Ala Thr Leu Gly Leu Glu Leu Asp Arg Ala Leu Leu
1               5                   10                  15


Pro Ala Ser Gly Leu Gly Trp Leu Val Asp Tyr Gly Lys Leu Pro Pro
            20                  25                  30


Ala Pro Ala Pro Leu Ala Pro Tyr Glu Val Leu Gly Gly Ala Leu Glu
        35                  40                  45


Gly Gly Leu Pro Val Gly Gly Glu Pro Leu Ala Gly Asp Gly Phe Ser
    50                  55                  60
```

```
Asp Trp Met Thr Glu Arg Val Asp Phe Thr Ala Leu Leu Pro Leu Glu
65                  70                  75                  80

Pro Pro Leu Pro Pro Gly Thr Leu Pro Gln Pro Ser Pro Thr Pro Pro
                85                  90                  95

Asp Leu Glu Ala Met Ala Ser Leu Leu Lys Lys Glu Leu Glu Gln Met
            100                 105                 110

Glu Asp Phe Phe Leu Asp Ala Pro Pro Leu Pro Pro Pro Ser Pro Pro
        115                 120                 125

Pro
```

<210> 1650
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 464; "

<220>
<221> source
<223> /note="Gene Symbol: ATF5; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
5; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y2D1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470633"

<400> 1650

```
Met Ser Leu Leu Ala Thr Leu Gly Leu Glu Leu Asp Arg Ala Leu Leu
1               5                   10                  15

Pro Ala Ser Gly Leu Gly Trp Leu Val Asp Tyr Gly Lys Leu Pro Pro
            20                  25                  30
```

```
Ala Pro Ala Pro Leu Ala Pro Tyr Glu Val Leu Gly Gly Ala Leu Glu
        35                  40                  45

Gly Gly Leu Pro Val Gly Gly Glu Pro Leu Ala Gly Asp Gly Phe Ser
    50                  55                  60

Asp Trp Met Thr Glu Arg Val Asp Phe Thr Ala Leu Leu Pro Leu Glu
65                  70                  75                  80

Pro Pro Leu Pro Pro Gly Thr Leu Pro Gln Pro Ser Pro Thr Pro Pro
                85                  90                  95

Asp Leu Glu Ala Met Ala Ser Leu Leu Lys Lys Glu Leu Glu Gln Met
            100                 105                 110

Glu Asp Phe Phe Leu Asp Ala Pro Pro Leu Pro Pro Pro Ser Pro Pro
        115                 120                 125

Pro Leu Pro Pro Pro Pro Leu Pro Pro Ala Pro Ser Leu Pro Leu Ser
    130                 135                 140

Leu Pro Ser Phe Asp Leu Pro Gln Pro Pro Val Leu Asp Thr Leu Asp
145                 150                 155                 160

Leu Leu Ala Ile Tyr Cys Arg Asn Glu Ala Gly Gln Glu Glu Val Gly
                165                 170                 175

Met Pro Pro Leu Pro Pro Pro Gln Gln Pro Pro Pro Pro Ser Pro Pro
            180                 185                 190

Gln Pro Ser Arg Leu Ala Pro Tyr Pro His Pro Ala Thr Thr Arg Gly
        195                 200                 205

Asp Arg Lys Gln Lys Lys Arg Asp Gln Asn Lys Ser Ala Ala Leu Arg
    210                 215                 220

Tyr Arg Gln Arg Lys Arg Ala Glu Gly Glu Ala Leu Glu Gly Glu Cys
225                 230                 235                 240

Gln Gly Leu Glu Ala Arg Asn Arg Glu Leu Lys Glu Arg Ala Glu Ser
                245                 250                 255
```

```
Val Glu Arg Glu Ile Gln Tyr Val Lys Asp Leu Leu Ile Glu Val Tyr
            260                 265                 270


Lys Ala Arg Ser Gln Arg Thr Arg Ser Cys
        275                 280


<210> 1651
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 464; "

<220>
<221> source
<223> /note="Gene Symbol: ATF5; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470978"

<400> 1651
Met Ser Leu Leu Ala Thr Leu Gly Leu Glu Leu Asp Arg Ala Leu Leu
1               5                   10                  15


Pro Ala Ser Gly Leu Gly Trp Leu Val Asp Tyr Gly Lys Leu Pro Pro
            20                  25                  30


Ala Pro Ala Pro Leu Ala Pro Tyr Glu Val Leu Gly Gly Ala Leu Glu
        35                  40                  45


Gly Gly Leu Pro Val Gly Gly Glu Pro Leu Ala Gly Asp Gly Phe Ser
    50                  55                  60


Asp Trp Met Thr Glu Arg Val Asp Phe Thr Ala Leu Leu Pro Leu Glu
65                  70                  75                  80


Pro Pro Leu Pro Pro Gly Thr Leu Pro Gln Pro Ser Pro Thr Pro Pro
                85                  90                  95
```

```
Asp Leu Glu Ala Met Ala Ser Leu Leu Lys Lys Glu Leu Glu Gln Met
            100                 105                 110


Glu Asp Phe Phe Leu Asp Ala Pro Pro
        115                 120


<210> 1652
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 464; "

<220>
<221> source
<223> /note="Gene Symbol: ATF5; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000471162"

<400> 1652
Met Ser Leu Leu Ala Thr Leu Gly Leu Glu Leu Asp Arg Ala Leu Leu
1               5                   10                  15


Pro Ala Ser Gly Leu Gly Trp Leu Val Asp Tyr Gly Lys Leu Pro Pro
            20                  25                  30


Ala Pro Ala Pro Leu Ala Pro Tyr Glu Val Leu Gly Gly Ala Leu Glu
        35                  40                  45


Gly Gly Leu Pro Val Gly Gly Glu Pro Leu Ala Gly Lys Gly Arg Trp
    50                  55                  60


Lys Val Glu Leu Gly Ser Gly Gly Gln Gly Lys Met Gly Glu Glu Glu
65                  70                  75                  80


Leu Ile His Val Phe Asn Lys Tyr
                85
```

<210> 1653
<211> 670
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 465; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
6; "

<220>
<221> source
<223> /note="Uniprot ID: P18850; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356919"

<400> 1653
Met Gly Glu Pro Ala Gly Val Ala Gly Thr Met Glu Ser Pro Phe Ser
1   5   10   15

Pro Gly Leu Phe His Arg Leu Asp Glu Asp Trp Asp Ser Ala Leu Phe
            20   25   30

Ala Glu Leu Gly Tyr Phe Thr Asp Thr Asp Glu Leu Gln Leu Glu Ala
        35   40   45

Ala Asn Glu Thr Tyr Glu Asn Asn Phe Asp Asn Leu Asp Phe Asp Leu
    50   55   60

Asp Leu Met Pro Trp Glu Ser Asp Ile Trp Asp Ile Asn Asn Gln Ile
65   70   75   80

Cys Thr Val Lys Asp Ile Lys Ala Glu Pro Gln Pro Leu Ser Pro Ala
                85   90   95

Ser Ser Ser Tyr Ser Val Ser Ser Pro Arg Ser Val Asp Ser Tyr Ser
            100   105   110

```
Ser Thr Gln His Val Pro Glu Glu Leu Asp Leu Ser Ser Ser Ser Gln
        115                 120                 125

Met Ser Pro Leu Ser Leu Tyr Gly Glu Asn Ser Asn Ser Leu Ser Ser
    130                 135                 140

Ala Glu Pro Leu Lys Glu Asp Lys Pro Val Thr Gly Pro Arg Asn Lys
145                 150                 155                 160

Thr Glu Asn Gly Leu Thr Pro Lys Lys Lys Ile Gln Val Asn Ser Lys
                165                 170                 175

Pro Ser Ile Gln Pro Lys Pro Leu Leu Leu Pro Ala Ala Pro Lys Thr
            180                 185                 190

Gln Thr Asn Ser Ser Val Pro Ala Lys Thr Ile Ile Ile Gln Thr Val
        195                 200                 205

Pro Thr Leu Met Pro Leu Ala Lys Gln Gln Pro Ile Ile Ser Leu Gln
    210                 215                 220

Pro Ala Pro Thr Lys Gly Gln Thr Val Leu Leu Ser Gln Pro Thr Val
225                 230                 235                 240

Val Gln Leu Gln Ala Pro Gly Val Leu Pro Ser Ala Gln Pro Val Leu
                245                 250                 255

Ala Val Ala Gly Gly Val Thr Gln Leu Pro Asn His Val Val Asn Val
            260                 265                 270

Val Pro Ala Pro Ser Ala Asn Ser Pro Val Asn Gly Lys Leu Ser Val
        275                 280                 285

Thr Lys Pro Val Leu Gln Ser Thr Met Arg Asn Val Gly Ser Asp Ile
    290                 295                 300

Ala Val Leu Arg Arg Gln Gln Arg Met Ile Lys Asn Arg Glu Ser Ala
305                 310                 315                 320

Cys Gln Ser Arg Lys Lys Lys Lys Glu Tyr Met Leu Gly Leu Glu Ala
                325                 330                 335

Arg Leu Lys Ala Ala Leu Ser Glu Asn Glu Gln Leu Lys Lys Glu Asn
```

```
            340                 345                 350

Gly Thr Leu Lys Arg Gln Leu Asp Glu Val Val Ser Glu Asn Gln Arg
        355                 360                 365

Leu Lys Val Pro Ser Pro Lys Arg Arg Val Val Cys Val Met Ile Val
    370                 375                 380

Leu Ala Phe Ile Ile Leu Asn Tyr Gly Pro Met Ser Met Leu Glu Gln
385                 390                 395                 400

Asp Ser Arg Arg Met Asn Pro Ser Val Ser Pro Ala Asn Gln Arg Arg
                405                 410                 415

His Leu Leu Gly Phe Ser Ala Lys Glu Ala Gln Asp Thr Ser Asp Gly
            420                 425                 430

Ile Ile Gln Lys Asn Ser Tyr Arg Tyr Asp His Ser Val Ser Asn Asp
        435                 440                 445

Lys Ala Leu Met Val Leu Thr Glu Glu Pro Leu Leu Tyr Ile Pro Pro
    450                 455                 460

Pro Pro Cys Gln Pro Leu Ile Asn Thr Thr Glu Ser Leu Arg Leu Asn
465                 470                 475                 480

His Glu Leu Arg Gly Trp Val His Arg His Glu Val Glu Arg Thr Lys
                485                 490                 495

Ser Arg Arg Met Thr Asn Asn Gln Gln Lys Thr Arg Ile Leu Gln Gly
            500                 505                 510

Ala Leu Glu Gln Gly Ser Asn Ser Gln Leu Met Ala Val Gln Tyr Thr
        515                 520                 525

Glu Thr Thr Ser Ser Ile Ser Arg Asn Ser Gly Ser Glu Leu Gln Val
    530                 535                 540

Tyr Tyr Ala Ser Pro Arg Ser Tyr Gln Asp Phe Phe Glu Ala Ile Arg
545                 550                 555                 560

Arg Arg Gly Asp Thr Phe Tyr Val Val Ser Phe Arg Arg Asp His Leu
                565                 570                 575
```

```
Leu Leu Pro Ala Thr Thr His Asn Lys Thr Thr Arg Pro Lys Met Ser
            580                 585                 590

Ile Val Leu Pro Ala Ile Asn Ile Asn Glu Asn Val Ile Asn Gly Gln
        595                 600                 605

Asp Tyr Glu Val Met Met Gln Ile Asp Cys Gln Val Met Asp Thr Arg
    610                 615                 620

Ile Leu His Ile Lys Ser Ser Ser Val Pro Pro Tyr Leu Arg Asp Gln
625                 630                 635                 640

Gln Arg Asn Gln Thr Asn Thr Phe Phe Gly Ser Pro Pro Ala Ala Thr
                645                 650                 655

Glu Ala Thr His Val Val Ser Thr Ile Pro Glu Ser Leu Gln
            660                 665                 670


<210> 1654
<211> 703
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      6 beta; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99941; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000293709"

<400> 1654
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1               5                   10                  15
```

```
Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Gly Leu Gln Asn Ser
            20                  25                  30

Thr Leu Tyr Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu
        35                  40                  45

Phe Arg Cys Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp
    50                  55                  60

Val Gly Met Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro
65                  70                  75                  80

Ile Phe Pro Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser
                85                  90                  95

Ser Ser Ser Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser
            100                 105                 110

Ser Glu Ala Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser
        115                 120                 125

Leu Ala Pro Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe
    130                 135                 140

Glu Thr Val Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp
145                 150                 155                 160

Val Gln Thr Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser
                165                 170                 175

Glu Ala Ser Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly
            180                 185                 190

Glu Glu Val Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys
        195                 200                 205

Leu Leu Trp Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser
    210                 215                 220

Met Gly Pro Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg
225                 230                 235                 240
```

Lys Pro Pro Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met
245 250 255

Pro Ser Arg Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu
260 265 270

Val Gln Pro Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile
275 280 285

Arg Val Gln Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg
290 295 300

Lys Ser Ile Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu
305 310 315 320

Val Asp Ala Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg
325 330 335

Glu Ser Ala Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly
340 345 350

Leu Glu Ala Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg
355 360 365

Arg Glu Asn Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu
370 375 380

Asn Ser Glu Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile
385 390 395 400

Met Val Phe Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile
405 410 415

Ser Glu Pro Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu
420 425 430

Pro Gln Pro Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val
435 440 445

Gln Gly Val Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro
450 455 460

```
Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe
465                 470                 475                 480

Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe
                485                 490                 495

Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu
            500                 505                 510

Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg
        515                 520                 525

Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys
    530                 535                 540

Lys Ser Pro Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro
545                 550                 555                 560

Glu Arg Asp Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg
                565                 570                 575

Ser Gln Pro Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe
            580                 585                 590

Tyr Val Val Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser
        595                 600                 605

His Asn Lys Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met
    610                 615                 620

Ala Pro Asn Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu
625                 630                 635                 640

Glu Met Met Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His
                645                 650                 655

Ile Lys Thr Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro
            660                 665                 670

Thr Pro Gly Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser
        675                 680                 685

Gln Ala His Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
```

690 695 700

<210> 1655
<211> 700
<212> PRT
<213> Homo sapiens

<220>
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<220>
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activating transcription
factor
6 beta; "

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<220>
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<400> 1655
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1 5 10 15

Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Asp Ser Thr Leu Tyr
20 25 30

Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu Phe Arg Cys
35 40 45

Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp Val Gly Met
50 55 60

Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro Ile Phe Pro
65 70 75 80

Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser Ser Ser Ser
85 90 95

Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser Ser Glu Ala

```
            100                 105                 110

Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser Leu Ala Pro
        115                 120                 125

Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe Glu Thr Val
    130                 135                 140

Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp Val Gln Thr
145                 150                 155                 160

Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser Glu Ala Ser
                165                 170                 175

Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly Glu Glu Val
            180                 185                 190

Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys Leu Leu Trp
        195                 200                 205

Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser Met Gly Pro
    210                 215                 220

Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg Lys Pro Pro
225                 230                 235                 240

Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met Pro Ser Arg
                245                 250                 255

Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu Val Gln Pro
            260                 265                 270

Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile Arg Val Gln
        275                 280                 285

Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg Lys Ser Ile
    290                 295                 300

Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu Val Asp Ala
305                 310                 315                 320

Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg Glu Ser Ala
                325                 330                 335
```

```
Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly Leu Glu Ala
            340                 345                 350

Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg Arg Glu Asn
        355                 360                 365

Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu Asn Ser Glu
    370                 375                 380

Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile Met Val Phe
385                 390                 395                 400

Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile Ser Glu Pro
                405                 410                 415

Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu Pro Gln Pro
            420                 425                 430

Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val Gln Gly Val
        435                 440                 445

Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro Gln Pro Ser
    450                 455                 460

Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe Pro Gly Gly
465                 470                 475                 480

Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe Leu Ser Ser
                485                 490                 495

Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu Ala Asp Glu
            500                 505                 510

Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg Lys Ile Pro
        515                 520                 525

Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys Lys Ser Pro
    530                 535                 540

Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro Glu Arg Asp
545                 550                 555                 560
```

```
Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg Ser Gln Pro
                565                 570                 575

Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe Tyr Val Val
            580                 585                 590

Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser His Asn Lys
        595                 600                 605

Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met Ala Pro Asn
    610                 615                 620

Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu Glu Met Met
625                 630                 635                 640

Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His Ile Lys Thr
                645                 650                 655

Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro Thr Pro Gly
            660                 665                 670

Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser Gln Ala His
        675                 680                 685

Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700
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<210> 1656
<211> 703
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 466; "

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
6 beta; "

<220>
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<220>
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<400> 1656
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1   5   10   15

Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Gly Leu Gln Asn Ser
            20   25   30

Thr Leu Tyr Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu
        35   40   45

Phe Arg Cys Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp
    50   55   60

Val Gly Met Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro
65   70   75   80

Ile Phe Pro Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser
                85   90   95

Ser Ser Ser Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser
            100   105   110

Ser Glu Ala Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser
        115   120   125

Leu Ala Pro Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe
    130   135   140

Glu Thr Val Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp
145   150   155   160

Val Gln Thr Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser
                165   170   175

Glu Ala Ser Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly
            180   185   190

```
Glu Glu Val Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys
        195                 200                 205

Leu Leu Trp Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser
    210                 215                 220

Met Gly Pro Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg
225                 230                 235                 240

Lys Pro Pro Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met
                245                 250                 255

Pro Ser Arg Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu
            260                 265                 270

Val Gln Pro Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile
        275                 280                 285

Arg Val Gln Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg
    290                 295                 300

Lys Ser Ile Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu
305                 310                 315                 320

Val Asp Ala Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg
                325                 330                 335

Glu Ser Ala Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly
            340                 345                 350

Leu Glu Ala Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg
        355                 360                 365

Arg Glu Asn Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu
    370                 375                 380

Asn Ser Glu Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile
385                 390                 395                 400

Met Val Phe Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile
                405                 410                 415

Ser Glu Pro Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu
```

```
            420                 425                 430

Pro Gln Pro Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val
        435                 440                 445

Gln Gly Val Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro
    450                 455                 460

Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe
465                 470                 475                 480

Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe
                485                 490                 495

Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu
            500                 505                 510

Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg
        515                 520                 525

Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys
    530                 535                 540

Lys Ser Pro Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro
545                 550                 555                 560

Glu Arg Asp Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg
                565                 570                 575

Ser Gln Pro Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe
            580                 585                 590

Tyr Val Val Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser
        595                 600                 605

His Asn Lys Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met
    610                 615                 620

Ala Pro Asn Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu
625                 630                 635                 640

Glu Met Met Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His
                645                 650                 655
```

```
Ile Lys Thr Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro
            660                 665                 670

Thr Pro Gly Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser
        675                 680                 685

Gln Ala His Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700


<210> 1657
<211> 700
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      6 beta; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99941; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000372642"

<400> 1657
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1               5                  10                  15

Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Asp Ser Thr Leu Tyr
            20                  25                  30

Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu Phe Arg Cys
        35                  40                  45

Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp Val Gly Met
    50                  55                  60
```

```
Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro Ile Phe Pro
65                  70                  75                  80

Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser Ser Ser Ser
                85                  90                  95

Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser Ser Glu Ala
            100                 105                 110

Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser Leu Ala Pro
        115                 120                 125

Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe Glu Thr Val
    130                 135                 140

Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp Val Gln Thr
145                 150                 155                 160

Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser Glu Ala Ser
                165                 170                 175

Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly Glu Glu Val
            180                 185                 190

Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys Leu Leu Trp
        195                 200                 205

Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser Met Gly Pro
    210                 215                 220

Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg Lys Pro Pro
225                 230                 235                 240

Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met Pro Ser Arg
                245                 250                 255

Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu Val Gln Pro
            260                 265                 270

Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile Arg Val Gln
        275                 280                 285
```

```
Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg Lys Ser Ile
    290                 295                 300

Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu Val Asp Ala
305                 310                 315                 320

Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg Glu Ser Ala
                325                 330                 335

Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly Leu Glu Ala
            340                 345                 350

Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg Arg Glu Asn
        355                 360                 365

Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu Asn Ser Glu
    370                 375                 380

Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile Met Val Phe
385                 390                 395                 400

Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile Ser Glu Pro
                405                 410                 415

Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu Pro Gln Pro
            420                 425                 430

Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val Gln Gly Val
        435                 440                 445

Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro Gln Pro Ser
    450                 455                 460

Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe Pro Gly Gly
465                 470                 475                 480

Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe Leu Ser Ser
                485                 490                 495

Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu Ala Asp Glu
            500                 505                 510
```

```
Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg Lys Ile Pro
        515                 520                 525

Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys Lys Ser Pro
    530                 535                 540

Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro Glu Arg Asp
545                 550                 555                 560

Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg Ser Gln Pro
                565                 570                 575

Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe Tyr Val Val
            580                 585                 590

Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser His Asn Lys
        595                 600                 605

Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met Ala Pro Asn
    610                 615                 620

Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu Glu Met Met
625                 630                 635                 640

Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His Ile Lys Thr
                645                 650                 655

Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro Thr Pro Gly
            660                 665                 670

Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser Gln Ala His
        675                 680                 685

Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700


<210> 1658
<211> 142
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 466; "
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<220>
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<223> /note="Gene Symbol: ATF6B; "

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activating transcription
factor
6 beta; "

<220>
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<223> /note="ENSP ID: ENSP00000389467"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1658
Xaa Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala
1 5 10 15

Phe Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu
20 25 30

Phe Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg
35 40 45

Leu Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg
50 55 60

Arg Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Ser Leu Asp Thr Ser
65 70 75 80

Pro Ser Arg Ser Leu Ser His Gly Arg Ser His Leu Gln Leu Arg Gln
85 90 95

Ser Pro Ser Asn Pro Leu Asp Pro Gln Lys Gly Ile Leu Trp Ala Ser
100 105 110

Cys Asn Tyr Ile Ala Thr Gln Thr Val Arg Ser Gln His Ser Trp Met
115 120 125

Gln Leu Thr Asp Gly Lys Thr His Phe Met Leu Ser Leu Ser
130 135 140

<210> 1659
<211> 700
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 466; "

<220>
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<220>
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activating transcription
factor
6 beta; "

<220>
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<223> /note="Uniprot ID: Q99941; "

<220>
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<400> 1659
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1   5   10   15

Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Asp Ser Thr Leu Tyr
            20   25   30

Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu Phe Arg Cys
        35   40   45

Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp Val Gly Met
    50   55   60

Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro Ile Phe Pro
65   70   75   80

Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser Ser Ser Ser
                85   90   95

Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser Ser Glu Ala
            100   105   110

```
Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser Leu Ala Pro
        115                 120                 125

Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe Glu Thr Val
    130                 135                 140

Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp Val Gln Thr
145                 150                 155                 160

Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser Glu Ala Ser
                165                 170                 175

Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly Glu Glu Val
            180                 185                 190

Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys Leu Leu Trp
        195                 200                 205

Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser Met Gly Pro
    210                 215                 220

Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg Lys Pro Pro
225                 230                 235                 240

Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met Pro Ser Arg
                245                 250                 255

Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu Val Gln Pro
            260                 265                 270

Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile Arg Val Gln
        275                 280                 285

Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg Lys Ser Ile
    290                 295                 300

Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu Val Asp Ala
305                 310                 315                 320

Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg Glu Ser Ala
                325                 330                 335
```

```
Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly Leu Glu Ala
            340                 345                 350

Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg Arg Glu Asn
        355                 360                 365

Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu Asn Ser Glu
    370                 375                 380

Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile Met Val Phe
385                 390                 395                 400

Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile Ser Glu Pro
                405                 410                 415

Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu Pro Gln Pro
            420                 425                 430

Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val Gln Gly Val
        435                 440                 445

Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro Gln Pro Ser
    450                 455                 460

Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe Pro Gly Gly
465                 470                 475                 480

Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe Leu Ser Ser
                485                 490                 495

Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu Ala Asp Glu
            500                 505                 510

Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg Lys Ile Pro
        515                 520                 525

Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys Lys Ser Pro
    530                 535                 540

Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro Glu Arg Asp
545                 550                 555                 560

Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg Ser Gln Pro
```

```
                565                 570                 575

Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe Tyr Val Val
            580                 585                 590

Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser His Asn Lys
        595                 600                 605

Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met Ala Pro Asn
    610                 615                 620

Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu Glu Met Met
625                 630                 635                 640

Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His Ile Lys Thr
                645                 650                 655

Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro Thr Pro Gly
            660                 665                 670

Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser Gln Ala His
        675                 680                 685

Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700


<210> 1660
<211> 142
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 466; "

<220>
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<223> /note="Gene Symbol: ATF6B; "

<220>
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      factor
      6 beta; "

<220>
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<223> /note="ENSP ID: ENSP00000393419"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1660
Xaa Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala
1 5 10 15

Phe Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu
20 25 30

Phe Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg
35 40 45

Leu Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg
50 55 60

Arg Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Ser Leu Asp Thr Ser
65 70 75 80

Pro Ser Arg Ser Leu Ser His Gly Arg Ser His Leu Gln Leu Arg Gln
85 90 95

Ser Pro Ser Asn Pro Leu Asp Pro Gln Lys Gly Ile Leu Trp Ala Ser
100 105 110

Cys Asn Tyr Ile Ala Thr Gln Thr Val Arg Ser Gln His Ser Trp Met
115 120 125

Gln Leu Thr Asp Gly Lys Thr His Phe Met Leu Ser Leu Ser
130 135 140

<210> 1661
<211> 700
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
6 beta; "

<220>
<221> source
<223> /note="Uniprot ID: Q99941; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399764"

<400> 1661
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1   5   10   15

Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Asp Ser Thr Leu Tyr
            20   25   30

Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu Phe Arg Cys
        35   40   45

Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp Val Gly Met
    50   55   60

Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro Ile Phe Pro
65   70   75   80

Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser Ser Ser Ser
                85   90   95

Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser Ser Glu Ala
            100   105   110

Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser Leu Ala Pro
        115   120   125

Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe Glu Thr Val
    130   135   140

Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp Val Gln Thr
145   150   155   160

```
Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser Glu Ala Ser
                165                 170                 175

Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly Glu Glu Val
            180                 185                 190

Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys Leu Leu Trp
        195                 200                 205

Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser Met Gly Pro
    210                 215                 220

Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg Lys Pro Pro
225                 230                 235                 240

Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met Pro Ser Arg
                245                 250                 255

Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu Val Gln Pro
            260                 265                 270

Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile Arg Val Gln
        275                 280                 285

Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg Lys Ser Ile
    290                 295                 300

Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu Val Asp Ala
305                 310                 315                 320

Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg Glu Ser Ala
                325                 330                 335

Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly Leu Glu Ala
            340                 345                 350

Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg Arg Glu Asn
        355                 360                 365

Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu Asn Ser Glu
    370                 375                 380

Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile Met Val Phe
```

385 390 395 400

Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile Ser Glu Pro
405 410 415

Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu Pro Gln Pro
420 425 430

Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val Gln Gly Val
435 440 445

Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro Gln Pro Ser
450 455 460

Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe Pro Gly Gly
465 470 475 480

Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe Leu Ser Ser
485 490 495

Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu Ala Asp Glu
500 505 510

Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg Lys Ile Pro
515 520 525

Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys Lys Ser Pro
530 535 540

Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro Glu Arg Asp
545 550 555 560

Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg Ser Gln Pro
565 570 575

Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe Tyr Val Val
580 585 590

Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser His Asn Lys
595 600 605

Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met Ala Pro Asn
610 615 620

```
Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu Glu Met Met
625                 630                 635                 640

Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His Ile Lys Thr
                645                 650                 655

Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro Thr Pro Gly
            660                 665                 670

Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser Gln Ala His
        675                 680                 685

Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700


<210> 1662
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      6 beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399944"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1662
Xaa Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala
1               5                   10                  15
```

```
Phe Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu
            20                  25                  30

Phe Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg
        35                  40                  45

Leu Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg
    50                  55                  60

Arg Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Ser Leu Asp Thr Ser
65                  70                  75                  80

Pro Ser Arg Ser Leu Ser His Gly Arg Ser His Leu Gln Leu Arg Gln
                85                  90                  95

Ser Pro Ser Asn Pro Leu Asp Pro Gln Lys Gly Ile Leu Trp Ala Ser
            100                 105                 110

Cys Asn Tyr Ile Ala Thr Gln Thr Val Arg Ser Gln His Ser Trp Met
        115                 120                 125

Gln Leu Thr Asp Gly Lys Thr His Phe Met Leu Ser Leu Ser
    130                 135                 140


<210> 1663
<211> 703
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      6 beta; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99941; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000404725"

<400> 1663
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1 5 10 15

Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Gly Leu Gln Asn Ser
20 25 30

Thr Leu Tyr Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu
35 40 45

Phe Arg Cys Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp
50 55 60

Val Gly Met Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro
65 70 75 80

Ile Phe Pro Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser
85 90 95

Ser Ser Ser Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser
100 105 110

Ser Glu Ala Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser
115 120 125

Leu Ala Pro Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe
130 135 140

Glu Thr Val Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp
145 150 155 160

Val Gln Thr Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser
165 170 175

Glu Ala Ser Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly
180 185 190

Glu Glu Val Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys
195 200 205

Leu Leu Trp Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser

```
    210                 215                 220

Met Gly Pro Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg
225                 230                 235                 240

Lys Pro Pro Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met
                245                 250                 255

Pro Ser Arg Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu
            260                 265                 270

Val Gln Pro Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile
        275                 280                 285

Arg Val Gln Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg
    290                 295                 300

Lys Ser Ile Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu
305                 310                 315                 320

Val Asp Ala Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg
                325                 330                 335

Glu Ser Ala Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly
            340                 345                 350

Leu Glu Ala Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg
        355                 360                 365

Arg Glu Asn Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu
    370                 375                 380

Asn Ser Glu Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile
385                 390                 395                 400

Met Val Phe Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile
                405                 410                 415

Ser Glu Pro Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu
            420                 425                 430

Pro Gln Pro Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val
        435                 440                 445
```

```
Gln Gly Val Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro
    450                 455                 460

Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe
465                 470                 475                 480

Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe
                485                 490                 495

Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu
            500                 505                 510

Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg
        515                 520                 525

Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys
    530                 535                 540

Lys Ser Pro Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro
545                 550                 555                 560

Glu Arg Asp Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg
                565                 570                 575

Ser Gln Pro Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe
            580                 585                 590

Tyr Val Val Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser
        595                 600                 605

His Asn Lys Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met
    610                 615                 620

Ala Pro Asn Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu
625                 630                 635                 640

Glu Met Met Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His
                645                 650                 655

Ile Lys Thr Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro
            660                 665                 670
```

```
Thr Pro Gly Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser
        675                 680                 685


Gln Ala His Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700


<210> 1664
<211> 703
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      6 beta; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99941; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000404814"

<400> 1664
Met Ala Glu Leu Met Leu Leu Ser Glu Ile Ala Asp Pro Thr Arg Phe
1               5                   10                  15


Phe Thr Asp Asn Leu Leu Ser Pro Glu Asp Trp Gly Leu Gln Asn Ser
            20                  25                  30


Thr Leu Tyr Ser Gly Leu Asp Glu Val Ala Glu Glu Gln Thr Gln Leu
        35                  40                  45


Phe Arg Cys Pro Glu Gln Asp Val Pro Phe Asp Gly Ser Ser Leu Asp
    50                  55                  60


Val Gly Met Asp Val Ser Pro Ser Glu Pro Pro Trp Glu Leu Leu Pro
65                  70                  75                  80
```

```
Ile Phe Pro Asp Leu Gln Val Lys Ser Glu Pro Ser Ser Pro Cys Ser
                85                  90                  95

Ser Ser Ser Leu Ser Ser Glu Ser Ser Arg Leu Ser Thr Glu Pro Ser
            100                 105                 110

Ser Glu Ala Leu Gly Val Gly Glu Val Leu His Val Lys Thr Glu Ser
        115                 120                 125

Leu Ala Pro Pro Leu Cys Leu Leu Gly Asp Asp Pro Thr Ser Ser Phe
    130                 135                 140

Glu Thr Val Gln Ile Asn Val Ile Pro Thr Ser Asp Asp Ser Ser Asp
145                 150                 155                 160

Val Gln Thr Lys Ile Glu Pro Val Ser Pro Cys Ser Ser Val Asn Ser
                165                 170                 175

Glu Ala Ser Leu Leu Ser Ala Asp Ser Ser Ser Gln Ala Phe Ile Gly
            180                 185                 190

Glu Glu Val Leu Glu Val Lys Thr Glu Ser Leu Ser Pro Ser Gly Cys
        195                 200                 205

Leu Leu Trp Asp Val Pro Ala Pro Ser Leu Gly Ala Val Gln Ile Ser
    210                 215                 220

Met Gly Pro Ser Leu Asp Gly Ser Ser Gly Lys Ala Leu Pro Thr Arg
225                 230                 235                 240

Lys Pro Pro Leu Gln Pro Lys Pro Val Val Leu Thr Thr Val Pro Met
                245                 250                 255

Pro Ser Arg Ala Val Pro Pro Ser Thr Thr Val Leu Leu Gln Ser Leu
            260                 265                 270

Val Gln Pro Pro Pro Val Ser Pro Val Val Leu Ile Gln Gly Ala Ile
        275                 280                 285

Arg Val Gln Pro Glu Gly Pro Ala Pro Ser Leu Pro Arg Pro Glu Arg
    290                 295                 300
```

```
Lys Ser Ile Val Pro Ala Pro Met Pro Gly Asn Ser Cys Pro Pro Glu
305                 310                 315                 320

Val Asp Ala Lys Leu Leu Lys Arg Gln Gln Arg Met Ile Lys Asn Arg
                325                 330                 335

Glu Ser Ala Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr Leu Gln Gly
            340                 345                 350

Leu Glu Ala Arg Leu Gln Ala Val Leu Ala Asp Asn Gln Gln Leu Arg
        355                 360                 365

Arg Glu Asn Ala Ala Leu Arg Arg Arg Leu Glu Ala Leu Leu Ala Glu
    370                 375                 380

Asn Ser Glu Leu Lys Leu Gly Ser Gly Asn Arg Lys Val Val Cys Ile
385                 390                 395                 400

Met Val Phe Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro Val Ser Ile
                405                 410                 415

Ser Glu Pro Pro Ser Ala Pro Ile Ser Pro Arg Met Asn Lys Gly Glu
            420                 425                 430

Pro Gln Pro Arg Arg His Leu Leu Gly Phe Ser Glu Gln Glu Pro Val
        435                 440                 445

Gln Gly Val Glu Pro Leu Gln Gly Ser Ser Gln Gly Pro Lys Glu Pro
    450                 455                 460

Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala Phe
465                 470                 475                 480

Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu Phe
                485                 490                 495

Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg Leu
            500                 505                 510

Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg Arg
        515                 520                 525

Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Lys Ser Gln Pro Arg Lys
```

```
    530                 535                 540

Lys Ser Pro Pro Val Lys Ala Val Pro Ile Gln Pro Pro Gly Pro Pro
545                 550                 555                 560

Glu Arg Asp Ser Val Gly Gln Leu Gln Leu Tyr Arg His Pro Asp Arg
                565                 570                 575

Ser Gln Pro Ala Phe Leu Asp Ala Ile Asp Arg Arg Glu Asp Thr Phe
            580                 585                 590

Tyr Val Val Ser Phe Arg Arg Asp His Leu Leu Leu Pro Ala Ile Ser
        595                 600                 605

His Asn Lys Thr Ser Arg Pro Lys Met Ser Leu Val Met Pro Ala Met
    610                 615                 620

Ala Pro Asn Glu Thr Leu Ser Gly Arg Gly Ala Pro Gly Asp Tyr Glu
625                 630                 635                 640

Glu Met Met Gln Ile Glu Cys Glu Val Met Asp Thr Arg Val Ile His
                645                 650                 655

Ile Lys Thr Ser Thr Val Pro Pro Ser Leu Arg Lys Gln Pro Ser Pro
            660                 665                 670

Thr Pro Gly Asn Ala Thr Gly Gly Pro Leu Pro Val Ser Ala Ala Ser
        675                 680                 685

Gln Ala His Gln Ala Ser His Gln Pro Leu Tyr Leu Asn His Pro
    690                 695                 700


<210> 1665
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 466; "

<220>
<221> source
<223> /note="Gene Symbol: ATF6B; "

<220>
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<221> source
<223> /note="Gene Name:
activating transcription
factor
6 beta; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412066"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1665
Xaa Gln Pro Ser Pro Thr Asp Gln Pro Ser Phe Ser Asn Leu Thr Ala
1 5 10 15

Phe Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp Gln Leu
20 25 30

Phe Leu Ser Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser Leu Arg
35 40 45

Leu Ala Asp Glu Leu Ser Gly Trp Val Gln Arg His Gln Arg Gly Arg
50 55 60

Arg Lys Ile Pro Gln Arg Ala Gln Glu Arg Gln Ser Leu Asp Thr Ser
65 70 75 80

Pro Ser Arg Ser Leu Ser His Gly Arg Ser His Leu Gln Leu Arg Gln
85 90 95

Ser Pro Ser Asn Pro Leu Asp Pro Gln Lys Gly Ile Leu Trp Ala Ser
100 105 110

Cys Asn Tyr Ile Ala Thr Gln Thr Val Arg Ser Gln His Ser Trp Met
115 120 125

Gln Leu Thr Asp Gly Lys Thr His Phe Met Leu Ser Leu Ser
130 135 140

<210> 1666
<211> 483
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 467; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
7; "

<220>
<221> source
<223> /note="Uniprot ID: P17544; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387406"

<400> 1666
Met Gly Asp Asp Arg Pro Phe Val Cys Asn Ala Pro Gly Cys Gly Gln
1   5   10   15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
            20   25   30

Met Thr Leu Lys Phe Gly Pro Ala Arg Thr Asp Ser Val Ile Ile Ala
        35   40   45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
    50   55   60

Gly Leu Phe Asn Glu Leu Ala Ser Ser Phe Glu His Glu Phe Lys Lys
65   70   75   80

Ala Ala Asp Glu Asp Glu Lys Lys Ala Ala Ala Gly Pro Leu Asp Met
                85   90   95

Ser Leu Pro Ser Thr Pro Asp Ile Lys Ile Lys Glu Glu Glu Pro Val
            100   105   110

Glu Val Asp Ser Ser Pro Pro Asp Ser Pro Ala Ser Ser Pro Cys Ser
        115   120   125

```
Pro Pro Leu Lys Glu Lys Glu Val Thr Pro Lys Pro Val Leu Ile Ser
    130                 135                 140

Thr Pro Thr Pro Thr Ile Val Arg Pro Gly Ser Leu Pro Leu His Leu
145                 150                 155                 160

Gly Tyr Asp Pro Leu His Pro Thr Leu Pro Ser Pro Thr Ser Val Ile
                165                 170                 175

Thr Gln Ala Pro Pro Ser Asn Arg Gln Met Gly Ser Pro Thr Gly Ser
            180                 185                 190

Leu Pro Leu Val Met His Leu Ala Asn Gly Gln Thr Met Pro Val Leu
        195                 200                 205

Pro Gly Pro Pro Val Gln Met Pro Ser Val Ile Ser Leu Ala Arg Pro
    210                 215                 220

Val Ser Met Val Pro Asn Ile Pro Gly Ile Pro Gly Pro Pro Val Asn
225                 230                 235                 240

Ser Ser Gly Ser Ile Ser Pro Ser Gly His Pro Ile Pro Ser Glu Ala
                245                 250                 255

Lys Met Arg Leu Lys Ala Thr Leu Thr His Gln Val Ser Ser Ile Asn
            260                 265                 270

Gly Gly Cys Gly Met Val Val Gly Thr Ala Ser Thr Met Val Thr Ala
        275                 280                 285

Arg Pro Glu Gln Ser Gln Ile Leu Ile Gln His Pro Asp Ala Pro Ser
    290                 295                 300

Pro Ala Gln Pro Gln Val Ser Pro Ala Gln Pro Thr Pro Ser Thr Gly
305                 310                 315                 320

Gly Arg Arg Arg Arg Thr Val Asp Glu Asp Pro Asp Glu Arg Arg Gln
                325                 330                 335

Arg Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg Cys Arg Gln Lys
            340                 345                 350

Arg Lys Leu Trp Val Ser Ser Leu Glu Lys Lys Ala Glu Glu Leu Thr
```

```
        355                 360                 365

Ser Gln Asn Ile Gln Leu Ser Asn Glu Val Thr Leu Leu Arg Asn Glu
    370                 375                 380

Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys Asp Cys Pro Val
385                 390                 395                 400

Thr Ala Leu Gln Lys Lys Thr Gln Gly Tyr Leu Glu Ser Pro Lys Glu
                405                 410                 415

Ser Ser Glu Pro Thr Gly Ser Pro Ala Pro Val Ile Gln His Ser Ser
            420                 425                 430

Ala Thr Ala Pro Ser Asn Gly Leu Ser Val Arg Ser Ala Ala Glu Ala
        435                 440                 445

Val Ala Thr Ser Val Leu Thr Gln Met Ala Ser Gln Arg Thr Glu Leu
    450                 455                 460

Ser Met Pro Ile Gln Ser His Val Ile Met Thr Pro Gln Ser Gln Ser
465                 470                 475                 480

Ala Gly Arg
```

<210> 1667
<211> 483
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 467; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
7; "

<220>
<221> source

<223> /note="Uniprot ID: P17544; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399465"

<400> 1667
Met Gly Asp Asp Arg Pro Phe Val Cys Asn Ala Pro Gly Cys Gly Gln
1   5   10   15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
            20   25   30

Met Thr Leu Lys Phe Gly Pro Ala Arg Thr Asp Ser Val Ile Ile Ala
        35   40   45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
    50   55   60

Gly Leu Phe Asn Glu Leu Ala Ser Ser Phe Glu His Glu Phe Lys Lys
65   70   75   80

Ala Ala Asp Glu Asp Glu Lys Lys Ala Ala Ala Gly Pro Leu Asp Met
                85   90   95

Ser Leu Pro Ser Thr Pro Asp Ile Lys Ile Lys Glu Glu Glu Pro Val
            100   105   110

Glu Val Asp Ser Ser Pro Pro Asp Ser Pro Ala Ser Ser Pro Cys Ser
        115   120   125

Pro Pro Leu Lys Glu Lys Glu Val Thr Pro Lys Pro Val Leu Ile Ser
    130   135   140

Thr Pro Thr Pro Thr Ile Val Arg Pro Gly Ser Leu Pro Leu His Leu
145   150   155   160

Gly Tyr Asp Pro Leu His Pro Thr Leu Pro Ser Pro Thr Ser Val Ile
                165   170   175

Thr Gln Ala Pro Pro Ser Asn Arg Gln Met Gly Ser Pro Thr Gly Ser
            180   185   190

Leu Pro Leu Val Met His Leu Ala Asn Gly Gln Thr Met Pro Val Leu
        195   200   205

```
Pro Gly Pro Pro Val Gln Met Pro Ser Val Ile Ser Leu Ala Arg Pro
    210                 215                 220

Val Ser Met Val Pro Asn Ile Pro Gly Ile Pro Gly Pro Pro Val Asn
225                 230                 235                 240

Ser Ser Gly Ser Ile Ser Pro Ser Gly His Pro Ile Pro Ser Glu Ala
                245                 250                 255

Lys Met Arg Leu Lys Ala Thr Leu Thr His Gln Val Ser Ser Ile Asn
            260                 265                 270

Gly Gly Cys Gly Met Val Val Gly Thr Ala Ser Thr Met Val Thr Ala
        275                 280                 285

Arg Pro Glu Gln Ser Gln Ile Leu Ile Gln His Pro Asp Ala Pro Ser
    290                 295                 300

Pro Ala Gln Pro Gln Val Ser Pro Ala Gln Pro Thr Pro Ser Thr Gly
305                 310                 315                 320

Gly Arg Arg Arg Arg Thr Val Asp Glu Asp Pro Asp Glu Arg Arg Gln
                325                 330                 335

Arg Phe Leu Glu Arg Asn Arg Ala Ala Ala Ser Arg Cys Arg Gln Lys
            340                 345                 350

Arg Lys Leu Trp Val Ser Ser Leu Glu Lys Lys Ala Glu Glu Leu Thr
        355                 360                 365

Ser Gln Asn Ile Gln Leu Ser Asn Glu Val Thr Leu Leu Arg Asn Glu
    370                 375                 380

Val Ala Gln Leu Lys Gln Leu Leu Leu Ala His Lys Asp Cys Pro Val
385                 390                 395                 400

Thr Ala Leu Gln Lys Lys Thr Gln Gly Tyr Leu Glu Ser Pro Lys Glu
                405                 410                 415

Ser Ser Glu Pro Thr Gly Ser Pro Ala Pro Val Ile Gln His Ser Ser
            420                 425                 430
```

```
Ala Thr Ala Pro Ser Asn Gly Leu Ser Val Arg Ser Ala Ala Glu Ala
        435                 440                 445

Val Ala Thr Ser Val Leu Thr Gln Met Ala Ser Gln Arg Thr Glu Leu
    450                 455                 460

Ser Met Pro Ile Gln Ser His Val Ile Met Thr Pro Gln Ser Gln Ser
465                 470                 475                 480

Ala Gly Arg



<210> 1668
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 467; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000449817"

<400> 1668
Met Ser Leu Pro Ser Thr Pro Asp Ile Lys Ile Lys Glu Glu Glu Pro
1               5                   10                  15

Val Glu Val Asp Ser Ser Pro Pro Asp Ser Pro Ala Ser Ser Pro Cys
            20                  25                  30

Ser Pro Pro Leu Lys Glu Lys Glu Val Thr Pro Lys Pro Val Leu Ile
        35                  40                  45

Ser Thr Pro Thr Pro Thr Ile Val Arg Pro Gly Ser Leu Pro Leu His
    50                  55                  60
```

```
Leu Gly Tyr Asp Pro Leu His Pro Thr Leu Pro Ser Pro Thr
65                  70                  75


<210> 1669
<211> 494
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 467; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
      factor
      7; "

<220>
<221> source
<223> /note="Uniprot ID:  P17544; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000449938"

<400> 1669
Met Gly Asp Asp Arg Pro Phe Val Cys Asn Ala Pro Gly Cys Gly Gln
1               5                   10                  15


Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
            20                  25                  30


Met Thr Leu Lys Phe Gly Pro Ala Arg Thr Asp Ser Val Ile Ile Ala
        35                  40                  45


Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
    50                  55                  60


Gly Leu Phe Asn Glu Leu Ala Ser Ser Phe Glu His Glu Phe Lys Lys
65                  70                  75                  80


Ala Ala Asp Glu Asp Glu Lys Lys Ala Arg Ser Arg Thr Val Ala Lys
                85                  90                  95
```

```
Lys Leu Val Ala Ala Ala Gly Pro Leu Asp Met Ser Leu Pro Ser Thr
            100                 105                 110

Pro Asp Ile Lys Ile Lys Glu Glu Glu Pro Val Glu Val Asp Ser Ser
        115                 120                 125

Pro Pro Asp Ser Pro Ala Ser Ser Pro Cys Ser Pro Pro Leu Lys Glu
    130                 135                 140

Lys Glu Val Thr Pro Lys Pro Val Leu Ile Ser Thr Pro Thr Pro Thr
145                 150                 155                 160

Ile Val Arg Pro Gly Ser Leu Pro Leu His Leu Gly Tyr Asp Pro Leu
                165                 170                 175

His Pro Thr Leu Pro Ser Pro Thr Ser Val Ile Thr Gln Ala Pro Pro
            180                 185                 190

Ser Asn Arg Gln Met Gly Ser Pro Thr Gly Ser Leu Pro Leu Val Met
        195                 200                 205

His Leu Ala Asn Gly Gln Thr Met Pro Val Leu Pro Gly Pro Pro Val
    210                 215                 220

Gln Met Pro Ser Val Ile Ser Leu Ala Arg Pro Val Ser Met Val Pro
225                 230                 235                 240

Asn Ile Pro Gly Ile Pro Gly Pro Pro Val Asn Ser Ser Gly Ser Ile
                245                 250                 255

Ser Pro Ser Gly His Pro Ile Pro Ser Glu Ala Lys Met Arg Leu Lys
            260                 265                 270

Ala Thr Leu Thr His Gln Val Ser Ser Ile Asn Gly Gly Cys Gly Met
        275                 280                 285

Val Val Gly Thr Ala Ser Thr Met Val Thr Ala Arg Pro Glu Gln Ser
    290                 295                 300

Gln Ile Leu Ile Gln His Pro Asp Ala Pro Ser Pro Ala Gln Pro Gln
305                 310                 315                 320
```

```
Val Ser Pro Ala Gln Pro Thr Pro Ser Thr Gly Gly Arg Arg Arg Arg
                325                 330                 335

Thr Val Asp Glu Asp Pro Asp Glu Arg Arg Gln Arg Phe Leu Glu Arg
            340                 345                 350

Asn Arg Ala Ala Ala Ser Arg Cys Arg Gln Lys Arg Lys Leu Trp Val
        355                 360                 365

Ser Ser Leu Glu Lys Lys Ala Glu Glu Leu Thr Ser Gln Asn Ile Gln
    370                 375                 380

Leu Ser Asn Glu Val Thr Leu Leu Arg Asn Glu Val Ala Gln Leu Lys
385                 390                 395                 400

Gln Leu Leu Leu Ala His Lys Asp Cys Pro Val Thr Ala Leu Gln Lys
                405                 410                 415

Lys Thr Gln Gly Tyr Leu Glu Ser Pro Lys Glu Ser Ser Glu Pro Thr
            420                 425                 430

Gly Ser Pro Ala Pro Val Ile Gln His Ser Ser Ala Thr Ala Pro Ser
        435                 440                 445

Asn Gly Leu Ser Val Arg Ser Ala Ala Glu Ala Val Ala Thr Ser Val
    450                 455                 460

Leu Thr Gln Met Ala Ser Gln Arg Thr Glu Leu Ser Met Pro Ile Gln
465                 470                 475                 480

Ser His Val Ile Met Thr Pro Gln Ser Gln Ser Ala Gly Arg
                485                 490


<210> 1670
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 467; "

<220>
<221> source
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<220>
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activating transcription
factor
7; "

<220>
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<223> /note="Uniprot ID: P17544; "

<220>
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<400> 1670
Met Gly Asp Asp Arg Pro Phe Val Cys Asn Ala Pro Gly Cys Gly Gln
1   5   10   15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
            20   25   30

Met Thr Leu Lys Phe Gly Pro Ala Arg Thr Asp Ser Val Ile Ile Ala
        35   40   45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
    50   55   60

Gly Leu Phe Asn Glu Leu Ala Ser Ser Phe Glu His Glu Phe Lys Lys
65   70   75   80

Ala Ala Asp Glu Asp Glu Lys Lys Ala Arg Ser Arg Thr Val Ala Lys
                85   90   95

Lys Leu Val Val Phe Arg Pro Arg Leu Phe Leu Leu Cys Phe Gly Ile
            100   105   110

Ile Phe Leu Ile Gly
        115

<210> 1671
<211> 117
<212> PRT
<213> Homo sapiens

<220>
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<220>
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7; "

<220>
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<220>
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<400> 1671
Met Gly Asp Asp Arg Pro Phe Val Cys Asn Ala Pro Gly Cys Gly Gln
1   5   10   15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
            20   25   30

Met Thr Leu Lys Phe Gly Pro Ala Arg Thr Asp Ser Val Ile Ile Ala
        35   40   45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
    50   55   60

Gly Leu Phe Asn Glu Leu Ala Ser Ser Phe Glu His Glu Phe Lys Lys
65   70   75   80

Ala Ala Asp Glu Asp Glu Lys Lys Ala Arg Ser Arg Thr Val Ala Lys
                85   90   95

Lys Leu Val Val Phe Arg Pro Arg Leu Phe Leu Leu Cys Phe Gly Ile
            100   105   110

Ile Phe Leu Ile Gly
        115

<210> 1672
<211> 79
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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factor
7; "

<220>
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<400> 1672
Met Ser Leu Pro Ser Thr Pro Asp Ile Lys Ile Lys Glu Glu Glu Pro
1 5 10 15

Val Glu Val Asp Ser Ser Pro Pro Asp Ser Pro Ala Ser Ser Pro Cys
20 25 30

Ser Pro Pro Leu Lys Glu Lys Glu Val Thr Pro Lys Pro Val Leu Ile
35 40 45

Ser Thr Pro Thr Pro Thr Ile Val Arg Pro Gly Ser Leu Pro Leu His
50 55 60

Leu Gly Tyr Asp Pro Leu His Pro Thr Leu Pro Ser Pro Thr Ser
65 70 75

<210> 1673
<211> 163
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
activating transcription

factor
7; "

<220>
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<223> /note="ENSP ID: ENSP00000468623"

<400> 1673
Met Gly Asp Asp Arg Pro Phe Val Cys Asn Ala Pro Gly Cys Gly Gln
1 5 10 15

Arg Phe Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu
20 25 30

Met Thr Leu Lys Phe Gly Pro Ala Arg Thr Asp Ser Val Ile Ile Ala
35 40 45

Asp Gln Thr Pro Thr Pro Thr Arg Phe Leu Lys Asn Cys Glu Glu Val
50 55 60

Gly Leu Phe Asn Glu Leu Ala Ser Ser Phe Glu His Glu Phe Lys Lys
65 70 75 80

Ala Ala Asp Glu Asp Glu Lys Lys Ala Arg Ser Arg Thr Val Ala Lys
85 90 95

Lys Leu Val Ala Ala Ala Gly Pro Leu Asp Met Ser Leu Pro Ser Thr
100 105 110

Pro Asp Ile Lys Ile Lys Glu Glu Glu Pro Val Glu Val Asp Ser Ser
115 120 125

Pro Pro Asp Ser Pro Ala Ser Ser Pro Cys Ser Pro Pro Leu Lys Glu
130 135 140

Lys Glu Val Thr Pro Lys Pro Val Leu Ile Ser Thr Pro Thr Pro Thr
145 150 155 160

Ile Val Arg

<210> 1674
<211> 1270
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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factor
7 interacting prt; "

<220>
<221> source
<223> /note="Uniprot ID: Q6VMQ6; "

<220>
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<223> /note="ENSP ID: ENSP00000261168"

<400> 1674
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1   5   10   15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20   25   30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35   40   45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50   55   60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65   70   75   80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85   90   95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
            100   105   110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
        115   120   125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro

```
    130                 135                 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145                 150                 155                 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
                165                 170                 175

Gly Asp Ala Pro Ser Gly Asp Val Ser Pro Gly Asp Ala Thr Ser Gly
            180                 185                 190

Asp Ala Thr Ala Asp Asp Leu Ser Ser Gly Asp Pro Thr Ser Ser Asp
        195                 200                 205

Pro Ile Pro Gly Glu Pro Val Pro Val Glu Pro Ile Ser Gly Asp Cys
    210                 215                 220

Ala Ala Asp Asp Ile Ala Ser Ser Glu Ile Thr Ser Val Asp Leu Ala
225                 230                 235                 240

Ser Gly Ala Pro Ala Ser Thr Asp Pro Ala Ser Asp Asp Leu Ala Ser
                245                 250                 255

Gly Asp Leu Ser Ser Ser Glu Leu Ala Ser Asp Asp Leu Ala Thr Gly
            260                 265                 270

Glu Leu Ala Ser Asp Glu Leu Thr Ser Glu Ser Thr Phe Asp Arg Thr
        275                 280                 285

Phe Glu Pro Lys Ser Val Pro Val Cys Glu Pro Val Pro Glu Ile Asp
    290                 295                 300

Asn Ile Glu Pro Ser Ser Asn Lys Asp Asp Asp Phe Leu Glu Lys Asn
305                 310                 315                 320

Gly Ala Asp Glu Lys Leu Glu Gln Ile Gln Ser Lys Asp Ser Leu Asp
                325                 330                 335

Glu Lys Asn Lys Ala Asp Asn Asn Ile Asp Ala Asn Glu Glu Thr Leu
            340                 345                 350

Glu Thr Asp Asp Thr Thr Ile Cys Ser Asp Arg Pro Pro Glu Asn Glu
        355                 360                 365
```

```
Lys Lys Val Glu Glu Asp Ile Ile Thr Glu Leu Ala Leu Gly Glu Asp
    370                 375                 380

Ala Ile Ser Ser Ser Met Glu Ile Asp Gln Gly Glu Lys Asn Glu Asp
385                 390                 395                 400

Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu Asn Val Ile Glu
                405                 410                 415

Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp Ser Met Glu Thr
            420                 425                 430

Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro Ser Glu Asp Glu
        435                 440                 445

Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile Asp Glu Thr Asn
    450                 455                 460

Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly Ser Pro Ser Lys
465                 470                 475                 480

Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe Leu Val Leu Ser
                485                 490                 495

Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser Glu Val Ile Ser
            500                 505                 510

Gln Asn Glu Thr Cys Ser Pro Ala Glu Val Glu Ser Asn Glu Lys Asp
        515                 520                 525

Asn Lys Pro Glu Glu Glu Glu Gln Val Ile His Glu Asp Asp Glu Arg
    530                 535                 540

Pro Ser Glu Lys Asn Glu Phe Ser Arg Arg Lys Arg Ser Lys Ser Glu
545                 550                 555                 560

Asp Met Asp Asn Val Gln Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu
                565                 570                 575

Tyr Glu Ala Glu Phe Gln Val Lys Ile Thr Ala Lys Gly Asp Ile Asn
            580                 585                 590
```

```
Gln Lys Leu Gln Lys Val Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys
        595                 600                 605

Ala Leu Gln Cys Ala Val Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr
    610                 615                 620

Arg Val Glu Lys Ile Glu Cys Asn Lys Arg His Lys Thr Val Leu Thr
625                 630                 635                 640

Glu Leu Gln Ala Lys Ile Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala
                645                 650                 655

Lys Glu Asp Leu Lys Lys Arg His Glu His Pro Pro Asn Pro Pro Val
            660                 665                 670

Ser Pro Gly Lys Thr Val Asn Asp Val Asn Ser Asn Asn Asn Met Ser
        675                 680                 685

Tyr Arg Asn Ala Gly Thr Val Arg Gln Met Leu Glu Ser Lys Arg Asn
    690                 695                 700

Val Ser Glu Ser Ala Pro Pro Ser Phe Gln Thr Pro Val Asn Thr Val
705                 710                 715                 720

Ser Ser Thr Asn Leu Val Thr Pro Pro Ala Val Val Ser Ser Gln Pro
                725                 730                 735

Lys Leu Gln Thr Pro Val Thr Ser Gly Ser Leu Thr Ala Thr Ser Val
            740                 745                 750

Leu Pro Ala Pro Asn Thr Ala Thr Val Val Ala Thr Thr Gln Val Pro
        755                 760                 765

Ser Gly Asn Pro Gln Pro Thr Ile Ser Leu Gln Pro Leu Pro Val Ile
    770                 775                 780

Leu His Val Pro Val Ala Val Ser Ser Gln Pro Gln Leu Leu Gln Ser
785                 790                 795                 800

His Pro Gly Thr Leu Val Thr Asn Gln Pro Ser Gly Asn Val Glu Phe
                805                 810                 815
```

```
Ile Ser Val Gln Ser Pro Pro Thr Val Ser Gly Leu Thr Lys Asn Pro
            820                 825                 830

Val Ser Leu Pro Ser Leu Pro Asn Pro Thr Lys Pro Asn Asn Val Pro
        835                 840                 845

Ser Val Pro Ser Pro Ser Ile Gln Arg Asn Pro Thr Ala Ser Ala Ala
    850                 855                 860

Pro Leu Gly Thr Thr Leu Ala Val Gln Ala Val Pro Thr Ala His Ser
865                 870                 875                 880

Ile Val Gln Ala Thr Arg Thr Ser Leu Pro Thr Val Gly Pro Ser Gly
                885                 890                 895

Leu Tyr Ser Pro Ser Thr Asn Arg Gly Pro Ile Gln Met Lys Ile Pro
            900                 905                 910

Ile Ser Ala Phe Ser Thr Ser Ser Ala Ala Glu Gln Asn Ser Asn Thr
        915                 920                 925

Thr Pro Arg Ile Glu Asn Gln Thr Asn Lys Thr Ile Asp Ala Ser Val
    930                 935                 940

Ser Lys Lys Ala Ala Asp Ser Thr Ser Gln Cys Gly Lys Ala Thr Gly
945                 950                 955                 960

Ser Asp Ser Ser Gly Val Ile Asp Leu Thr Met Asp Asp Glu Glu Ser
                965                 970                 975

Gly Ala Ser Gln Asp Pro Lys Lys Leu Asn His Thr Pro Val Ser Thr
            980                 985                 990

Met Ser Ser Ser Gln Pro Val Ser  Arg Pro Leu Gln Pro  Ile Gln
Pro
        995                 1000                1005

Ala Pro  Pro Leu Gln Pro Ser  Gly Val Pro Thr Ser  Gly Pro Ser
    1010                1015                1020

Gln Thr  Thr Ile His Leu Leu  Pro Thr Ala Pro Thr  Thr Val Asn
    1025                1030                1035
```

```
Val Thr  His Arg Pro Val Thr  Gln Val Thr Thr Arg  Leu Pro Val
    1040                1045                1050

Pro Arg  Ala Pro Ala Asn His  Gln Val Val Tyr Thr  Thr Leu Pro
    1055                1060                1065

Ala Pro  Pro Ala Gln Ala Pro  Leu Arg Gly Thr Val  Met Gln Ala
    1070                1075                1080

Pro Ala  Val Arg Gln Val Asn  Pro Gln Asn Ser Val  Thr Val Arg
    1085                1090                1095

Val Pro  Gln Thr Thr Thr Tyr  Val Val Asn Asn Gly  Leu Thr Leu
    1100                1105                1110

Gly Ser  Thr Gly Pro Gln Leu  Thr Val His His Arg  Pro Pro Gln
    1115                1120                1125

Val His  Thr Glu Pro Pro Arg  Pro Val His Pro Ala  Pro Leu Pro
    1130                1135                1140

Glu Ala  Pro Gln Pro Gln Arg  Leu Pro Pro Glu Ala  Ala Ser Thr
    1145                1150                1155

Ser Leu  Pro Gln Lys Pro His  Leu Lys Leu Ala Arg  Val Gln Ser
    1160                1165                1170

Gln Asn  Gly Ile Val Leu Ser  Trp Ser Val Leu Glu  Val Asp Arg
    1175                1180                1185

Ser Cys  Ala Thr Val Asp Ser  Tyr His Leu Tyr Ala  Tyr His Glu
    1190                1195                1200

Glu Pro  Ser Ala Thr Val Pro  Ser Gln Trp Lys Lys  Ile Gly Glu
    1205                1210                1215

Val Lys  Ala Leu Pro Leu Pro  Met Ala Cys Thr Leu  Thr Gln Phe
    1220                1225                1230

Val Ser  Gly Ser Lys Tyr Tyr  Phe Ala Val Arg Ala  Lys Asp Ile
    1235                1240                1245

Tyr Gly  Arg Phe Gly Pro Phe  Cys Asp Pro Gln Ser  Thr Asp Val
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1250 1255 1260

Ile Ser Ser Thr Gln Ser Ser
1265 1270

<210> 1675
<211> 515
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ATF7IP; "

<220>
<221> source
<223> /note="Gene Name:
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factor
7 interacting prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000379575"

<400> 1675
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
85 90 95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu

100 105 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
115 120 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
130 135 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145 150 155 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
165 170 175

Gly Asp Ala Pro Ser Gly Asp Val Ser Pro Gly Asp Ala Thr Ser Gly
180 185 190

Asp Ala Thr Ala Asp Asp Leu Ser Ser Gly Asp Pro Thr Ser Ser Asp
195 200 205

Pro Ile Pro Gly Glu Pro Val Pro Val Glu Pro Ile Ser Gly Asp Cys
210 215 220

Ala Ala Asp Asp Ile Ala Ser Ser Glu Ile Thr Ser Val Asp Leu Ala
225 230 235 240

Ser Gly Ala Pro Ala Ser Thr Asp Pro Ala Ser Asp Asp Leu Ala Ser
245 250 255

Gly Asp Leu Ser Ser Ser Glu Leu Ala Ser Asp Asp Leu Ala Thr Gly
260 265 270

Glu Leu Ala Ser Asp Glu Leu Thr Ser Glu Ser Thr Phe Asp Arg Thr
275 280 285

Phe Glu Pro Lys Ser Val Pro Val Cys Glu Pro Val Pro Glu Ile Asp
290 295 300

Asn Ile Glu Pro Ser Ser Asn Lys Asp Asp Asp Phe Leu Glu Lys Asn
305 310 315 320

Gly Ala Asp Glu Lys Leu Glu Gln Ile Gln Ser Lys Asp Ser Leu Asp
325 330 335

```
Glu Lys Asn Lys Ala Asp Asn Asn Ile Asp Ala Asn Glu Glu Thr Leu
            340                 345                 350

Glu Thr Asp Asp Thr Thr Ile Cys Ser Asp Arg Pro Pro Glu Asn Glu
        355                 360                 365

Lys Lys Val Glu Glu Asp Ile Ile Thr Glu Leu Ala Leu Gly Glu Asp
    370                 375                 380

Ala Ile Ser Ser Ser Met Glu Ile Asp Gln Gly Glu Lys Asn Glu Asp
385                 390                 395                 400

Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu Asn Val Ile Glu
                405                 410                 415

Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp Ser Met Glu Thr
            420                 425                 430

Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro Ser Glu Asp Glu
        435                 440                 445

Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile Asp Glu Thr Asn
    450                 455                 460

Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly Ser Pro Ser Lys
465                 470                 475                 480

Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe Leu Val Leu Ser
                485                 490                 495

Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser Glu Val Ile Ser
            500                 505                 510

Gln Asn Glu
        515
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<210> 1676
<211> 125
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 468; "

<220>
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<220>
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factor
7 interacting prt; "

<220>
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<400> 1676
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
85 90 95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
100 105 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu
115 120 125

<210> 1677
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 468; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
7 interacting prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437711"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1677

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Xaa Thr Pro Val Ser Thr Met Ser Ser Ser Gln Pro Val Ser Arg Pro
1               5                   10                  15

Leu Gln Pro Ile Gln Pro Ala Pro Pro Leu Gln Pro Ser Gly Val Pro
            20                  25                  30

Thr Ser Gly Pro Ser Gln Thr Thr Ile His Leu Leu Pro Thr Ala Pro
        35                  40                  45

Thr Thr Val Asn Val Thr His Arg Pro Val Thr Gln Val Thr Thr Arg
    50                  55                  60

Leu Pro Val Pro Arg Ala Pro Ala Asn His Gln Val Val Tyr Thr Thr
65                  70                  75                  80

Leu Pro Ala Pro Pro Ala Gln Ala Pro Leu Arg Gly Thr Val Met Gln
                85                  90                  95

Ala Pro Ala Val Arg Gln Val Asn Pro Gln Asn Arg Glu Leu Asn Arg
            100                 105                 110

Glu Asn Cys
        115
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<210> 1678

<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 468; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7IP; "

<220>
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<223> /note="Gene Name:
activating transcription
factor
7 interacting prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439192"

<400> 1678
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

<210> 1679
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
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<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
7 interacting prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439279"

<400> 1679

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Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1               5                  10                  15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20                  25                  30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35                  40                  45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50                  55                  60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65                  70                  75                  80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85                  90                  95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
            100                 105                 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
        115                 120                 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
    130                 135                 140

Ala Ser Gly Val Leu Ala Ser Gly
145                 150


<210> 1680
<211> 176
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ATF7IP; "

<220>
<221> source
<223> /note="Gene Name:
      activating transcription
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factor
7 interacting prt; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439578"

<400> 1680
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
85 90 95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
100 105 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
115 120 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
130 135 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145 150 155 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
165 170 175

<210> 1681
<211> 1278
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 468; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7IP; "

<220>
<221> source
<223> /note="Gene Name:
activating transcription
factor
7 interacting prt; "

<220>
<221> source
<223> /note="Uniprot ID: Q6VMQ6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000440440"

<400> 1681
Met His Gln Asp Gln Arg Phe Arg Met Asp Ser Leu Glu Glu Pro Gln
1   5   10   15

Lys Lys Val Phe Lys Ala Arg Lys Thr Met Arg Val Ser Asp Arg Gln
            20   25   30

Gln Leu Glu Ala Val Tyr Lys Val Lys Glu Glu Leu Leu Lys Thr Asp
        35   40   45

Val Lys Leu Leu Asn Gly Asn His Glu Asn Gly Asp Leu Asp Pro Thr
    50   55   60

Ser Pro Leu Glu Asn Met Asp Tyr Ile Lys Asp Lys Glu Glu Val Asn
65   70   75   80

Gly Ile Glu Glu Ile Cys Phe Asp Pro Glu Gly Ser Lys Ala Glu Trp
                85   90   95

Lys Glu Thr Pro Cys Ile Leu Ser Val Asn Val Lys Asn Lys Gln Asp
            100   105   110

Asp Asp Leu Asn Cys Glu Pro Leu Ser Pro His Asn Ile Thr Pro Glu
        115   120   125

Pro Val Ser Lys Leu Pro Ala Glu Pro Val Ser Gly Asp Pro Ala Pro

```
    130                 135                 140

Gly Asp Leu Asp Ala Gly Asp Pro Ala Ser Gly Val Leu Ala Ser Gly
145                 150                 155                 160

Asp Ser Thr Ser Gly Asp Pro Thr Ser Ser Glu Pro Ser Ser Ser Asp
                165                 170                 175

Ala Ala Ser Gly Asp Ala Thr Ser Gly Asp Ala Pro Ser Gly Asp Val
            180                 185                 190

Ser Pro Gly Asp Ala Thr Ser Gly Asp Ala Thr Ala Asp Asp Leu Ser
        195                 200                 205

Ser Gly Asp Pro Thr Ser Ser Asp Pro Ile Pro Gly Glu Pro Val Pro
    210                 215                 220

Val Glu Pro Ile Ser Gly Asp Cys Ala Ala Asp Asp Ile Ala Ser Ser
225                 230                 235                 240

Glu Ile Thr Ser Val Asp Leu Ala Ser Gly Ala Pro Ala Ser Thr Asp
                245                 250                 255

Pro Ala Ser Asp Asp Leu Ala Ser Gly Asp Leu Ser Ser Ser Glu Leu
            260                 265                 270

Ala Ser Asp Asp Leu Ala Thr Gly Glu Leu Ala Ser Asp Glu Leu Thr
        275                 280                 285

Ser Glu Ser Thr Phe Asp Arg Thr Phe Glu Pro Lys Ser Val Pro Val
    290                 295                 300

Cys Glu Pro Val Pro Glu Ile Asp Asn Ile Glu Pro Ser Ser Asn Lys
305                 310                 315                 320

Asp Asp Asp Phe Leu Glu Lys Asn Gly Ala Asp Glu Lys Leu Glu Gln
                325                 330                 335

Ile Gln Ser Lys Asp Ser Leu Asp Glu Lys Asn Lys Ala Asp Asn Asn
            340                 345                 350

Ile Asp Ala Asn Glu Glu Thr Leu Glu Thr Asp Asp Thr Thr Ile Cys
        355                 360                 365
```

```
Ser Asp Arg Pro Pro Glu Asn Glu Lys Lys Val Glu Glu Asp Ile Ile
    370                 375                 380

Thr Glu Leu Ala Leu Gly Glu Asp Ala Ile Ser Ser Ser Met Glu Ile
385                 390                 395                 400

Asp Gln Gly Glu Lys Asn Glu Asp Glu Thr Ser Ala Asp Leu Val Glu
                405                 410                 415

Thr Ile Asn Glu Asn Val Ile Glu Asp Asn Lys Ser Glu Asn Ile Leu
            420                 425                 430

Glu Asn Thr Asp Ser Met Glu Thr Asp Glu Ile Ile Pro Ile Leu Glu
        435                 440                 445

Lys Leu Ala Pro Ser Glu Asp Glu Leu Thr Cys Phe Ser Lys Thr Ser
    450                 455                 460

Leu Leu Pro Ile Asp Glu Thr Asn Pro Asp Leu Glu Glu Lys Met Glu
465                 470                 475                 480

Ser Ser Phe Gly Ser Pro Ser Lys Gln Glu Ser Ser Glu Ser Leu Pro
                485                 490                 495

Lys Glu Ala Phe Leu Val Leu Ser Asp Glu Glu Asp Ile Ser Gly Glu
            500                 505                 510

Lys Asp Glu Ser Glu Val Ile Ser Gln Asn Glu Thr Cys Ser Pro Ala
        515                 520                 525

Glu Val Glu Ser Asn Glu Lys Asp Asn Lys Pro Glu Glu Glu Glu Gln
    530                 535                 540

Val Ile His Glu Asp Asp Glu Arg Pro Ser Glu Lys Asn Glu Phe Ser
545                 550                 555                 560

Arg Arg Lys Arg Ser Lys Ser Glu Asp Met Asp Asn Val Gln Ser Lys
                565                 570                 575

Arg Arg Arg Tyr Met Glu Glu Glu Tyr Glu Ala Glu Phe Gln Val Lys
            580                 585                 590
```

```
Ile Thr Ala Lys Gly Asp Ile Asn Gln Lys Leu Gln Lys Val Ile Gln
        595                 600                 605

Trp Leu Leu Glu Glu Lys Leu Cys Ala Leu Gln Cys Ala Val Phe Asp
    610                 615                 620

Lys Thr Leu Ala Glu Leu Lys Thr Arg Val Glu Lys Ile Glu Cys Asn
625                 630                 635                 640

Lys Arg His Lys Thr Val Leu Thr Glu Leu Gln Ala Lys Ile Ala Arg
                645                 650                 655

Leu Thr Lys Arg Phe Glu Ala Ala Lys Glu Asp Leu Lys Lys Arg His
            660                 665                 670

Glu His Pro Pro Asn Pro Pro Val Ser Pro Gly Lys Thr Val Asn Asp
        675                 680                 685

Val Asn Ser Asn Asn Asn Met Ser Tyr Arg Asn Ala Gly Thr Val Arg
    690                 695                 700

Gln Met Leu Glu Ser Lys Arg Asn Val Ser Glu Ser Ala Pro Pro Ser
705                 710                 715                 720

Phe Gln Thr Pro Val Asn Thr Val Ser Ser Thr Asn Leu Val Thr Pro
                725                 730                 735

Pro Ala Val Val Ser Ser Gln Pro Lys Leu Gln Thr Pro Val Thr Ser
            740                 745                 750

Gly Ser Leu Thr Ala Thr Ser Val Leu Pro Ala Pro Asn Thr Ala Thr
        755                 760                 765

Val Val Ala Thr Thr Gln Val Pro Ser Gly Asn Pro Gln Pro Thr Ile
    770                 775                 780

Ser Leu Gln Pro Leu Pro Val Ile Leu His Val Pro Val Ala Val Ser
785                 790                 795                 800

Ser Gln Pro Gln Leu Leu Gln Ser His Pro Gly Thr Leu Val Thr Asn
                805                 810                 815
```

```
Gln Pro Ser Gly Asn Val Glu Phe Ile Ser Val Gln Ser Pro Pro Thr
            820                 825                 830

Val Ser Gly Leu Thr Lys Asn Pro Val Ser Leu Pro Ser Leu Pro Asn
        835                 840                 845

Pro Thr Lys Pro Asn Asn Val Pro Ser Val Pro Ser Pro Ser Ile Gln
    850                 855                 860

Arg Asn Pro Thr Ala Ser Ala Ala Pro Leu Gly Thr Thr Leu Ala Val
865                 870                 875                 880

Gln Ala Val Pro Thr Ala His Ser Ile Val Gln Ala Thr Arg Thr Ser
                885                 890                 895

Leu Pro Thr Val Gly Pro Ser Gly Leu Tyr Ser Pro Ser Thr Asn Arg
            900                 905                 910

Gly Pro Ile Gln Met Lys Ile Pro Ile Ser Ala Phe Ser Thr Ser Ser
        915                 920                 925

Ala Ala Glu Gln Asn Ser Asn Thr Thr Pro Arg Ile Glu Asn Gln Thr
    930                 935                 940

Asn Lys Thr Ile Asp Ala Ser Val Ser Lys Lys Ala Ala Asp Ser Thr
945                 950                 955                 960

Ser Gln Cys Gly Lys Ala Thr Gly Ser Asp Ser Ser Gly Val Ile Asp
                965                 970                 975

Leu Thr Met Asp Asp Glu Glu Ser Gly Ala Ser Gln Asp Pro Lys Lys
            980                 985                 990

Leu Asn His Thr Pro Val Ser Thr  Met Ser Ser Ser Gln  Pro Val
Ser
        995                 1000                1005

Arg Pro  Leu Gln Pro Ile Gln  Pro Ala Pro Pro Leu  Gln Pro Ser
    1010                1015                1020

Gly Val  Pro Thr Ser Gly Pro  Ser Gln Thr Thr Ile  His Leu Leu
    1025                1030                1035
```

```
Pro Thr  Ala Pro Thr Thr Val  Asn Val Thr His Arg  Pro Val Thr
    1040                1045                1050

Gln Val  Thr Thr Arg Leu Pro  Val Pro Arg Ala Pro  Ala Asn His
    1055                1060                1065

Gln Val  Val Tyr Thr Thr Leu  Pro Ala Pro Pro Ala  Gln Ala Pro
    1070                1075                1080

Leu Arg  Gly Thr Val Met Gln  Ala Pro Ala Val Arg  Gln Val Asn
    1085                1090                1095

Pro Gln  Asn Ser Val Thr Val  Arg Val Pro Gln Thr  Thr Thr Tyr
    1100                1105                1110

Val Val  Asn Asn Gly Leu Thr  Leu Gly Ser Thr Gly  Pro Gln Leu
    1115                1120                1125

Thr Val  His His Arg Pro Pro  Gln Val His Thr Glu  Pro Pro Arg
    1130                1135                1140

Pro Val  His Pro Ala Pro Leu  Pro Glu Ala Pro Gln  Pro Gln Arg
    1145                1150                1155

Leu Pro  Pro Glu Ala Ala Ser  Thr Ser Leu Pro Gln  Lys Pro His
    1160                1165                1170

Leu Lys  Leu Ala Arg Val Gln  Ser Gln Asn Gly Ile  Val Leu Ser
    1175                1180                1185

Trp Ser  Val Leu Glu Val Asp  Arg Ser Cys Ala Thr  Val Asp Ser
    1190                1195                1200

Tyr His  Leu Tyr Ala Tyr His  Glu Glu Pro Ser Ala  Thr Val Pro
    1205                1210                1215

Ser Gln  Trp Lys Lys Ile Gly  Glu Val Lys Ala Leu  Pro Leu Pro
    1220                1225                1230

Met Ala  Cys Thr Leu Thr Gln  Phe Val Ser Gly Ser  Lys Tyr Tyr
    1235                1240                1245

Phe Ala  Val Arg Ala Lys Asp  Ile Tyr Gly Arg Phe  Gly Pro Phe
```

```
    1250                1255                1260

Cys Asp  Pro Gln Ser Thr Asp  Val Ile Ser Ser Thr  Gln Ser Ser
    1265                1270                1275


<210> 1682
<211> 96
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      factor
      7 interacting prt; "

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<400> 1682
Met Asp Asn Val Gln Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu Tyr
1               5                   10                  15


Glu Ala Glu Phe Gln Val Lys Ile Thr Ala Lys Gly Asp Ile Asn Gln
            20                  25                  30


Lys Leu Gln Lys Val Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys Ala
        35                  40                  45


Leu Gln Cys Ala Val Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr Arg
    50                  55                  60


Val Glu Lys Ile Glu Cys Asn Lys Arg His Lys Thr Val Leu Thr Glu
65                  70                  75                  80


Leu Gln Ala Lys Ile Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala Lys
                85                  90                  95


<210> 1683
```

<211> 169
<212> PRT
<213> Homo sapiens

<220>
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<220>
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factor
7 interacting prt; "

<220>
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<223> /note="ENSP ID: ENSP00000441483"

<400> 1683
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
85 90 95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
100 105 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
115 120 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro

130 135 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145 150 155 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala
165

<210> 1684
<211> 89
<212> PRT
<213> Homo sapiens

<220>
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<220>
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factor
7 interacting prt; "

<220>
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<400> 1684
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys

85

<210> 1685
<211> 1105
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<400> 1685
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1   5   10   15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20   25   30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35   40   45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50   55   60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65   70   75   80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85   90   95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu

100 105 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
115 120 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
130 135 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145 150 155 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
165 170 175

Gly Asp Ala Pro Ser Gly Asp Val Ser Pro Gly Asp Ala Thr Ser Gly
180 185 190

Asp Ala Thr Ala Asp Asp Leu Ser Ser Gly Asp Pro Thr Ser Ser Asp
195 200 205

Pro Ile Pro Gly Glu Pro Val Pro Val Glu Pro Ile Ser Gly Asp Cys
210 215 220

Ala Ala Asp Asp Ile Ala Ser Ser Glu Ile Thr Ser Val Asp Leu Ala
225 230 235 240

Ser Gly Ala Pro Ala Ser Thr Asp Pro Ala Ser Asp Asp Leu Ala Ser
245 250 255

Gly Asp Leu Ser Ser Ser Glu Leu Ala Ser Asp Asp Leu Ala Thr Gly
260 265 270

Glu Leu Ala Ser Asp Glu Leu Thr Ser Glu Ser Thr Phe Asp Arg Thr
275 280 285

Phe Glu Pro Lys Ser Val Pro Val Cys Glu Pro Val Pro Glu Ile Asp
290 295 300

Asn Ile Glu Pro Ser Ser Asn Lys Asp Asp Asp Phe Leu Glu Lys Asn
305 310 315 320

Gly Ala Asp Glu Lys Leu Glu Gln Ile Gln Ser Lys Asp Ser Leu Asp
325 330 335

```
Glu Lys Asn Lys Ala Asp Asn Asn Ile Asp Ala Asn Glu Glu Thr Leu
            340                 345                 350

Glu Thr Asp Asp Thr Thr Ile Cys Ser Asp Arg Pro Pro Glu Asn Glu
        355                 360                 365

Lys Lys Val Glu Glu Asp Ile Ile Thr Glu Leu Ala Leu Gly Glu Asp
    370                 375                 380

Ala Ile Ser Ser Ser Met Glu Ile Asp Gln Gly Glu Lys Asn Glu Asp
385                 390                 395                 400

Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu Asn Val Ile Glu
                405                 410                 415

Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp Ser Met Glu Thr
            420                 425                 430

Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro Ser Glu Asp Glu
        435                 440                 445

Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile Asp Glu Thr Asn
    450                 455                 460

Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly Ser Pro Ser Lys
465                 470                 475                 480

Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe Leu Val Leu Ser
                485                 490                 495

Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser Glu Val Ile Ser
            500                 505                 510

Gln Asn Glu Thr Cys Ser Pro Glu Val Glu Ser Asn Glu Lys Asp Asn
        515                 520                 525

Lys Pro Glu Glu Glu Glu Gln Val Ile His Glu Asp Asp Glu Arg Pro
    530                 535                 540

Ser Glu Lys Asn Glu Phe Ser Arg Arg Lys Arg Ser Lys Ser Glu Asp
545                 550                 555                 560
```

```
Met Asp Asn Val Gln Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu Tyr
                565                 570                 575

Glu Ala Glu Phe Gln Val Lys Ile Thr Ala Lys Gly Asp Ile Asn Gln
            580                 585                 590

Lys Leu Gln Lys Val Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys Ala
        595                 600                 605

Leu Gln Cys Ala Val Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr Arg
    610                 615                 620

Val Glu Lys Ile Glu Cys Asn Lys Arg His Lys Thr Val Leu Thr Glu
625                 630                 635                 640

Leu Gln Ala Lys Ile Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala Lys
                645                 650                 655

Glu Asp Leu Lys Lys Arg His Glu His Pro Pro Asn Pro Pro Val Ser
            660                 665                 670

Pro Gly Lys Thr Val Asn Asp Val Asn Ser Asn Asn Asn Met Ser Tyr
        675                 680                 685

Arg Asn Ala Gly Thr Val Arg Gln Met Leu Glu Ser Lys Arg Asn Val
    690                 695                 700

Ser Glu Ser Ala Pro Pro Ser Phe Gln Thr Pro Val Asn Thr Val Ser
705                 710                 715                 720

Ser Thr Asn Leu Val Thr Pro Pro Ala Val Val Ser Ser Gln Pro Lys
                725                 730                 735

Leu Gln Thr Pro Val Thr Ser Gly Ser Leu Thr Ala Thr Ser Val Leu
            740                 745                 750

Pro Ala Pro Asn Thr Ala Thr Val Val Ala Thr Thr Gln Val Pro Ser
        755                 760                 765

Gly Asn Pro Gln Pro Thr Ile Ser Leu Gln Pro Leu Pro Val Ile Leu
    770                 775                 780
```

```
His Val Pro Val Ala Val Ser Ser Gln Pro Gln Leu Leu Gln Ser His
785                 790                 795                 800

Pro Gly Thr Leu Val Thr Asn Gln Pro Ser Gly Asn Val Glu Phe Ile
                805                 810                 815

Ser Val Gln Ser Pro Pro Thr Val Ser Gly Leu Thr Lys Asn Pro Val
            820                 825                 830

Ser Leu Pro Ser Leu Pro Asn Pro Thr Lys Pro Asn Asn Val Pro Ser
        835                 840                 845

Val Pro Ser Pro Ser Ile Gln Arg Asn Pro Thr Ala Ser Ala Ala Pro
    850                 855                 860

Leu Gly Thr Thr Leu Ala Val Gln Ala Val Pro Thr Ala His Ser Ile
865                 870                 875                 880

Val Gln Ala Thr Arg Thr Ser Leu Pro Thr Val Gly Pro Ser Gly Leu
                885                 890                 895

Tyr Ser Pro Ser Thr Asn Arg Gly Pro Ile Gln Met Lys Ile Pro Ile
            900                 905                 910

Ser Ala Phe Ser Thr Ser Ser Ala Ala Glu Gln Asn Ser Asn Thr Thr
        915                 920                 925

Pro Arg Ile Glu Asn Gln Thr Asn Lys Thr Ile Asp Ala Ser Val Ser
    930                 935                 940

Lys Lys Ala Ala Asp Ser Thr Ser Gln Cys Gly Lys Ala Thr Gly Ser
945                 950                 955                 960

Asp Ser Ser Gly Val Ile Asp Leu Thr Met Asp Asp Glu Glu Ser Gly
                965                 970                 975

Ala Ser Gln Asp Pro Lys Lys Leu Asn His Thr Pro Val Ser Thr Met
            980                 985                 990

Ser Ser Ser Gln Pro Val Ser Arg  Pro Leu Gln Pro Ile  Gln Pro
Ala
        995                 1000                1005
```

```
Pro Pro  Leu Gln Pro Ser Gly  Val Pro Thr Ser Gly  Pro Ser Gln
    1010                1015                1020

Thr Thr  Ile His Leu Leu Pro  Thr Ala Pro Thr Thr  Val Asn Val
    1025                1030                1035

Thr His  Arg Pro Val Thr Gln  Val Thr Thr Arg Leu  Pro Val Pro
    1040                1045                1050

Arg Ala  Pro Ala Asn His Gln  Val Val Tyr Thr Thr  Leu Pro Ala
    1055                1060                1065

Pro Pro  Ala Gln Ala Pro Leu  Arg Gly Thr Val Met  Gln Ala Pro
    1070                1075                1080

Ala Val  Arg Gln Val Asn Pro  Gln Asn Ser Lys Arg  Phe Phe Leu
    1085                1090                1095

Tyr Met  Ala Pro Arg Tyr Met
    1100                1105


<210> 1686
<211> 132
<212> PRT
<213> Homo sapiens

<220>
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      factor
      7 interacting prt; "

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<400> 1686
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1               5                  10                  15
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```
Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20                  25                  30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35                  40                  45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50                  55                  60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65                  70                  75                  80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85                  90                  95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
            100                 105                 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
        115                 120                 125

Pro Val Ser Gly
    130


<210> 1687
<211> 59
<212> PRT
<213> Homo sapiens

<220>
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      factor
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<223> /note="ENSP ID: ENSP00000443855"

<400> 1687
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```
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1               5                   10                  15


Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20                  25                  30


Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35                  40                  45


Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu
    50                  55


<210> 1688
<211> 1270
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      factor
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<220>
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<223> /note="ENSP ID: ENSP00000444589"

<400> 1688
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1               5                   10                  15


Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20                  25                  30


Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35                  40                  45
```

```
Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50                  55                  60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65                  70                  75                  80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85                  90                  95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
            100                 105                 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
        115                 120                 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
    130                 135                 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145                 150                 155                 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
                165                 170                 175

Gly Asp Ala Pro Ser Gly Asp Val Ser Pro Gly Asp Ala Thr Ser Gly
            180                 185                 190

Asp Ala Thr Ala Asp Asp Leu Ser Ser Gly Asp Pro Thr Ser Ser Asp
        195                 200                 205

Pro Ile Pro Gly Glu Pro Val Pro Val Glu Pro Ile Ser Gly Asp Cys
    210                 215                 220

Ala Ala Asp Asp Ile Ala Ser Ser Glu Ile Thr Ser Val Asp Leu Ala
225                 230                 235                 240

Ser Gly Ala Pro Ala Ser Thr Asp Pro Ala Ser Asp Asp Leu Ala Ser
                245                 250                 255

Gly Asp Leu Ser Ser Ser Glu Leu Ala Ser Asp Asp Leu Ala Thr Gly
            260                 265                 270

Glu Leu Ala Ser Asp Glu Leu Thr Ser Glu Ser Thr Phe Asp Arg Thr
```

```
        275                 280                 285

Phe Glu Pro Lys Ser Val Pro Val Cys Glu Pro Val Pro Glu Ile Asp
    290                 295                 300

Asn Ile Glu Pro Ser Ser Asn Lys Asp Asp Asp Phe Leu Glu Lys Asn
305                 310                 315                 320

Gly Ala Asp Glu Lys Leu Glu Gln Ile Gln Ser Lys Asp Ser Leu Asp
                325                 330                 335

Glu Lys Asn Lys Ala Asp Asn Asn Ile Asp Ala Asn Glu Glu Thr Leu
            340                 345                 350

Glu Thr Asp Asp Thr Thr Ile Cys Ser Asp Arg Pro Pro Glu Asn Glu
        355                 360                 365

Lys Lys Val Glu Glu Asp Ile Ile Thr Glu Leu Ala Leu Gly Glu Asp
    370                 375                 380

Ala Ile Ser Ser Ser Met Glu Ile Asp Gln Gly Glu Lys Asn Glu Asp
385                 390                 395                 400

Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu Asn Val Ile Glu
                405                 410                 415

Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp Ser Met Glu Thr
            420                 425                 430

Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro Ser Glu Asp Glu
        435                 440                 445

Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile Asp Glu Thr Asn
    450                 455                 460

Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly Ser Pro Ser Lys
465                 470                 475                 480

Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe Leu Val Leu Ser
                485                 490                 495

Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser Glu Val Ile Ser
            500                 505                 510
```

```
Gln Asn Glu Thr Cys Ser Pro Ala Glu Val Glu Ser Asn Glu Lys Asp
        515                 520                 525

Asn Lys Pro Glu Glu Glu Glu Gln Val Ile His Glu Asp Asp Glu Arg
    530                 535                 540

Pro Ser Glu Lys Asn Glu Phe Ser Arg Arg Lys Arg Ser Lys Ser Glu
545                 550                 555                 560

Asp Met Asp Asn Val Gln Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu
                565                 570                 575

Tyr Glu Ala Glu Phe Gln Val Lys Ile Thr Ala Lys Gly Asp Ile Asn
            580                 585                 590

Gln Lys Leu Gln Lys Val Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys
        595                 600                 605

Ala Leu Gln Cys Ala Val Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr
    610                 615                 620

Arg Val Glu Lys Ile Glu Cys Asn Lys Arg His Lys Thr Val Leu Thr
625                 630                 635                 640

Glu Leu Gln Ala Lys Ile Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala
                645                 650                 655

Lys Glu Asp Leu Lys Lys Arg His Glu His Pro Pro Asn Pro Pro Val
            660                 665                 670

Ser Pro Gly Lys Thr Val Asn Asp Val Asn Ser Asn Asn Asn Met Ser
        675                 680                 685

Tyr Arg Asn Ala Gly Thr Val Arg Gln Met Leu Glu Ser Lys Arg Asn
    690                 695                 700

Val Ser Glu Ser Ala Pro Pro Ser Phe Gln Thr Pro Val Asn Thr Val
705                 710                 715                 720

Ser Ser Thr Asn Leu Val Thr Pro Pro Ala Val Val Ser Ser Gln Pro
                725                 730                 735
```

```
Lys Leu Gln Thr Pro Val Thr Ser Gly Ser Leu Thr Ala Thr Ser Val
            740                 745                 750

Leu Pro Ala Pro Asn Thr Ala Thr Val Val Ala Thr Thr Gln Val Pro
        755                 760                 765

Ser Gly Asn Pro Gln Pro Thr Ile Ser Leu Gln Pro Leu Pro Val Ile
    770                 775                 780

Leu His Val Pro Val Ala Val Ser Ser Gln Pro Gln Leu Leu Gln Ser
785                 790                 795                 800

His Pro Gly Thr Leu Val Thr Asn Gln Pro Ser Gly Asn Val Glu Phe
                805                 810                 815

Ile Ser Val Gln Ser Pro Pro Thr Val Ser Gly Leu Thr Lys Asn Pro
            820                 825                 830

Val Ser Leu Pro Ser Leu Pro Asn Pro Thr Lys Pro Asn Asn Val Pro
        835                 840                 845

Ser Val Pro Ser Pro Ser Ile Gln Arg Asn Pro Thr Ala Ser Ala Ala
    850                 855                 860

Pro Leu Gly Thr Thr Leu Ala Val Gln Ala Val Pro Thr Ala His Ser
865                 870                 875                 880

Ile Val Gln Ala Thr Arg Thr Ser Leu Pro Thr Val Gly Pro Ser Gly
                885                 890                 895

Leu Tyr Ser Pro Ser Thr Asn Arg Gly Pro Ile Gln Met Lys Ile Pro
            900                 905                 910

Ile Ser Ala Phe Ser Thr Ser Ser Ala Ala Glu Gln Asn Ser Asn Thr
        915                 920                 925

Thr Pro Arg Ile Glu Asn Gln Thr Asn Lys Thr Ile Asp Ala Ser Val
    930                 935                 940

Ser Lys Lys Ala Ala Asp Ser Thr Ser Gln Cys Gly Lys Ala Thr Gly
945                 950                 955                 960
```

```
Ser Asp Ser Ser Gly Val Ile Asp Leu Thr Met Asp Asp Glu Glu Ser
                965                 970                 975

Gly Ala Ser Gln Asp Pro Lys Lys Leu Asn His Thr Pro Val Ser Thr
            980                 985                 990

Met Ser Ser Ser Gln Pro Val Ser  Arg Pro Leu Gln Pro  Ile Gln
Pro
        995                 1000                1005

Ala Pro  Pro Leu Gln Pro Ser  Gly Val Pro Thr Ser  Gly Pro Ser
    1010                1015                1020

Gln Thr  Thr Ile His Leu Leu  Pro Thr Ala Pro Thr  Thr Val Asn
    1025                1030                1035

Val Thr  His Arg Pro Val Thr  Gln Val Thr Thr Arg  Leu Pro Val
    1040                1045                1050

Pro Arg  Ala Pro Ala Asn His  Gln Val Val Tyr Thr  Thr Leu Pro
    1055                1060                1065

Ala Pro  Pro Ala Gln Ala Pro  Leu Arg Gly Thr Val  Met Gln Ala
    1070                1075                1080

Pro Ala  Val Arg Gln Val Asn  Pro Gln Asn Ser Val  Thr Val Arg
    1085                1090                1095

Val Pro  Gln Thr Thr Thr Tyr  Val Val Asn Asn Gly  Leu Thr Leu
    1100                1105                1110

Gly Ser  Thr Gly Pro Gln Leu  Thr Val His His Arg  Pro Pro Gln
    1115                1120                1125

Val His  Thr Glu Pro Pro Arg  Pro Val His Pro Ala  Pro Leu Pro
    1130                1135                1140

Glu Ala  Pro Gln Pro Gln Arg  Leu Pro Pro Glu Ala  Ala Ser Thr
    1145                1150                1155

Ser Leu  Pro Gln Lys Pro His  Leu Lys Leu Ala Arg  Val Gln Ser
    1160                1165                1170
```

```
Gln Asn  Gly Ile Val Leu Ser  Trp Ser Val Leu Glu  Val Asp Arg
    1175                1180                1185

Ser Cys  Ala Thr Val Asp Ser  Tyr His Leu Tyr Ala  Tyr His Glu
    1190                1195                1200

Glu Pro  Ser Ala Thr Val Pro  Ser Gln Trp Lys Lys  Ile Gly Glu
    1205                1210                1215

Val Lys  Ala Leu Pro Leu Pro  Met Ala Cys Thr Leu  Thr Gln Phe
    1220                1225                1230

Val Ser  Gly Ser Lys Tyr Tyr  Phe Ala Val Arg Ala  Lys Asp Ile
    1235                1240                1245

Tyr Gly  Arg Phe Gly Pro Phe  Cys Asp Pro Gln Ser  Thr Asp Val
    1250                1255                1260

Ile Ser  Ser Thr Gln Ser Ser
    1265                1270


<210> 1689
<211> 143
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ATF7IP; "

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      factor
      7 interacting prt; "

<220>
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<400> 1689
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1               5                  10                  15
```

```
Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20                  25                  30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35                  40                  45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50                  55                  60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65                  70                  75                  80

Pro Glu Gly Ser Lys Ala Glu Phe Gln Val Lys Ile Thr Ala Lys Gly
                85                  90                  95

Asp Ile Asn Gln Lys Leu Gln Lys Val Ile Gln Trp Leu Leu Glu Glu
            100                 105                 110

Lys Leu Cys Ala Leu Gln Cys Ala Val Phe Asp Lys Thr Leu Ala Glu
        115                 120                 125

Leu Lys Thr Arg Val Glu Lys Ile Glu Cys Asn Lys Arg His Lys
    130                 135                 140


<210> 1690
<211> 176
<212> PRT
<213> Homo sapiens

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<220>
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<400> 1690
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```
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1               5                  10                  15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20                  25                  30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35                  40                  45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50                  55                  60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65                  70                  75                  80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85                  90                  95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
            100                 105                 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
        115                 120                 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
    130                 135                 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145                 150                 155                 160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
                165                 170                 175


<210> 1691
<211> 103
<212> PRT
<213> Homo sapiens

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factor
7 interacting prt; "

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<400> 1691
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
85 90 95

Val Asn Val Lys Asn Lys Gln
100

<210> 1692
<211> 1269
<212> PRT
<213> Homo sapiens

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factor
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<220>
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<400> 1692
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1   5   10   15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
            20   25   30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
        35   40   45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
    50   55   60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65   70   75   80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
                85   90   95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
            100   105   110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
        115   120   125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
    130   135   140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr
145   150   155   160

Ser Ser Glu Pro Ser Ser Ser Asp Ala Ala Ser Gly Asp Ala Thr Ser
                165   170   175

Gly Asp Ala Pro Ser Gly Asp Val Ser Pro Gly Asp Ala Thr Ser Gly

```
            180                 185                 190

Asp Ala Thr Ala Asp Asp Leu Ser Ser Gly Asp Pro Thr Ser Ser Asp
        195                 200                 205

Pro Ile Pro Gly Glu Pro Val Pro Val Glu Pro Ile Ser Gly Asp Cys
    210                 215                 220

Ala Ala Asp Asp Ile Ala Ser Ser Glu Ile Thr Ser Val Asp Leu Ala
225                 230                 235                 240

Ser Gly Ala Pro Ala Ser Thr Asp Pro Ala Ser Asp Asp Leu Ala Ser
                245                 250                 255

Gly Asp Leu Ser Ser Ser Glu Leu Ala Ser Asp Asp Leu Ala Thr Gly
            260                 265                 270

Glu Leu Ala Ser Asp Glu Leu Thr Ser Glu Ser Thr Phe Asp Arg Thr
        275                 280                 285

Phe Glu Pro Lys Ser Val Pro Val Cys Glu Pro Val Pro Glu Ile Asp
    290                 295                 300

Asn Ile Glu Pro Ser Ser Asn Lys Asp Asp Asp Phe Leu Glu Lys Asn
305                 310                 315                 320

Gly Ala Asp Glu Lys Leu Glu Gln Ile Gln Ser Lys Asp Ser Leu Asp
                325                 330                 335

Glu Lys Asn Lys Ala Asp Asn Asn Ile Asp Ala Asn Glu Glu Thr Leu
            340                 345                 350

Glu Thr Asp Asp Thr Thr Ile Cys Ser Asp Arg Pro Pro Glu Asn Glu
        355                 360                 365

Lys Lys Val Glu Glu Asp Ile Ile Thr Glu Leu Ala Leu Gly Glu Asp
    370                 375                 380

Ala Ile Ser Ser Ser Met Glu Ile Asp Gln Gly Glu Lys Asn Glu Asp
385                 390                 395                 400

Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu Asn Val Ile Glu
                405                 410                 415
```

```
Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp Ser Met Glu Thr
            420                 425                 430

Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro Ser Glu Asp Glu
        435                 440                 445

Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile Asp Glu Thr Asn
    450                 455                 460

Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly Ser Pro Ser Lys
465                 470                 475                 480

Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe Leu Val Leu Ser
                485                 490                 495

Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser Glu Val Ile Ser
            500                 505                 510

Gln Asn Glu Thr Cys Ser Pro Glu Val Glu Ser Asn Glu Lys Asp Asn
        515                 520                 525

Lys Pro Glu Glu Glu Glu Gln Val Ile His Glu Asp Asp Glu Arg Pro
    530                 535                 540

Ser Glu Lys Asn Glu Phe Ser Arg Arg Lys Arg Ser Lys Ser Glu Asp
545                 550                 555                 560

Met Asp Asn Val Gln Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu Tyr
                565                 570                 575

Glu Ala Glu Phe Gln Val Lys Ile Thr Ala Lys Gly Asp Ile Asn Gln
            580                 585                 590

Lys Leu Gln Lys Val Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys Ala
        595                 600                 605

Leu Gln Cys Ala Val Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr Arg
    610                 615                 620

Val Glu Lys Ile Glu Cys Asn Lys Arg His Lys Thr Val Leu Thr Glu
625                 630                 635                 640
```

Leu Gln Ala Lys Ile Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala Lys
645 650 655

Glu Asp Leu Lys Lys Arg His Glu His Pro Pro Asn Pro Pro Val Ser
660 665 670

Pro Gly Lys Thr Val Asn Asp Val Asn Ser Asn Asn Asn Met Ser Tyr
675 680 685

Arg Asn Ala Gly Thr Val Arg Gln Met Leu Glu Ser Lys Arg Asn Val
690 695 700

Ser Glu Ser Ala Pro Pro Ser Phe Gln Thr Pro Val Asn Thr Val Ser
705 710 715 720

Ser Thr Asn Leu Val Thr Pro Pro Ala Val Val Ser Ser Gln Pro Lys
725 730 735

Leu Gln Thr Pro Val Thr Ser Gly Ser Leu Thr Ala Thr Ser Val Leu
740 745 750

Pro Ala Pro Asn Thr Ala Thr Val Val Ala Thr Thr Gln Val Pro Ser
755 760 765

Gly Asn Pro Gln Pro Thr Ile Ser Leu Gln Pro Leu Pro Val Ile Leu
770 775 780

His Val Pro Val Ala Val Ser Ser Gln Pro Gln Leu Leu Gln Ser His
785 790 795 800

Pro Gly Thr Leu Val Thr Asn Gln Pro Ser Gly Asn Val Glu Phe Ile
805 810 815

Ser Val Gln Ser Pro Pro Thr Val Ser Gly Leu Thr Lys Asn Pro Val
820 825 830

Ser Leu Pro Ser Leu Pro Asn Pro Thr Lys Pro Asn Asn Val Pro Ser
835 840 845

Val Pro Ser Pro Ser Ile Gln Arg Asn Pro Thr Ala Ser Ala Ala Pro
850 855 860

```
Leu Gly Thr Thr Leu Ala Val Gln Ala Val Pro Thr Ala His Ser Ile
865                 870                 875                 880

Val Gln Ala Thr Arg Thr Ser Leu Pro Thr Val Gly Pro Ser Gly Leu
                885                 890                 895

Tyr Ser Pro Ser Thr Asn Arg Gly Pro Ile Gln Met Lys Ile Pro Ile
            900                 905                 910

Ser Ala Phe Ser Thr Ser Ser Ala Ala Glu Gln Asn Ser Asn Thr Thr
        915                 920                 925

Pro Arg Ile Glu Asn Gln Thr Asn Lys Thr Ile Asp Ala Ser Val Ser
    930                 935                 940

Lys Lys Ala Ala Asp Ser Thr Ser Gln Cys Gly Lys Ala Thr Gly Ser
945                 950                 955                 960

Asp Ser Ser Gly Val Ile Asp Leu Thr Met Asp Asp Glu Glu Ser Gly
                965                 970                 975

Ala Ser Gln Asp Pro Lys Lys Leu Asn His Thr Pro Val Ser Thr Met
            980                 985                 990

Ser Ser Ser Gln Pro Val Ser Arg  Pro Leu Gln Pro Ile  Gln Pro
Ala
        995                 1000                1005

Pro Pro  Leu Gln Pro Ser Gly  Val Pro Thr Ser Gly  Pro Ser Gln
    1010                1015                1020

Thr Thr  Ile His Leu Leu Pro  Thr Ala Pro Thr Thr  Val Asn Val
    1025                1030                1035

Thr His  Arg Pro Val Thr Gln  Val Thr Thr Arg Leu  Pro Val Pro
    1040                1045                1050

Arg Ala  Pro Ala Asn His Gln  Val Val Tyr Thr Thr  Leu Pro Ala
    1055                1060                1065

Pro Pro  Ala Gln Ala Pro Leu  Arg Gly Thr Val Met  Gln Ala Pro
    1070                1075                1080
```

```
Ala Val  Arg Gln Val Asn Pro  Gln Asn Ser Val Thr  Val Arg Val
    1085                1090                1095

Pro Gln  Thr Thr Thr Tyr Val  Val Asn Asn Gly Leu  Thr Leu Gly
    1100                1105                1110

Ser Thr  Gly Pro Gln Leu Thr  Val His His Arg Pro  Pro Gln Val
    1115                1120                1125

His Thr  Glu Pro Pro Arg Pro  Val His Pro Ala Pro  Leu Pro Glu
    1130                1135                1140

Ala Pro  Gln Pro Gln Arg Leu  Pro Pro Glu Ala Ala  Ser Thr Ser
    1145                1150                1155

Leu Pro  Gln Lys Pro His Leu  Lys Leu Ala Arg Val  Gln Ser Gln
    1160                1165                1170

Asn Gly  Ile Val Leu Ser Trp  Ser Val Leu Glu Val  Asp Arg Ser
    1175                1180                1185

Cys Ala  Thr Val Asp Ser Tyr  His Leu Tyr Ala Tyr  His Glu Glu
    1190                1195                1200

Pro Ser  Ala Thr Val Pro Ser  Gln Trp Lys Lys Ile  Gly Glu Val
    1205                1210                1215

Lys Ala  Leu Pro Leu Pro Met  Ala Cys Thr Leu Thr  Gln Phe Val
    1220                1225                1230

Ser Gly  Ser Lys Tyr Tyr Phe  Ala Val Arg Ala Lys  Asp Ile Tyr
    1235                1240                1245

Gly Arg  Phe Gly Pro Phe Cys  Asp Pro Gln Ser Thr  Asp Val Ile
    1250                1255                1260

Ser Ser  Thr Gln Ser Ser
    1265
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<210> 1693
<211> 168
<212> PRT
<213> Homo sapiens

<220>
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factor
7 interacting prt; "

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<400> 1693
Met Asp Ser Leu Glu Glu Pro Gln Lys Lys Val Phe Lys Ala Arg Lys
1 5 10 15

Thr Met Arg Val Ser Asp Arg Gln Gln Leu Glu Ala Val Tyr Lys Val
20 25 30

Lys Glu Glu Leu Leu Lys Thr Asp Val Lys Leu Leu Asn Gly Asn His
35 40 45

Glu Asn Gly Asp Leu Asp Pro Thr Ser Pro Leu Glu Asn Met Asp Tyr
50 55 60

Ile Lys Asp Lys Glu Glu Val Asn Gly Ile Glu Glu Ile Cys Phe Asp
65 70 75 80

Pro Glu Gly Ser Lys Ala Glu Trp Lys Glu Thr Pro Cys Ile Leu Ser
85 90 95

Val Asn Val Lys Asn Lys Gln Asp Asp Asp Leu Asn Cys Glu Pro Leu
100 105 110

Ser Pro His Asn Ile Thr Pro Glu Pro Val Ser Lys Leu Pro Ala Glu
115 120 125

Pro Val Ser Gly Asp Pro Ala Pro Gly Asp Leu Asp Ala Gly Asp Pro
130 135 140

Ala Ser Gly Val Leu Ala Ser Gly Asp Ser Thr Ser Gly Asp Pro Thr

145 150 155 160

Ser Ser Glu Pro Ser Ser Ser Asp
165

<210> 1694
<211> 543
<212> PRT
<213> Homo sapiens

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<400> 1694
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1 5 10 15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
20 25 30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
35 40 45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
50 55 60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65 70 75 80

Lys Asn Ser Ile Ser Glu Lys Ser Lys Val Phe Ser Gln Asn Cys Ile
85 90 95

```
Lys Pro Val Glu Glu Ile Val His Ser Glu Thr Lys Leu Glu Gln Val
            100                 105                 110

Val Cys Ser Tyr Gln Lys Pro Ser Arg Thr Thr Glu Ser Pro Ser Arg
        115                 120                 125

Val Phe Thr Glu Glu Ala Lys Asp Ser Leu Asn Thr Ser Glu Asn Asp
    130                 135                 140

Ser Glu His Gln Thr Asn Val Thr Arg Ser Leu Phe Glu His Glu Gly
145                 150                 155                 160

Ala Cys Ser Leu Lys Ser Ser Cys Cys Pro Pro Ser Val Leu Ser Gly
                165                 170                 175

Val Val Gln Met Pro Glu Ser Thr Val Thr Ser Thr Val Gly Asp Lys
            180                 185                 190

Lys Thr Asp Gln Met Val Phe His Leu Glu Thr Asn Ser Asn Ser Glu
        195                 200                 205

Ser His Asp Lys Arg Gln Ser Asp Asn Ile Leu Cys Ser Glu Asp Ser
    210                 215                 220

Gly Phe Val Pro Val Glu Lys Thr Pro Asn Leu Val Asn Ser Val Thr
225                 230                 235                 240

Ser Asn Asn Cys Ala Asp Asp Ile Leu Lys Thr Asp Glu Cys Ser Arg
                245                 250                 255

Thr Ser Ile Ser Asn Cys Glu Ser Ala Asp Ser Thr Trp Gln Ser Ser
            260                 265                 270

Leu Asp Thr Asn Asn Asn Ser His Tyr Gln Lys Lys Arg Met Phe Ser
        275                 280                 285

Glu Asn Glu Glu Asn Val Lys Arg Met Lys Thr Ser Glu Gln Ile Asn
    290                 295                 300

Glu Asn Ile Cys Val Ser Leu Glu Arg Gln Thr Ala Phe Leu Glu Gln
305                 310                 315                 320
```

Val Arg His Leu Ile Gln Gln Glu Ile Tyr Ser Ile Asn Tyr Glu Leu
325 330 335

Phe Asp Lys Lys Leu Lys Glu Leu Asn Gln Arg Ile Gly Lys Thr Glu
340 345 350

Cys Arg Asn Lys His Glu Gly Ile Ala Asp Lys Leu Leu Ala Lys Ile
355 360 365

Ala Lys Leu Gln Arg Arg Ile Lys Thr Val Leu Leu Phe Gln Arg Asn
370 375 380

Cys Leu Lys Pro Asn Met Leu Ser Ser Asn Gly Ala Ser Lys Val Ala
385 390 395 400

Asn Ser Glu Ala Met Ile Leu Asp Lys Asn Leu Glu Ser Val Asn Ser
405 410 415

Pro Ile Glu Lys Ser Ser Val Asn Tyr Glu Pro Ser Asn Pro Ser Glu
420 425 430

Lys Gly Ser Lys Lys Ile Asn Leu Ser Ser Asp Gln Asn Lys Ser Val
435 440 445

Ser Glu Ser Asn Asn Asp Asp Val Met Leu Ile Ser Val Glu Ser Pro
450 455 460

Asn Leu Thr Thr Pro Ile Thr Ser Asn Pro Thr Asp Thr Arg Lys Ile
465 470 475 480

Thr Ser Gly Asn Ser Ser Asn Ser Pro Asn Ala Glu Val Met Lys Val
485 490 495

Gln Tyr Pro Pro Trp Ser His Ile Arg Lys Leu Leu Gln Thr Gln Arg
500 505 510

Lys Gln Pro His Trp His Lys Met Gln Ser Arg Phe Leu Ser Pro Leu
515 520 525

Ser Thr Cys His Leu Ser Gln Asn His Gln His His Tyr Leu Asn
530 535 540

<210> 1695
<211> 682
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Uniprot ID: Q5U623; "

<220>
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<400> 1695
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1   5   10   15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20   25   30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
        35   40   45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50   55   60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65   70   75   80

Lys Asn Ser Ile Ser Glu Lys Ser Lys Val Phe Ser Gln Asn Cys Ile
                85   90   95

Lys Pro Val Glu Glu Ile Val His Ser Glu Thr Lys Leu Glu Gln Val
            100   105   110

Val Cys Ser Tyr Gln Lys Pro Ser Arg Thr Thr Glu Ser Pro Ser Arg

```
        115                 120                 125

Val Phe Thr Glu Glu Ala Lys Asp Ser Leu Asn Thr Ser Glu Asn Asp
    130                 135                 140

Ser Glu His Gln Thr Asn Val Thr Arg Ser Leu Phe Glu His Glu Gly
145                 150                 155                 160

Ala Cys Ser Leu Lys Ser Ser Cys Cys Pro Pro Ser Val Leu Ser Gly
                165                 170                 175

Val Val Gln Met Pro Glu Ser Thr Val Thr Ser Thr Val Gly Asp Lys
            180                 185                 190

Lys Thr Asp Gln Met Val Phe His Leu Glu Thr Asn Ser Asn Ser Glu
        195                 200                 205

Ser His Asp Lys Arg Gln Ser Asp Asn Ile Leu Cys Ser Glu Asp Ser
    210                 215                 220

Gly Phe Val Pro Val Glu Lys Thr Pro Asn Leu Val Asn Ser Val Thr
225                 230                 235                 240

Ser Asn Asn Cys Ala Asp Asp Ile Leu Lys Thr Asp Glu Cys Ser Arg
                245                 250                 255

Thr Ser Ile Ser Asn Cys Glu Ser Ala Asp Ser Thr Trp Gln Ser Ser
            260                 265                 270

Leu Asp Thr Asn Asn Asn Ser His Tyr Gln Lys Lys Arg Met Phe Ser
        275                 280                 285

Glu Asn Glu Glu Asn Val Lys Arg Met Lys Thr Ser Glu Gln Ile Asn
    290                 295                 300

Glu Asn Ile Cys Val Ser Leu Glu Arg Gln Thr Ala Phe Leu Glu Gln
305                 310                 315                 320

Val Arg His Leu Ile Gln Gln Glu Ile Tyr Ser Ile Asn Tyr Glu Leu
                325                 330                 335

Phe Asp Lys Lys Leu Lys Glu Leu Asn Gln Arg Ile Gly Lys Thr Glu
            340                 345                 350
```

```
Cys Arg Asn Lys His Glu Gly Ile Ala Asp Lys Leu Leu Ala Lys Ile
        355                 360                 365

Ala Lys Leu Gln Arg Arg Ile Lys Thr Val Leu Leu Phe Gln Arg Asn
    370                 375                 380

Cys Leu Lys Pro Asn Met Leu Ser Ser Asn Gly Ala Ser Lys Val Ala
385                 390                 395                 400

Asn Ser Glu Ala Met Ile Leu Asp Lys Asn Leu Glu Ser Val Asn Ser
                405                 410                 415

Pro Ile Glu Lys Ser Ser Val Asn Tyr Glu Pro Ser Asn Pro Ser Glu
            420                 425                 430

Lys Gly Ser Lys Lys Ile Asn Leu Ser Ser Asp Gln Asn Lys Ser Val
        435                 440                 445

Ser Glu Ser Asn Asn Asp Asp Val Met Leu Ile Ser Val Glu Ser Pro
    450                 455                 460

Asn Leu Thr Thr Pro Ile Thr Ser Asn Pro Thr Asp Thr Arg Lys Ile
465                 470                 475                 480

Thr Ser Gly Asn Ser Ser Asn Ser Pro Asn Ala Glu Val Met Ala Val
                485                 490                 495

Gln Lys Lys Leu Asp Ser Ile Ile Asp Leu Thr Lys Glu Gly Leu Ser
            500                 505                 510

Asn Cys Asn Thr Glu Ser Pro Val Ser Pro Leu Glu Ser His Ser Lys
        515                 520                 525

Ala Ala Ser Asn Ser Lys Glu Thr Thr Pro Leu Ala Gln Asn Ala Val
    530                 535                 540

Gln Val Pro Glu Ser Phe Glu His Leu Pro Pro Leu Pro Glu Pro Pro
545                 550                 555                 560

Ala Pro Leu Pro Glu Leu Val Asp Lys Thr Arg Asp Thr Leu Pro Pro
                565                 570                 575
```

```
Gln Lys Pro Glu Leu Lys Val Lys Arg Val Phe Arg Pro Asn Gly Ile
            580                 585                 590

Ala Leu Thr Trp Asn Ile Thr Lys Ile Asn Pro Lys Cys Ala Pro Val
        595                 600                 605

Glu Ser Tyr His Leu Phe Leu Cys His Glu Asn Ser Asn Asn Lys Leu
    610                 615                 620

Ile Trp Lys Lys Ile Gly Glu Ile Lys Ala Leu Pro Leu Pro Met Ala
625                 630                 635                 640

Cys Thr Leu Ser Gln Phe Leu Ala Ser Asn Arg Tyr Tyr Phe Thr Val
                645                 650                 655

Gln Ser Lys Asp Ile Phe Gly Arg Tyr Gly Pro Phe Cys Asp Ile Lys
            660                 665                 670

Ser Ile Pro Gly Phe Ser Glu Asn Leu Thr
        675                 680


<210> 1696
<211> 543
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<220>
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<223> /note="Uniprot ID:  Q5U623; "

<220>
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<223> /note="ENSP ID: ENSP00000379807"

<400> 1696
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```
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1               5                  10                  15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20                  25                  30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
        35                  40                  45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50                  55                  60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65                  70                  75                  80

Lys Asn Ser Ile Ser Glu Lys Ser Lys Val Phe Ser Gln Asn Cys Ile
                85                  90                  95

Lys Pro Val Glu Glu Ile Val His Ser Glu Thr Lys Leu Glu Gln Val
            100                 105                 110

Val Cys Ser Tyr Gln Lys Pro Ser Arg Thr Thr Glu Ser Pro Ser Arg
        115                 120                 125

Val Phe Thr Glu Glu Ala Lys Asp Ser Leu Asn Thr Ser Glu Asn Asp
    130                 135                 140

Ser Glu His Gln Thr Asn Val Thr Arg Ser Leu Phe Glu His Glu Gly
145                 150                 155                 160

Ala Cys Ser Leu Lys Ser Ser Cys Cys Pro Pro Ser Val Leu Ser Gly
                165                 170                 175

Val Val Gln Met Pro Glu Ser Thr Val Thr Ser Thr Val Gly Asp Lys
            180                 185                 190

Lys Thr Asp Gln Met Val Phe His Leu Glu Thr Asn Ser Asn Ser Glu
        195                 200                 205

Ser His Asp Lys Arg Gln Ser Asp Asn Ile Leu Cys Ser Glu Asp Ser
    210                 215                 220

Gly Phe Val Pro Val Glu Lys Thr Pro Asn Leu Val Asn Ser Val Thr
```

225 230 235 240

Ser Asn Asn Cys Ala Asp Asp Ile Leu Lys Thr Asp Glu Cys Ser Arg
245 250 255

Thr Ser Ile Ser Asn Cys Glu Ser Ala Asp Ser Thr Trp Gln Ser Ser
260 265 270

Leu Asp Thr Asn Asn Asn Ser His Tyr Gln Lys Lys Arg Met Phe Ser
275 280 285

Glu Asn Glu Glu Asn Val Lys Arg Met Lys Thr Ser Glu Gln Ile Asn
290 295 300

Glu Asn Ile Cys Val Ser Leu Glu Arg Gln Thr Ala Phe Leu Glu Gln
305 310 315 320

Val Arg His Leu Ile Gln Gln Glu Ile Tyr Ser Ile Asn Tyr Glu Leu
325 330 335

Phe Asp Lys Lys Leu Lys Glu Leu Asn Gln Arg Ile Gly Lys Thr Glu
340 345 350

Cys Arg Asn Lys His Glu Gly Ile Ala Asp Lys Leu Leu Ala Lys Ile
355 360 365

Ala Lys Leu Gln Arg Arg Ile Lys Thr Val Leu Leu Phe Gln Arg Asn
370 375 380

Cys Leu Lys Pro Asn Met Leu Ser Ser Asn Gly Ala Ser Lys Val Ala
385 390 395 400

Asn Ser Glu Ala Met Ile Leu Asp Lys Asn Leu Glu Ser Val Asn Ser
405 410 415

Pro Ile Glu Lys Ser Ser Val Asn Tyr Glu Pro Ser Asn Pro Ser Glu
420 425 430

Lys Gly Ser Lys Lys Ile Asn Leu Ser Ser Asp Gln Asn Lys Ser Val
435 440 445

Ser Glu Ser Asn Asn Asp Asp Val Met Leu Ile Ser Val Glu Ser Pro
450 455 460

```
Asn Leu Thr Thr Pro Ile Thr Ser Asn Pro Thr Asp Thr Arg Lys Ile
465                 470                 475                 480


Thr Ser Gly Asn Ser Ser Asn Ser Pro Asn Ala Glu Val Met Lys Val
                485                 490                 495


Gln Tyr Pro Pro Trp Ser His Ile Arg Lys Leu Leu Gln Thr Gln Arg
            500                 505                 510


Lys Gln Pro His Trp His Lys Met Gln Ser Arg Phe Leu Ser Pro Leu
        515                 520                 525


Ser Thr Cys His Leu Ser Gln Asn His Gln His His Tyr Leu Asn
    530                 535                 540


<210> 1697
<211> 682
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 469; "

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<220>
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<220>
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<400> 1697
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1               5                   10                  15


Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20                  25                  30
```

```
Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
        35                  40                  45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50                  55                  60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65                  70                  75                  80

Lys Asn Ser Ile Ser Glu Lys Ser Lys Val Phe Ser Gln Asn Cys Ile
                85                  90                  95

Lys Pro Val Glu Glu Ile Val His Ser Glu Thr Lys Leu Glu Gln Val
            100                 105                 110

Val Cys Ser Tyr Gln Lys Pro Ser Arg Thr Thr Glu Ser Pro Ser Arg
        115                 120                 125

Val Phe Thr Glu Glu Ala Lys Asp Ser Leu Asn Thr Ser Glu Asn Asp
    130                 135                 140

Ser Glu His Gln Thr Asn Val Thr Arg Ser Leu Phe Glu His Glu Gly
145                 150                 155                 160

Ala Cys Ser Leu Lys Ser Ser Cys Cys Pro Pro Ser Val Leu Ser Gly
                165                 170                 175

Val Val Gln Met Pro Glu Ser Thr Val Thr Ser Thr Val Gly Asp Lys
            180                 185                 190

Lys Thr Asp Gln Met Val Phe His Leu Glu Thr Asn Ser Asn Ser Glu
        195                 200                 205

Ser His Asp Lys Arg Gln Ser Asp Asn Ile Leu Cys Ser Glu Asp Ser
    210                 215                 220

Gly Phe Val Pro Val Glu Lys Thr Pro Asn Leu Val Asn Ser Val Thr
225                 230                 235                 240

Ser Asn Asn Cys Ala Asp Asp Ile Leu Lys Thr Asp Glu Cys Ser Arg
                245                 250                 255
```

```
Thr Ser Ile Ser Asn Cys Glu Ser Ala Asp Ser Thr Trp Gln Ser Ser
            260                 265                 270

Leu Asp Thr Asn Asn Asn Ser His Tyr Gln Lys Lys Arg Met Phe Ser
        275                 280                 285

Glu Asn Glu Glu Asn Val Lys Arg Met Lys Thr Ser Glu Gln Ile Asn
    290                 295                 300

Glu Asn Ile Cys Val Ser Leu Glu Arg Gln Thr Ala Phe Leu Glu Gln
305                 310                 315                 320

Val Arg His Leu Ile Gln Gln Glu Ile Tyr Ser Ile Asn Tyr Glu Leu
                325                 330                 335

Phe Asp Lys Lys Leu Lys Glu Leu Asn Gln Arg Ile Gly Lys Thr Glu
            340                 345                 350

Cys Arg Asn Lys His Glu Gly Ile Ala Asp Lys Leu Leu Ala Lys Ile
        355                 360                 365

Ala Lys Leu Gln Arg Arg Ile Lys Thr Val Leu Leu Phe Gln Arg Asn
    370                 375                 380

Cys Leu Lys Pro Asn Met Leu Ser Ser Asn Gly Ala Ser Lys Val Ala
385                 390                 395                 400

Asn Ser Glu Ala Met Ile Leu Asp Lys Asn Leu Glu Ser Val Asn Ser
                405                 410                 415

Pro Ile Glu Lys Ser Ser Val Asn Tyr Glu Pro Ser Asn Pro Ser Glu
            420                 425                 430

Lys Gly Ser Lys Lys Ile Asn Leu Ser Ser Asp Gln Asn Lys Ser Val
        435                 440                 445

Ser Glu Ser Asn Asn Asp Asp Val Met Leu Ile Ser Val Glu Ser Pro
    450                 455                 460

Asn Leu Thr Thr Pro Ile Thr Ser Asn Pro Thr Asp Thr Arg Lys Ile
465                 470                 475                 480

Thr Ser Gly Asn Ser Ser Asn Ser Pro Asn Ala Glu Val Met Ala Val
```

485 490 495

Gln Lys Lys Leu Asp Ser Ile Ile Asp Leu Thr Lys Glu Gly Leu Ser
500 505 510

Asn Cys Asn Thr Glu Ser Pro Val Ser Pro Leu Glu Ser His Ser Lys
515 520 525

Ala Ala Ser Asn Ser Lys Glu Thr Thr Pro Leu Ala Gln Asn Ala Val
530 535 540

Gln Val Pro Glu Ser Phe Glu His Leu Pro Pro Leu Pro Glu Pro Pro
545 550 555 560

Ala Pro Leu Pro Glu Leu Val Asp Lys Thr Arg Asp Thr Leu Pro Pro
565 570 575

Gln Lys Pro Glu Leu Lys Val Lys Arg Val Phe Arg Pro Asn Gly Ile
580 585 590

Ala Leu Thr Trp Asn Ile Thr Lys Ile Asn Pro Lys Cys Ala Pro Val
595 600 605

Glu Ser Tyr His Leu Phe Leu Cys His Glu Asn Ser Asn Asn Lys Leu
610 615 620

Ile Trp Lys Lys Ile Gly Glu Ile Lys Ala Leu Pro Leu Pro Met Ala
625 630 635 640

Cys Thr Leu Ser Gln Phe Leu Ala Ser Asn Arg Tyr Tyr Phe Thr Val
645 650 655

Gln Ser Lys Asp Ile Phe Gly Arg Tyr Gly Pro Phe Cys Asp Ile Lys
660 665 670

Ser Ile Pro Gly Phe Ser Glu Asn Leu Thr
675 680

<210> 1698
<211> 425
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 469; "

<220>
<221> source
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<220>
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<223> /note="Gene Name:
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factor 7 interacting prt 2; "

<220>
<221> source
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<400> 1698

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Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1               5                  10                  15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20                  25                  30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
        35                  40                  45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50                  55                  60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65                  70                  75                  80

Lys Asn Ser Ile Ser Glu Lys Ser Lys Val Phe Ser Gln Asn Cys Ile
                85                  90                  95

Lys Pro Val Glu Glu Ile Val His Ser Glu Thr Lys Leu Glu Gln Val
            100                 105                 110

Val Cys Ser Tyr Gln Lys Pro Ser Arg Thr Thr Glu Ser Pro Ser Arg
        115                 120                 125

Val Phe Thr Glu Glu Ala Lys Asp Ser Leu Asn Thr Ser Glu Asn Asp
    130                 135                 140

Ser Glu His Gln Thr Asn Val Thr Arg Ser Leu Phe Glu His Glu Gly
145                 150                 155                 160
```

```
Ala Cys Ser Leu Lys Ser Ser Cys Cys Pro Pro Ser Val Leu Ser Gly
                165                 170                 175

Val Val Gln Met Pro Glu Ser Thr Val Thr Ser Thr Val Gly Asp Lys
            180                 185                 190

Lys Thr Asp Gln Met Val Phe His Leu Glu Thr Asn Ser Asn Ser Glu
        195                 200                 205

Ser His Asp Lys Arg Gln Ser Asp Asn Ile Leu Cys Ser Glu Asp Ser
    210                 215                 220

Gly Phe Val Pro Val Glu Lys Thr Pro Asn Leu Val Asn Ser Val Thr
225                 230                 235                 240

Ser Asn Asn Cys Ala Asp Asp Ile Leu Lys Thr Asp Glu Cys Ser Arg
                245                 250                 255

Thr Ser Ile Ser Asn Cys Glu Ser Ala Asp Ser Thr Trp Gln Ser Ser
            260                 265                 270

Leu Asp Thr Asn Asn Asn Ser His Tyr Gln Lys Lys Arg Met Phe Ser
        275                 280                 285

Glu Asn Glu Glu Asn Val Lys Arg Met Lys Thr Ser Glu Gln Ile Asn
    290                 295                 300

Glu Asn Ile Cys Val Ser Leu Glu Arg Gln Thr Ala Phe Leu Glu Gln
305                 310                 315                 320

Val Arg His Leu Ile Gln Gln Glu Ile Tyr Ser Ile Asn Tyr Glu Leu
                325                 330                 335

Phe Asp Lys Lys Leu Lys Glu Leu Asn Gln Arg Ile Gly Lys Thr Glu
            340                 345                 350

Cys Arg Asn Lys His Glu Gly Ile Ala Asp Lys Leu Leu Ala Lys Ile
        355                 360                 365

Ala Lys Leu Gln Arg Arg Ile Lys Thr Val Leu Leu Phe Gln Arg Asn
    370                 375                 380
```

```
Cys Leu Lys Pro Asn Met Leu Ser Ser Asn Gly Ala Ser Lys Ile Pro
385                 390                 395                 400


Glu Lys Leu His Gln Glu Ile Leu Ala Ile Leu Pro Met Leu Lys Leu
                405                 410                 415


Trp Leu Tyr Arg Arg Asn Leu Ile Leu
            420                 425


<210> 1699
<211> 226
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 469; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7IP2; "

<220>
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<223> /note="Gene Name:
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      factor 7 interacting prt 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446119"

<400> 1699
Met Leu Ile Ser Val Glu Ser Pro Asn Leu Thr Thr Pro Ile Thr Ser
1               5                   10                  15


Asn Pro Thr Asp Thr Arg Lys Ile Thr Ser Gly Asn Ser Ser Asn Ser
            20                  25                  30


Pro Asn Ala Glu Val Met Ala Val Gln Lys Lys Leu Asp Ser Ile Ile
        35                  40                  45


Asp Leu Thr Lys Glu Gly Leu Ser Asn Cys Asn Thr Glu Ser Pro Val
    50                  55                  60


Ser Pro Leu Glu Ser His Ser Lys Ala Ala Ser Asn Ser Lys Glu Thr
65                  70                  75                  80


Thr Pro Leu Ala Gln Asn Ala Val Gln Val Pro Glu Ser Phe Glu His
```

```
                85                  90                  95

Leu Pro Pro Leu Pro Glu Pro Pro Ala Pro Leu Pro Glu Leu Val Asp
            100                 105                 110

Lys Thr Arg Asp Thr Leu Pro Pro Gln Lys Pro Glu Leu Lys Val Lys
        115                 120                 125

Arg Val Phe Arg Pro Asn Gly Ile Ala Leu Thr Trp Asn Ile Thr Lys
    130                 135                 140

Ile Asn Pro Lys Cys Ala Pro Val Glu Ser Tyr His Leu Phe Leu Cys
145                 150                 155                 160

His Glu Asn Ser Asn Asn Lys Leu Ile Trp Lys Lys Ile Gly Glu Ile
                165                 170                 175

Lys Ala Leu Pro Leu Pro Met Ala Cys Thr Leu Ser Gln Phe Leu Ala
            180                 185                 190

Ser Asn Arg Tyr Tyr Phe Thr Val Gln Ser Lys Asp Ile Phe Gly Arg
        195                 200                 205

Tyr Gly Pro Phe Cys Asp Ile Lys Ser Ile Pro Gly Phe Ser Glu Asn
    210                 215                 220

Leu Thr
225
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<210> 1700
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 469; "

<220>
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<223> /note="Gene Symbol: ATF7IP2; "

<220>
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<223> /note="Gene Name:
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factor 7 interacting prt 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454809"

<400> 1700
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1   5   10   15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val
            20   25

<210> 1701
<211> 398
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 469; "

<220>
<221> source
<223> /note="Gene Symbol: ATF7IP2; "

<220>
<221> source
<223> /note="Gene Name:
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      factor 7 interacting prt 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455259"

<400> 1701
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1   5   10   15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20   25   30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
        35   40   45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50   55   60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65   70   75   80

```
Lys Asn Ser Ile Ser Glu Lys Ser Lys Val Phe Ser Gln Asn Cys Ile
                85                  90                  95

Lys Pro Val Glu Glu Ile Val His Ser Glu Thr Lys Leu Glu Gln Val
            100                 105                 110

Val Cys Ser Tyr Gln Lys Pro Ser Arg Thr Thr Glu Ser Pro Ser Arg
        115                 120                 125

Val Phe Thr Glu Glu Ala Lys Asp Ser Leu Asn Thr Ser Glu Asn Asp
    130                 135                 140

Ser Glu His Gln Thr Asn Val Thr Arg Ser Leu Phe Glu His Glu Gly
145                 150                 155                 160

Ala Cys Ser Leu Lys Ser Ser Cys Cys Pro Pro Ser Val Leu Ser Gly
                165                 170                 175

Val Val Gln Met Pro Glu Ser Thr Val Thr Ser Thr Val Gly Asp Lys
            180                 185                 190

Lys Thr Asp Gln Met Val Phe His Leu Glu Thr Asn Ser Asn Ser Glu
        195                 200                 205

Ser His Asp Lys Arg Gln Ser Asp Asn Ile Leu Cys Ser Glu Asp Ser
    210                 215                 220

Gly Phe Val Pro Val Glu Lys Thr Pro Asn Leu Val Asn Ser Val Thr
225                 230                 235                 240

Ser Asn Asn Cys Ala Asp Asp Ile Leu Lys Thr Asp Glu Cys Ser Arg
                245                 250                 255

Thr Ser Ile Ser Asn Cys Glu Ser Ala Asp Ser Thr Trp Gln Ser Ser
            260                 265                 270

Leu Asp Thr Asn Asn Asn Ser His Tyr Gln Lys Lys Arg Met Phe Ser
        275                 280                 285

Glu Asn Glu Glu Asn Val Lys Arg Met Lys Thr Ser Glu Gln Ile Asn
    290                 295                 300
```

```
Glu Asn Ile Cys Val Ser Leu Glu Arg Gln Thr Ala Phe Leu Glu Gln
305                 310                 315                 320

Val Arg His Leu Ile Gln Gln Glu Ile Tyr Ser Ile Asn Tyr Glu Leu
                325                 330                 335

Phe Asp Lys Lys Leu Lys Glu Leu Asn Gln Arg Ile Gly Lys Thr Glu
            340                 345                 350

Cys Arg Asn Lys His Glu Gly Ile Ala Asp Lys Leu Leu Ala Lys Ile
        355                 360                 365

Ala Lys Leu Gln Arg Arg Ile Lys Thr Val Leu Leu Phe Gln Arg Asn
    370                 375                 380

Cys Leu Lys Pro Asn Met Leu Ser Ser Asn Gly Ala Ser Lys
385                 390                 395
```

<210> 1702
<211> 74
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ATF7IP2; "

<220>
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<223> /note="Gene Name:
activating transcription
factor 7 interacting prt 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456023"

<400> 1702

```
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1               5                   10                  15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20                  25                  30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
```

```
        35                  40                  45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50                  55                  60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala
65                  70


<210> 1703
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 469; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
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      factor 7 interacting prt 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457731"

<400> 1703
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1               5                   10                  15

Thr Met Pro Leu Ser Cys Arg Lys Gln Val Glu Met Leu Asn Lys Ser
            20                  25                  30

Arg Asn Val Glu Ala Leu Lys Thr Ala Ile Gly Ser Asn Val Pro Ser
        35                  40                  45

Gly Asn Gln Ser Phe Ser Pro Ser Val Ile Thr Arg Thr Thr Glu Ile
    50                  55                  60

Thr Lys Cys Ser Pro Ser Glu Asn Gly Ala Ser Ser Leu Asp Ser Asn
65                  70                  75                  80

Lys Asn Ser Ile
```

<210> 1704
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<220>
<221> source
<223> /note="Gene Name:
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factor 7 interacting prt 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461383"

<400> 1704
Met Ala Ser Pro Asp Arg Ser Lys Arg Lys Ile Leu Lys Ala Lys Lys
1 5 10 15

Thr

<210> 1705
<211> 198
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 470; "

<220>
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<223> /note="Gene Symbol: AICDA; "

<220>
<221> source
<223> /note="Gene Name:
activation-induced cytidine deaminase; "

<220>
<221> source
<223> /note="Uniprot ID: Q9GZX7; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000229335"

<400> 1705
Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
1 5 10 15

Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
20 25 30

Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
35 40 45

Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
50 55 60

Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
65 70 75 80

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
85 90 95

Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
100 105 110

Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
115 120 125

Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
130 135 140

Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
145 150 155 160

Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
165 170 175

Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
180 185 190

Phe Arg Thr Leu Gly Leu
195

<210> 1706

<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 470; "

<220>
<221> source
<223> /note="Gene Symbol: AICDA; "

<220>
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<223> /note="Gene Name:
activation-induced cytidine deaminase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439103"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1706
Xaa Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys Asn
1 5 10 15

Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val Val
20 25 30

Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr Leu
35 40 45

Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr Ile
50 55 60

Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp Phe
65 70 75 80

Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp Phe
85 90 95

Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg Leu
100 105 110

Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg Leu

115 120 125

His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Ala Pro Val
130 135 140

<210> 1707
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Symbol: AICDA; "

<220>
<221> source
<223> /note="Gene Name:
activation-induced cytidine deaminase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439538"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1707
Xaa Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys Asn
1 5 10 15

Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val Val
20 25 30

Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr Leu
35 40 45

Arg Asn Lys Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala Phe Arg
50 55 60

Thr Leu Gly Leu
65

<210> 1708

<211> 197
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 470; "

<220>
<221> source
<223> /note="Gene Symbol: AICDA; "

<220>
<221> source
<223> /note="Gene Name:
activation-induced cytidine deaminase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443060"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1708
Xaa Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys Asn
1 5 10 15

Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val Val
20 25 30

Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr Leu
35 40 45

Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr Ile
50 55 60

Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp Phe
65 70 75 80

Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp Phe
85 90 95

Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg Leu
100 105 110

Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg Leu

```
        115                 120                 125

His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr Phe
    130                 135                 140

Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys Ala
145                 150                 155                 160

Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu Arg
                165                 170                 175

Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala Phe
            180                 185                 190

Arg Thr Leu Gly Leu
        195


<210> 1709
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 470; "

<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  Q9GZX7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445691"

<400> 1709
Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
1               5                   10                  15

Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
            20                  25                  30
```

```
Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
        35                  40                  45

Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
    50                  55                  60

Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
65                  70                  75                  80

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
                85                  90                  95

Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
            100                 105                 110

Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
        115                 120                 125

Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Glu Asn
    130                 135                 140

His Glu Arg Thr Phe Lys Ala Trp Glu Gly Leu His Glu Asn Ser Val
145                 150                 155                 160

Arg Leu Ser Arg Gln Leu Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val
                165                 170                 175

Asp Asp Leu Arg Asp Ala Phe Arg Thr Leu Gly Leu
            180                 185


<210> 1710
<211> 272
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 471; "

<220>
<221> source
<223> /note="Gene Symbol: ABT1; "

<220>
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<223> /note="Gene Name:
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activator of basal transcription 1; "

<220>
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<223> /note="Uniprot ID: Q9ULW3; "

<220>
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<223> /note="ENSP ID: ENSP00000274849"

<400> 1710
Met Glu Ala Glu Glu Ser Glu Lys Ala Ala Thr Glu Gln Glu Pro Leu
1   5   10   15

Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu Glu Glu Gln Glu Glu Ser
            20   25   30

Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg Val Val Pro Gly Ile Val
        35   40   45

Tyr Leu Gly His Ile Pro Pro Arg Phe Arg Pro Leu His Val Arg Asn
    50   55   60

Leu Leu Ser Ala Tyr Gly Glu Val Gly Arg Val Phe Phe Gln Ala Glu
65   70   75   80

Asp Arg Phe Val Arg Arg Lys Lys Lys Ala Ala Ala Ala Ala Gly Gly
                85   90   95

Lys Lys Arg Ser Tyr Thr Lys Asp Tyr Thr Glu Gly Trp Val Glu Phe
            100   105   110

Arg Asp Lys Arg Ile Ala Lys Arg Val Ala Ala Ser Leu His Asn Thr
        115   120   125

Pro Met Gly Ala Arg Arg Arg Ser Pro Phe Arg Tyr Asp Leu Trp Asn
    130   135   140

Leu Lys Tyr Leu His Arg Phe Thr Trp Ser His Leu Ser Glu His Leu
145   150   155   160

Ala Phe Glu Arg Gln Val Arg Arg Gln Arg Leu Arg Ala Glu Val Ala
                165   170   175

Gln Ala Lys Arg Glu Thr Asp Phe Tyr Leu Gln Ser Val Glu Arg Gly
            180   185   190

```
Gln Arg Phe Leu Ala Ala Asp Gly Asp Pro Ala Arg Pro Asp Gly Ser
        195                 200                 205

Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys
    210                 215                 220

Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln
225                 230                 235                 240

Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala
                245                 250                 255

Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser
            260                 265                 270
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<210> 1711
<211> 822
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
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<223> /note="Gene Name:
active BCR-related; "

<220>
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<223> /note="Uniprot ID: Q12979; "

<220>
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<223> /note="ENSP ID: ENSP00000291107"

<400> 1711

```
Met Glu Glu Glu Glu Glu Ala Ile Gly Leu Leu Asp Lys Val Leu Glu
1               5                   10                  15

Asp Glu Asp Val Phe Leu Leu Glu Glu Cys Glu Leu Gly Thr Pro Thr
            20                  25                  30
```

```
Ser Pro Gly Ser Gly Ser Pro Phe Leu Val Ala Val Lys Val Glu Ala
        35                  40                  45

Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly Phe Leu Ala
    50                  55                  60

Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu Leu Pro Met
65                  70                  75                  80

Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val Leu Thr Ile
                85                  90                  95

Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile Tyr Glu Ile
            100                 105                 110

His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln Gln Trp Asp
        115                 120                 125

Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala Ser Gln Leu
    130                 135                 140

Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala Leu Glu Thr
145                 150                 155                 160

Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys Ile Ser Glu
                165                 170                 175

Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys Asp Ser His Thr Ser
            180                 185                 190

Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg
        195                 200                 205

Ser Thr Leu Val Leu His Asp Leu Leu Lys His Thr Pro Val Asp His
    210                 215                 220

Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe
225                 230                 235                 240

Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr
                245                 250                 255

Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val
```

260 265 270

Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr
275 280 285

Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His
290 295 300

Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe
305 310 315 320

Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro
325 330 335

Asp His Glu Leu Glu Asp Met Lys Met Lys Ile Ser Ala Leu Lys Ser
340 345 350

Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln Ser Arg Ala Ile Glu
355 360 365

Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe Leu Leu Leu Leu Asn
370 375 380

Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg Asn Gly Lys Ser Tyr
385 390 395 400

Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu Trp Arg Glu Ala
405 410 415

Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala Phe Val Leu Ser Ser
420 425 430

Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe Lys Leu Arg Thr Val
435 440 445

His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp Asp Glu Ser Pro Gly
450 455 460

Leu Tyr Gly Phe Leu His Val Ile Val His Ser Ala Lys Gly Phe Lys
465 470 475 480

Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr
485 490 495

Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr Ala Glu Pro
500 505 510

Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu Gly Ser Gln Ser Leu
515 520 525

Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys Thr Lys Val Asn Lys
530 535 540

Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly Lys Gly Gln Ile Gln
545 550 555 560

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
565 570 575

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
580 585 590

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
595 600 605

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
610 615 620

Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu
625 630 635 640

Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala
645 650 655

Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu
660 665 670

Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe
675 680 685

Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe
690 695 700

Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met
705 710 715 720

```
Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu
                725                 730                 735

Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn
            740                 745                 750

Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu
        755                 760                 765

Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp
    770                 775                 780

Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr
785                 790                 795                 800

Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu
                805                 810                 815

Tyr Phe Ser Thr Asp Val
            820


<210> 1712
<211> 859
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

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<223> /note="Gene Name:
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<221> source
<223> /note="Uniprot ID:  Q12979; "

<220>
<221> source
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<400> 1712
Met Glu Pro Leu Ser His Arg Gly Leu Pro Arg Leu Ser Trp Ile Asp
```

```
1               5                   10                  15

Thr Leu Tyr Ser Asn Phe Ser Tyr Gly Thr Asp Glu Tyr Asp Gly Glu
            20                  25                  30

Gly Asn Glu Glu Gln Lys Gly Pro Pro Glu Gly Ser Glu Thr Met Pro
        35                  40                  45

Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala Arg Ser
    50                  55                  60

Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly Leu Ala
65                  70                  75                  80

Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu
                85                  90                  95

Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala
            100                 105                 110

Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln
        115                 120                 125

Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln
    130                 135                 140

Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys
145                 150                 155                 160

Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln Lys
                165                 170                 175

Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys
            180                 185                 190

Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe
        195                 200                 205

Gln Lys Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys
    210                 215                 220

Asp Ser His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile
225                 230                 235                 240
```

```
Asp Arg Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu Lys His
                245                 250                 255

Thr Pro Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg
            260                 265                 270

Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg
        275                 280                 285

Arg Thr Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys
    290                 295                 300

Asp Gly Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His
305                 310                 315                 320

Val Phe Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr
                325                 330                 335

Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu
            340                 345                 350

Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln
        355                 360                 365

Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met Lys Ile
    370                 375                 380

Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln
385                 390                 395                 400

Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe
                405                 410                 415

Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg
            420                 425                 430

Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser
        435                 440                 445

Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala
    450                 455                 460
```

```
Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe
465                 470                 475                 480

Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp
                485                 490                 495

Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val His Ser
            500                 505                 510

Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val
        515                 520                 525

Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg
    530                 535                 540

Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu
545                 550                 555                 560

Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys
                565                 570                 575

Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly
            580                 585                 590

Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp
        595                 600                 605

His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met
    610                 615                 620

Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys
625                 630                 635                 640

Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu
                645                 650                 655

Arg Ser Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu
            660                 665                 670

Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala
        675                 680                 685
```

```
Thr Asp Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp
    690                 695                 700

Ile Leu Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr
705                 710                 715                 720

Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg
                725                 730                 735

Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala
            740                 745                 750

Lys Glu Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn
        755                 760                 765

Leu Ile Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu
    770                 775                 780

Lys Glu Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe
785                 790                 795                 800

Gly Pro Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu
                805                 810                 815

Thr Ser Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Val Gln
            820                 825                 830

Val Leu Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu
        835                 840                 845

Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp Val
    850                 855


<210> 1713
<211> 641
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

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<221> source
<223> /note="Gene Symbol: ABR; "
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<223> /note="Gene Name:
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<400> 1713
Met Glu Ile Leu Leu Ile Ile Arg Phe Cys Cys Asn Cys Thr Tyr Ala
1 5 10 15

Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu
20 25 30

His Asp Leu Leu Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu
35 40 45

Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn
50 55 60

Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu
65 70 75 80

Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser
85 90 95

Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys
100 105 110

Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys
115 120 125

Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu
130 135 140

Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu
145 150 155 160

Asp Met Lys Met Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu
165 170 175

Lys Ala Asn Lys Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys
180 185 190

```
Met Phe Glu Asn Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro
        195                 200                 205

Phe Arg Ile His Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser
    210                 215                 220

Ser Asp Tyr Glu Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln
225                 230                 235                 240

Lys Lys Asp Leu Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val
                245                 250                 255

Leu Thr Gly Ser Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val
            260                 265                 270

Thr Ser Asn Lys Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu
        275                 280                 285

His Val Ile Val His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu
    290                 295                 300

Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala
305                 310                 315                 320

Lys Thr Arg Val Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu
                325                 330                 335

Phe Glu Ile Glu Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr
            340                 345                 350

Glu Lys Cys Tyr Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile
        355                 360                 365

Val Asp Lys Ile Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr
    370                 375                 380

Val Glu Thr Lys Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile
385                 390                 395                 400

Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys
                405                 410                 415
```

Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser
420 425 430

Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln
435 440 445

Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr
450 455 460

Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe
465 470 475 480

Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile
485 490 495

Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu
500 505 510

Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala
515 520 525

Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg
530 535 540

Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His
545 550 555 560

Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His
565 570 575

Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val
580 585 590

Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp
595 600 605

Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro
610 615 620

Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp
625 630 635 640

Val

<210> 1714
<211> 813
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

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<223> /note="Gene Name:
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<223> /note="Uniprot ID: Q12979; "

<220>
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<223> /note="ENSP ID: ENSP00000442048"

<400> 1714
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1   5   10   15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20   25   30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
        35   40   45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
    50   55   60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65   70   75   80

Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys
                85   90   95

Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys
            100   105   110

```
Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe
        115                 120                 125

Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn
    130                 135                 140

Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn
145                 150                 155                 160

Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp
                165                 170                 175

Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys
            180                 185                 190

Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu
        195                 200                 205

Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala
    210                 215                 220

Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp
225                 230                 235                 240

Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu
                245                 250                 255

Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu
            260                 265                 270

Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys
        275                 280                 285

Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile
    290                 295                 300

Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser
305                 310                 315                 320

Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met
                325                 330                 335
```

```
Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys
            340                 345                 350

Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn
        355                 360                 365

Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His
    370                 375                 380

Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu
385                 390                 395                 400

Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu
                405                 410                 415

Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser
            420                 425                 430

Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys
        435                 440                 445

Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val
    450                 455                 460

His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu
465                 470                 475                 480

Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val
                485                 490                 495

Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
            500                 505                 510

Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
        515                 520                 525

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile
    530                 535                 540

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
545                 550                 555                 560

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
```

565 570 575

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
580 585 590

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
595 600 605

Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu
610 615 620

Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly
625 630 635 640

Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn
645 650 655

Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala
660 665 670

Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr
675 680 685

Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro
690 695 700

Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp
705 710 715 720

Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val
725 730 735

Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr
740 745 750

Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala
755 760 765

His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln
770 775 780

Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala
785 790 795 800

Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp Val
805 810

<210> 1715
<211> 310
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID: Q12979; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445198"

<400> 1715
Met Thr Asp Val Leu Pro Gln Pro Asp Cys Ser Pro Lys Ala Gly Arg
1 5 10 15

Glu Pro Leu Ala Leu Glu Glu Ser Gly Ser Lys Arg Pro Pro Asn Thr
20 25 30

Gly Ala Arg Leu Trp Gly Arg Val Arg Asn Lys Leu Leu Arg Asn Lys
35 40 45

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
50 55 60

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
65 70 75 80

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
85 90 95

```
Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
            100                 105                 110

Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu
        115                 120                 125

Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala
    130                 135                 140

Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu
145                 150                 155                 160

Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe
                165                 170                 175

Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe
            180                 185                 190

Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met
        195                 200                 205

Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu
    210                 215                 220

Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn
225                 230                 235                 240

Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu
                245                 250                 255

Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp
            260                 265                 270

Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr
        275                 280                 285

Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu
    290                 295                 300

Tyr Phe Ser Thr Asp Val
305                 310
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<210> 1716

<211> 189
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ABR; "

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<223> /note="Gene Name:
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 1716
Xaa Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr
1 5 10 15

Ile Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala
20 25 30

Ser Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys
35 40 45

Met Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn
50 55 60

Lys Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu
65 70 75 80

Asn Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile
85 90 95

His Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr
100 105 110

Glu Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp

```
        115                 120                 125

Leu Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly
    130                 135                 140

Ser Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn
145                 150                 155                 160

Lys Asp Asp Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe
                165                 170                 175

Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr Ala
            180                 185


<210> 1717
<211> 165
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

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<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000459118"

<400> 1717
Met Glu Ile Leu Leu Ile Ile Arg Phe Cys Cys Asn Cys Thr Tyr Gly
1               5                   10                  15

Asn Pro Ala Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr
            20                  25                  30

Leu Val Leu His Asp Leu Leu Lys His Thr Pro Val Asp His Pro Asp
        35                  40                  45

Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser
    50                  55                  60
```

```
Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr Thr Pro
65                  70                  75                  80

Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val Glu Val
                85                  90                  95

Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Val
            100                 105                 110

Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His Gln Gln
        115                 120                 125

Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe Pro Ser
    130                 135                 140

Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro Asp His
145                 150                 155                 160

Glu Leu Glu Asp Met
                165


<210> 1718
<211> 86
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000459406"

<400> 1718
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1               5                   10                  15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
```

20 25 30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
35 40 45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
50 55 60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65 70 75 80

Ser Gln Pro Val Leu Thr
85

<210> 1719
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
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<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459553"

<400> 1719
Met Thr Asp Val Leu Pro Gln Pro Asp Cys Ser Pro Lys Ala Gly Arg
1 5 10 15

Glu Pro Leu Ala Leu Glu Glu Ser Gly Ser Lys Arg Pro Pro Asn Thr
20 25 30

Gly Ala Arg Leu Trp Gly Arg Val Arg Asn Lys Leu Leu Arg Asn Lys
35 40 45

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
50 55 60

```
Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
65                  70                  75                  80

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
                85                  90                  95

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
            100                 105                 110

Tyr Ile Val Arg Gln Cys Val Glu Glu Ala Val Arg Leu Leu Arg Lys
        115                 120                 125

His His Arg Leu Asn Gly Gly Gly Met His Met Pro Arg Trp Val Ser
    130                 135                 140

Arg Val Ala Gly Arg Gln Leu Ser Ser
145                 150


<210> 1720
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459761"

<400> 1720
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1               5                   10                  15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20                  25                  30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
```

```
        35                  40                  45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
    50                  55                  60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65                  70                  75                  80

Ser Gln Pro Val Leu Thr Ile Gln
                85
```

<210> 1721
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459820"

<400> 1721

```
Met Arg Lys Leu Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr
1               5                   10                  15

Ile Asn Gln Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala
            20                  25                  30

Thr Ala Thr Thr Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr
        35                  40                  45

Ile Phe Tyr Lys Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr
    50                  55                  60

Asp Asn Leu Cys Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met
65                  70                  75                  80
```

```
Gly His Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala
                85                  90                  95

Phe Val Asp Asn Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser
            100                 105                 110

Gln Ser Asn Asn Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys
        115                 120                 125

Gly Pro Lys Asp Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala
    130                 135                 140

Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu
145                 150                 155                 160

His Asp Leu Leu Lys His Thr Pro
                165
```

<210> 1722
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000460248"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1722

```
Xaa Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
1               5                   10                  15
```

```
Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
            20                  25                  30

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile
        35                  40                  45

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
    50                  55                  60

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
65                  70                  75                  80

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
                85                  90                  95

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
            100                 105                 110

Trp Pro Val Trp Ile
        115


<210> 1723
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460770"

<400> 1723
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1               5                   10                  15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
```

```
            20                  25                  30

Leu Ala Pro Gly Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser
        35                  40                  45

Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile
    50                  55                  60

Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro
65                  70                  75                  80

Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln
                85                  90                  95

Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr
            100                 105                 110

Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln
        115                 120                 125

Phe Gln Lys Ile Ser
    130


<210> 1724
<211> 813
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
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<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID:  Q12979; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461565"
```

<400> 1724
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1 5 10 15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
20 25 30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
35 40 45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
50 55 60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65 70 75 80

Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys
85 90 95

Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys
100 105 110

Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe
115 120 125

Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn
130 135 140

Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn
145 150 155 160

Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp
165 170 175

Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys
180 185 190

Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu
195 200 205

Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala
210 215 220

```
Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp
225                 230                 235                 240

Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu
                245                 250                 255

Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu
            260                 265                 270

Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys
        275                 280                 285

Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile
    290                 295                 300

Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser
305                 310                 315                 320

Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met
                325                 330                 335

Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys
            340                 345                 350

Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn
        355                 360                 365

Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His
    370                 375                 380

Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu
385                 390                 395                 400

Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu
                405                 410                 415

Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser
            420                 425                 430

Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys
        435                 440                 445

Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val
```

```
    450                 455                 460

His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu
465                 470                 475                 480

Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val
                485                 490                 495

Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
            500                 505                 510

Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
        515                 520                 525

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile
    530                 535                 540

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
545                 550                 555                 560

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
                565                 570                 575

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
            580                 585                 590

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
        595                 600                 605

Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu
    610                 615                 620

Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly
625                 630                 635                 640

Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn
                645                 650                 655

Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala
            660                 665                 670

Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr
        675                 680                 685
```

```
Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro
    690                 695                 700

Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp
705                 710                 715                 720

Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val
                725                 730                 735

Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr
            740                 745                 750

Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala
        755                 760                 765

His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln
    770                 775                 780

Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala
785                 790                 795                 800

Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp Val
                805                 810


<210> 1725
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
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<223> /note="Gene Name:
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<223> /note="ENSP ID: ENSP00000461629"

<400> 1725
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```
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1               5                  10                  15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20                  25                  30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
        35                  40                  45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
    50                  55                  60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65                  70                  75                  80

Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys
                85                  90                  95

Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys
            100                 105                 110

Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe
        115                 120                 125

Gln
```

<210> 1726
<211> 191
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000461795"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1726
Xaa Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile
1 5 10 15

Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu
20 25 30

Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu
35 40 45

Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro
50 55 60

Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn
65 70 75 80

Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr
85 90 95

Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro
100 105 110

Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr
115 120 125

Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala
130 135 140

Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Asn Ser Ser Gly Thr
145 150 155 160

His Cys Thr Ser Pro Pro Thr Cys Ser Pro Arg Gln Gly Gly Cys Gly
165 170 175

Arg Val Val Glu Pro Ala Pro Pro Ala Trp Gly Pro Thr Gln Thr
180 185 190

<210> 1727

<211> 813
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

<220>
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<223> /note="Gene Symbol: ABR; "

<220>
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<223> /note="Gene Name:
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<223> /note="Uniprot ID: Q12979; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478880"

<400> 1727

```
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1               5                  10                  15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20                  25                  30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
        35                  40                  45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
    50                  55                  60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65                  70                  75                  80

Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys
                85                  90                  95

Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys
            100                 105                 110

Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe
        115                 120                 125
```

```
Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn
    130                 135                 140

Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn
145                 150                 155                 160

Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp
                165                 170                 175

Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys
            180                 185                 190

Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu
        195                 200                 205

Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala
    210                 215                 220

Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp
225                 230                 235                 240

Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu
                245                 250                 255

Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu
            260                 265                 270

Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys
        275                 280                 285

Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile
    290                 295                 300

Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser
305                 310                 315                 320

Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met
                325                 330                 335

Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys
            340                 345                 350
```

```
Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn
        355                 360                 365

Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His
    370                 375                 380

Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu
385                 390                 395                 400

Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu
                405                 410                 415

Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser
            420                 425                 430

Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys
        435                 440                 445

Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val
    450                 455                 460

His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu
465                 470                 475                 480

Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val
                485                 490                 495

Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
            500                 505                 510

Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
        515                 520                 525

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile
    530                 535                 540

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
545                 550                 555                 560

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
                565                 570                 575

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
```

580 585 590

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
595 600 605

Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu
610 615 620

Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly
625 630 635 640

Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn
645 650 655

Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala
660 665 670

Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr
675 680 685

Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro
690 695 700

Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp
705 710 715 720

Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val
725 730 735

Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr
740 745 750

Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala
755 760 765

His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln
770 775 780

Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala
785 790 795 800

Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp Val
805 810

<210> 1728
<211> 310
<212> PRT
<213> Homo sapiens

<220>
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<400> 1728
Met Thr Asp Val Leu Pro Gln Pro Asp Cys Ser Pro Lys Ala Gly Arg
1   5   10   15

Glu Pro Leu Ala Leu Glu Glu Ser Gly Ser Lys Arg Pro Pro Asn Thr
            20   25   30

Gly Ala Arg Leu Trp Gly Arg Val Arg Asn Lys Leu Leu Arg Asn Lys
        35   40   45

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
    50   55   60

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
65   70   75   80

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
                85   90   95

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
            100   105   110

```
Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu
        115                 120                 125

Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala
    130                 135                 140

Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu
145                 150                 155                 160

Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe
                165                 170                 175

Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe
            180                 185                 190

Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met
        195                 200                 205

Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu
    210                 215                 220

Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn
225                 230                 235                 240

Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu
                245                 250                 255

Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp
            260                 265                 270

Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr
        275                 280                 285

Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu
    290                 295                 300

Tyr Phe Ser Thr Asp Val
305                 310
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<210> 1729
<211> 641
<212> PRT
<213> Homo sapiens

<220>
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<400> 1729
Met Glu Ile Leu Leu Ile Ile Arg Phe Cys Cys Asn Cys Thr Tyr Ala
1 5 10 15

Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu
20 25 30

His Asp Leu Leu Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu
35 40 45

Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn
50 55 60

Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu
65 70 75 80

Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser
85 90 95

Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys
100 105 110

Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys
115 120 125

Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu
130 135 140

Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu
145 150 155 160

```
Asp Met Lys Met Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu
                165                 170                 175

Lys Ala Asn Lys Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys
            180                 185                 190

Met Phe Glu Asn Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro
        195                 200                 205

Phe Arg Ile His Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser
    210                 215                 220

Ser Asp Tyr Glu Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln
225                 230                 235                 240

Lys Lys Asp Leu Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val
                245                 250                 255

Leu Thr Gly Ser Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val
            260                 265                 270

Thr Ser Asn Lys Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu
        275                 280                 285

His Val Ile Val His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu
    290                 295                 300

Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala
305                 310                 315                 320

Lys Thr Arg Val Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu
                325                 330                 335

Phe Glu Ile Glu Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr
            340                 345                 350

Glu Lys Cys Tyr Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile
        355                 360                 365

Val Asp Lys Ile Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr
    370                 375                 380
```

```
Val Glu Thr Lys Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile
385                 390                 395                 400

Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys
                405                 410                 415

Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser
            420                 425                 430

Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln
        435                 440                 445

Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr
    450                 455                 460

Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe
465                 470                 475                 480

Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile
                485                 490                 495

Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu
            500                 505                 510

Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala
        515                 520                 525

Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg
    530                 535                 540

Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His
545                 550                 555                 560

Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His
                565                 570                 575

Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val
            580                 585                 590

Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp
        595                 600                 605

Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro
```

610 615 620

Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp
625 630 635 640

Val

<210> 1730
<211> 777
<212> PRT
<213> Homo sapiens

<220>
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<400> 1730
Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly
1 5 10 15

Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu
20 25 30

Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val
35 40 45

Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile
50 55 60

Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln
65 70 75 80

Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala
85 90 95

```
Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala
            100                 105                 110

Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys
        115                 120                 125

Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys Asp Ser
    130                 135                 140

His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile Asp Arg
145                 150                 155                 160

Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu Lys His Thr Pro
                165                 170                 175

Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser
            180                 185                 190

Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr
        195                 200                 205

Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly
    210                 215                 220

Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe
225                 230                 235                 240

Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala
                245                 250                 255

Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp
            260                 265                 270

Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His
        275                 280                 285

Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met Lys Ile Ser Ala
    290                 295                 300

Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln Ser Arg
305                 310                 315                 320
```

```
Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe Leu Leu
                325                 330                 335

Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg Asn Gly
            340                 345                 350

Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu Trp
        355                 360                 365

Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala Phe Val
    370                 375                 380

Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe Lys Leu
385                 390                 395                 400

Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp Asp Glu
                405                 410                 415

Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val His Ser Ala Lys
            420                 425                 430

Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser
        435                 440                 445

Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr
    450                 455                 460

Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu Gly Ser
465                 470                 475                 480

Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys Thr Lys
                485                 490                 495

Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly Lys Gly
            500                 505                 510

Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr
        515                 520                 525

Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe
    530                 535                 540

Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr
```

545 550 555 560

Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser
565 570 575

Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg
580 585 590

Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp
595 600 605

Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu
610 615 620

Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys
625 630 635 640

Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr
645 650 655

Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu
660 665 670

Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile
675 680 685

Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu
690 695 700

Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro
705 710 715 720

Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser
725 730 735

Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu
740 745 750

Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg
755 760 765

Asn Thr Leu Tyr Phe Ser Thr Asp Val
770 775

<210> 1731
<211> 859
<212> PRT
<213> Homo sapiens

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<400> 1731
Met Glu Pro Leu Ser His Arg Gly Leu Pro Arg Leu Ser Trp Ile Asp
1   5   10   15

Thr Leu Tyr Ser Asn Phe Ser Tyr Gly Thr Asp Glu Tyr Asp Gly Glu
            20   25   30

Gly Asn Glu Glu Gln Lys Gly Pro Pro Glu Gly Ser Glu Thr Met Pro
        35   40   45

Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala Arg Ser
    50   55   60

Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly Leu Ala
65   70   75   80

Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu
                85   90   95

Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala
            100   105   110

```
Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln
        115                 120                 125

Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln
    130                 135                 140

Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys
145                 150                 155                 160

Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln Lys
                165                 170                 175

Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys
            180                 185                 190

Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe
        195                 200                 205

Gln Lys Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys
    210                 215                 220

Asp Ser His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile
225                 230                 235                 240

Asp Arg Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu Lys His
                245                 250                 255

Thr Pro Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg
            260                 265                 270

Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg
        275                 280                 285

Arg Thr Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys
    290                 295                 300

Asp Gly Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His
305                 310                 315                 320

Val Phe Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr
                325                 330                 335

Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu
```

```
            340                 345                 350

Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln
        355                 360                 365

Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met Lys Ile
    370                 375                 380

Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln
385                 390                 395                 400

Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe
                405                 410                 415

Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg
            420                 425                 430

Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser
        435                 440                 445

Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala
    450                 455                 460

Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe
465                 470                 475                 480

Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp
                485                 490                 495

Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val His Ser
            500                 505                 510

Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val
        515                 520                 525

Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg
    530                 535                 540

Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu
545                 550                 555                 560

Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys
                565                 570                 575
```

```
Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly
            580                 585                 590

Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp
        595                 600                 605

His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met
    610                 615                 620

Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys
625                 630                 635                 640

Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu
                645                 650                 655

Arg Ser Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu
            660                 665                 670

Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala
        675                 680                 685

Thr Asp Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp
    690                 695                 700

Ile Leu Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr
705                 710                 715                 720

Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg
                725                 730                 735

Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala
            740                 745                 750

Lys Glu Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn
        755                 760                 765

Leu Ile Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu
    770                 775                 780

Lys Glu Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe
785                 790                 795                 800
```

Gly Pro Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu
805 810 815

Thr Ser Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Val Gln
820 825 830

Val Leu Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu
835 840 845

Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp Val
850 855

<210> 1732
<211> 822
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

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<400> 1732
Met Glu Glu Glu Glu Glu Ala Ile Gly Leu Leu Asp Lys Val Leu Glu
1 5 10 15

Asp Glu Asp Val Phe Leu Leu Glu Glu Cys Glu Leu Gly Thr Pro Thr
20 25 30

Ser Pro Gly Ser Gly Ser Pro Phe Leu Val Ala Val Lys Val Glu Ala
35 40 45

Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly Phe Leu Ala

50 55 60

Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu Leu Pro Met
65 70 75 80

Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val Leu Thr Ile
85 90 95

Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile Tyr Glu Ile
100 105 110

His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln Gln Trp Asp
115 120 125

Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala Ser Gln Leu
130 135 140

Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala Leu Glu Thr
145 150 155 160

Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys Ile Ser Glu
165 170 175

Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys Asp Ser His Thr Ser
180 185 190

Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg
195 200 205

Ser Thr Leu Val Leu His Asp Leu Leu Lys His Thr Pro Val Asp His
210 215 220

Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe
225 230 235 240

Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr
245 250 255

Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val
260 265 270

Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr
275 280 285

```
Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His
    290                 295                 300

Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe
305                 310                 315                 320

Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro
                325                 330                 335

Asp His Glu Leu Glu Asp Met Lys Met Lys Ile Ser Ala Leu Lys Ser
            340                 345                 350

Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln Ser Arg Ala Ile Glu
        355                 360                 365

Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe Leu Leu Leu Leu Asn
    370                 375                 380

Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg Asn Gly Lys Ser Tyr
385                 390                 395                 400

Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu Trp Arg Glu Ala
                405                 410                 415

Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala Phe Val Leu Ser Ser
            420                 425                 430

Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe Lys Leu Arg Thr Val
        435                 440                 445

His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp Asp Glu Ser Pro Gly
    450                 455                 460

Leu Tyr Gly Phe Leu His Val Ile Val His Ser Ala Lys Gly Phe Lys
465                 470                 475                 480

Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr
                485                 490                 495

Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr Ala Glu Pro
            500                 505                 510
```

```
Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu Gly Ser Gln Ser Leu
        515                 520                 525

Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys Thr Lys Val Asn Lys
    530                 535                 540

Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly Lys Gly Gln Ile Gln
545                 550                 555                 560

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
                565                 570                 575

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
            580                 585                 590

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
        595                 600                 605

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
    610                 615                 620

Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu
625                 630                 635                 640

Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala
                645                 650                 655

Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu
            660                 665                 670

Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe
        675                 680                 685

Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe
    690                 695                 700

Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met
705                 710                 715                 720

Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu
                725                 730                 735
```

```
Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn
            740                 745                 750

Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu
        755                 760                 765

Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp
    770                 775                 780

Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr
785                 790                 795                 800

Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu
                805                 810                 815

Tyr Phe Ser Thr Asp Val
            820


<210> 1733
<211> 310
<212> PRT
<213> Homo sapiens

<220>
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<400> 1733
Met Thr Asp Val Leu Pro Gln Pro Asp Cys Ser Pro Lys Ala Gly Arg
1               5                   10                  15

Glu Pro Leu Ala Leu Glu Glu Ser Gly Ser Lys Arg Pro Pro Asn Thr
            20                  25                  30
```

```
Gly Ala Arg Leu Trp Gly Arg Val Arg Asn Lys Leu Leu Arg Asn Lys
        35                  40                  45

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
    50                  55                  60

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
65                  70                  75                  80

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
                85                  90                  95

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
            100                 105                 110

Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu
        115                 120                 125

Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala
    130                 135                 140

Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu
145                 150                 155                 160

Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe
                165                 170                 175

Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe
            180                 185                 190

Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met
        195                 200                 205

Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu
    210                 215                 220

Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn
225                 230                 235                 240

Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu
                245                 250                 255
```

```
Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp
            260                 265                 270

Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr
        275                 280                 285

Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu
    290                 295                 300

Tyr Phe Ser Thr Asp Val
305                 310


<210> 1734
<211> 777
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000484899"

<400> 1734
Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly
1               5                   10                  15

Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu
            20                  25                  30

Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val
        35                  40                  45

Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile
    50                  55                  60

Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln
```

65 70 75 80

Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala
85 90 95

Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala
100 105 110

Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys
115 120 125

Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys Asp Ser
130 135 140

His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile Asp Arg
145 150 155 160

Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu Lys His Thr Pro
165 170 175

Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser
180 185 190

Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr
195 200 205

Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly
210 215 220

Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe
225 230 235 240

Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala
245 250 255

Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp
260 265 270

Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His
275 280 285

Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met Lys Ile Ser Ala
290 295 300

```
Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln Ser Arg
305                 310                 315                 320

Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe Leu Leu
                325                 330                 335

Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg Asn Gly
            340                 345                 350

Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu Trp
        355                 360                 365

Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala Phe Val
    370                 375                 380

Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe Lys Leu
385                 390                 395                 400

Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp Asp Glu
                405                 410                 415

Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val His Ser Ala Lys
            420                 425                 430

Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser
        435                 440                 445

Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr
    450                 455                 460

Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu Gly Ser
465                 470                 475                 480

Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys Thr Lys
                485                 490                 495

Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly Lys Gly
            500                 505                 510

Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr
        515                 520                 525
```

```
Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe
    530                 535                 540

Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr
545                 550                 555                 560

Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser
                565                 570                 575

Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg
            580                 585                 590

Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp
        595                 600                 605

Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu
    610                 615                 620

Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys
625                 630                 635                 640

Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr
                645                 650                 655

Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu
            660                 665                 670

Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile
        675                 680                 685

Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu
    690                 695                 700

Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro
705                 710                 715                 720

Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser
                725                 730                 735

Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu
            740                 745                 750
```

Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg
        755   760   765

Asn Thr Leu Tyr Phe Ser Thr Asp Val
    770   775

<210> 1735
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485727"

<400> 1735
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1   5   10   15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20   25   30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
        35   40   45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
    50   55   60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65   70   75   80

Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys
                85   90   95

Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys
            100   105   110

Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe
115 120 125

Gln

<210> 1736
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485918"

<400> 1736
Met Glu Ile Leu Leu Ile Ile Arg Phe Cys Cys Asn Cys Thr Tyr Gly
1 5 10 15

Asn Pro Ala Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr
20 25 30

Leu Val Leu His Asp Leu Leu Lys His Thr Pro Val Asp His Pro Asp
35 40 45

Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser
50 55 60

Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr Thr Pro
65 70 75 80

Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val Glu Val
85 90 95

```
Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Val
            100                 105                 110

Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His Gln Gln
        115                 120                 125

Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe Pro Ser
    130                 135                 140

Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro Asp His
145                 150                 155                 160

Glu Leu Glu Asp Met
                165


<210> 1737
<211> 189
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000485949"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1737
Xaa Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr
1               5                   10                  15

Ile Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala
            20                  25                  30
```

```
Ser Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys
        35                  40                  45

Met Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn
    50                  55                  60

Lys Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu
65                  70                  75                  80

Asn Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile
                85                  90                  95

His Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr
            100                 105                 110

Glu Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp
        115                 120                 125

Leu Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly
    130                 135                 140

Ser Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn
145                 150                 155                 160

Lys Asp Asp Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe
                165                 170                 175

Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr Ala
            180                 185


<210> 1738
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000485981"

<400> 1738
Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly
1   5   10   15

Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu
            20   25   30

Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val
        35   40   45

Leu Thr
    50

<210> 1739
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486137"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1739
Xaa Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile
1   5   10   15

Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu
            20   25   30

```
Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu
        35                  40                  45

Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro
    50                  55                  60

Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn
65                  70                  75                  80

Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr
                85                  90                  95

Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro
            100                 105                 110

Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr
        115                 120                 125

Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala
    130                 135                 140

Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Asn Ser Ser Gly Thr
145                 150                 155                 160

His Cys Thr Ser Pro Pro Thr Cys Ser Pro Arg Gln Gly Gly Cys Gly
                165                 170                 175

Arg Val Val Glu Pro Ala Pro Pro Ala Trp Gly Pro Thr Gln Thr
            180                 185                 190


<210> 1740
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
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<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486156"

<400> 1740
Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly
1 5 10 15

Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu
20 25 30

Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val
35 40 45

Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile
50 55 60

Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln
65 70 75 80

Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln
85 90

<210> 1741
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486157"

<400> 1741
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1 5 10 15

```
Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20                  25                  30

Leu Ala Pro Gly Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser
        35                  40                  45

Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile
    50                  55                  60

Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro
65                  70                  75                  80

Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln
                85                  90                  95

Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr
            100                 105                 110

Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln
        115                 120                 125

Phe Gln Lys Ile Ser
    130


<210> 1742
<211> 813
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID:  Q12979; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000486214"

<400> 1742
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1 5 10 15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
20 25 30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
35 40 45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
50 55 60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65 70 75 80

Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys
85 90 95

Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys
100 105 110

Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe
115 120 125

Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn
130 135 140

Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn
145 150 155 160

Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp
165 170 175

Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys
180 185 190

Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu
195 200 205

Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala

```
    210                 215                 220

Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp
225                 230                 235                 240

Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu
                245                 250                 255

Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu
            260                 265                 270

Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys
        275                 280                 285

Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile
    290                 295                 300

Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser
305                 310                 315                 320

Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met
                325                 330                 335

Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys
            340                 345                 350

Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn
        355                 360                 365

Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His
    370                 375                 380

Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu
385                 390                 395                 400

Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu
                405                 410                 415

Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser
            420                 425                 430

Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys
        435                 440                 445
```

```
Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val
    450                 455                 460

His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu
465                 470                 475                 480

Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val
                485                 490                 495

Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
            500                 505                 510

Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
        515                 520                 525

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile
    530                 535                 540

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
545                 550                 555                 560

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
                565                 570                 575

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
            580                 585                 590

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
        595                 600                 605

Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu
    610                 615                 620

Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly
625                 630                 635                 640

Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn
                645                 650                 655

Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala
            660                 665                 670
```

```
Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr
        675                 680                 685

Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro
    690                 695                 700

Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp
705                 710                 715                 720

Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val
                725                 730                 735

Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr
            740                 745                 750

Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala
        755                 760                 765

His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln
    770                 775                 780

Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala
785                 790                 795                 800

Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp Val
                805                 810


<210> 1743
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
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<223> /note="ENSP ID: ENSP00000486258"

<400> 1743
Met Arg Lys Leu Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr
1 5 10 15

Ile Asn Gln Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala
20 25 30

Thr Ala Thr Thr Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr
35 40 45

Ile Phe Tyr Lys Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr
50 55 60

Asp Asn Leu Cys Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met
65 70 75 80

Gly His Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala
85 90 95

Phe Val Asp Asn Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser
100 105 110

Gln Ser Asn Asn Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys
115 120 125

Gly Pro Lys Asp Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala
130 135 140

Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu
145 150 155 160

His Asp Leu Leu Lys His Thr Pro
165

<210> 1744
<211> 822
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>

<221> source
<223> /note="Gene Symbol: ABR; "

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<223> /note="Uniprot ID: Q12979; "

<220>
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<223> /note="ENSP ID: ENSP00000486511"

<400> 1744
Met Glu Glu Glu Glu Glu Ala Ile Gly Leu Leu Asp Lys Val Leu Glu
1   5   10   15

Asp Glu Asp Val Phe Leu Leu Glu Glu Cys Glu Leu Gly Thr Pro Thr
            20   25   30

Ser Pro Gly Ser Gly Ser Pro Phe Leu Val Ala Val Lys Val Glu Ala
        35   40   45

Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly Phe Leu Ala
    50   55   60

Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu Leu Pro Met
65   70   75   80

Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val Leu Thr Ile
                85   90   95

Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile Tyr Glu Ile
            100   105   110

His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln Gln Trp Asp
        115   120   125

Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala Ser Gln Leu
    130   135   140

Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala Leu Glu Thr
145   150   155   160

```
Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys Ile Ser Glu
                165                 170                 175

Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys Asp Ser His Thr Ser
            180                 185                 190

Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg
        195                 200                 205

Ser Thr Leu Val Leu His Asp Leu Leu Lys His Thr Pro Val Asp His
    210                 215                 220

Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe
225                 230                 235                 240

Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr
                245                 250                 255

Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val
            260                 265                 270

Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr
        275                 280                 285

Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His
    290                 295                 300

Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe
305                 310                 315                 320

Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro
                325                 330                 335

Asp His Glu Leu Glu Asp Met Lys Met Lys Ile Ser Ala Leu Lys Ser
            340                 345                 350

Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln Ser Arg Ala Ile Glu
        355                 360                 365

Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe Leu Leu Leu Leu Asn
    370                 375                 380

Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg Asn Gly Lys Ser Tyr
```

385 390 395 400

Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu Trp Arg Glu Ala
405 410 415

Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala Phe Val Leu Ser Ser
420 425 430

Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe Lys Leu Arg Thr Val
435 440 445

His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp Asp Glu Ser Pro Gly
450 455 460

Leu Tyr Gly Phe Leu His Val Ile Val His Ser Ala Lys Gly Phe Lys
465 470 475 480

Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr
485 490 495

Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr Ala Glu Pro
500 505 510

Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu Gly Ser Gln Ser Leu
515 520 525

Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys Thr Lys Val Asn Lys
530 535 540

Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly Lys Gly Gln Ile Gln
545 550 555 560

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
565 570 575

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
580 585 590

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
595 600 605

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
610 615 620

Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu
625 630 635 640

Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala
645 650 655

Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu
660 665 670

Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe
675 680 685

Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe
690 695 700

Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met
705 710 715 720

Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu
725 730 735

Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn
740 745 750

Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu
755 760 765

Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp
770 775 780

Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr
785 790 795 800

Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu
805 810 815

Tyr Phe Ser Thr Asp Val
820

<210> 1745
<211> 168
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

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active BCR-related; "

<220>
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<400> 1745

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Met Arg Lys Leu Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr
1               5                  10                  15

Ile Asn Gln Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala
            20                  25                  30

Thr Ala Thr Thr Ser Gln Pro Val Leu Thr Ile Gln Gln Ile Glu Thr
        35                  40                  45

Ile Phe Tyr Lys Ile Gln Asp Ile Tyr Glu Ile His Lys Glu Phe Tyr
    50                  55                  60

Asp Asn Leu Cys Pro Lys Val Gln Gln Trp Asp Ser Gln Val Thr Met
65                  70                  75                  80

Gly His Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Lys Ala
                85                  90                  95

Phe Val Asp Asn Tyr Lys Val Ala Leu Glu Thr Ala Glu Lys Cys Ser
            100                 105                 110

Gln Ser Asn Asn Gln Phe Gln Lys Ile Ser Glu Glu Leu Lys Val Lys
        115                 120                 125

Gly Pro Lys Asp Ser Lys Asp Ser His Thr Ser Val Thr Met Glu Ala
    130                 135                 140

Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu
```

145 150 155 160

His Asp Leu Leu Lys His Thr Pro
165

<210> 1746
<211> 20
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486625"

<400> 1746
Glu Thr Lys Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Val Ser
1 5 10 15

Arg Gly Trp Glu
20

<210> 1747
<211> 153
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
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<220>

<221> source
<223> /note="ENSP ID: ENSP00000486789"

<400> 1747
Met Thr Asp Val Leu Pro Gln Pro Asp Cys Ser Pro Lys Ala Gly Arg
1   5   10   15

Glu Pro Leu Ala Leu Glu Glu Ser Gly Ser Lys Arg Pro Pro Asn Thr
            20   25   30

Gly Ala Arg Leu Trp Gly Arg Val Arg Asn Lys Leu Leu Arg Asn Lys
        35   40   45

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
    50   55   60

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
65   70   75   80

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
                85   90   95

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
            100   105   110

Tyr Ile Val Arg Gln Cys Val Glu Glu Ala Val Arg Leu Leu Arg Lys
        115   120   125

His His Arg Leu Asn Gly Gly Gly Met His Met Pro Arg Trp Val Ser
    130   135   140

Arg Val Ala Gly Arg Gln Leu Ser Ser
145   150

<210> 1748
<211> 97
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
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<223> /note="ENSP ID: ENSP00000486808"

<400> 1748
Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val Leu
1 5 10 15

Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile Tyr
20 25 30

Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln Gln
35 40 45

Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala Ser
50 55 60

Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala Leu
65 70 75 80

Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys Ile
85 90 95

Ser

<210> 1749
<211> 86
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000486817"

<400> 1749
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1   5   10   15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
            20   25   30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
        35   40   45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
    50   55   60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65   70   75   80

Ser Gln Pro Val Leu Thr
                85

<210> 1750
<211> 777
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486868"

<400> 1750
Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly
1   5   10   15

Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu
            20   25   30

```
Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val
        35                  40                  45

Leu Thr Ile Gln Gln Ile Glu Thr Ile Phe Tyr Lys Ile Gln Asp Ile
    50                  55                  60

Tyr Glu Ile His Lys Glu Phe Tyr Asp Asn Leu Cys Pro Lys Val Gln
65                  70                  75                  80

Gln Trp Asp Ser Gln Val Thr Met Gly His Leu Phe Gln Lys Leu Ala
                85                  90                  95

Ser Gln Leu Gly Val Tyr Lys Ala Phe Val Asp Asn Tyr Lys Val Ala
            100                 105                 110

Leu Glu Thr Ala Glu Lys Cys Ser Gln Ser Asn Asn Gln Phe Gln Lys
        115                 120                 125

Ile Ser Glu Glu Leu Lys Val Lys Gly Pro Lys Asp Ser Lys Asp Ser
    130                 135                 140

His Thr Ser Val Thr Met Glu Ala Leu Leu Tyr Lys Pro Ile Asp Arg
145                 150                 155                 160

Val Thr Arg Ser Thr Leu Val Leu His Asp Leu Leu Lys His Thr Pro
                165                 170                 175

Val Asp His Pro Asp Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser
            180                 185                 190

Gln Asn Phe Leu Ser Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr
        195                 200                 205

Ala Val Thr Thr Pro Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly
    210                 215                 220

Phe Leu Val Glu Val Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe
225                 230                 235                 240

Leu Phe Thr Asp Val Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala
                245                 250                 255
```

```
Gly Lys His Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp
            260                 265                 270

Leu Val Phe Pro Ser Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His
        275                 280                 285

Pro Phe Pro Asp His Glu Leu Glu Asp Met Lys Met Lys Ile Ser Ala
    290                 295                 300

Leu Lys Ser Glu Ile Gln Lys Glu Lys Ala Asn Lys Gly Gln Ser Arg
305                 310                 315                 320

Ala Ile Glu Arg Leu Lys Lys Lys Met Phe Glu Asn Glu Phe Leu Leu
                325                 330                 335

Leu Leu Asn Ser Pro Thr Ile Pro Phe Arg Ile His Asn Arg Asn Gly
            340                 345                 350

Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu Trp
        355                 360                 365

Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Asp Leu Gln Ala Phe Val
    370                 375                 380

Leu Ser Ser Val Glu Leu Gln Val Leu Thr Gly Ser Cys Phe Lys Leu
385                 390                 395                 400

Arg Thr Val His Asn Ile Pro Val Thr Ser Asn Lys Asp Asp Asp Glu
                405                 410                 415

Ser Pro Gly Leu Tyr Gly Phe Leu His Val Ile Val His Ser Ala Lys
            420                 425                 430

Gly Phe Lys Gln Ser Ala Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser
        435                 440                 445

Phe Gly Tyr Phe Val Ser Lys Ala Lys Thr Arg Val Phe Arg Asp Thr
    450                 455                 460

Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu Leu Glu Gly Ser
465                 470                 475                 480
```

```
Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr Asp Lys Thr Lys
                485                 490                 495

Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile Met Gly Lys Gly
            500                 505                 510

Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr
        515                 520                 525

Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe
    530                 535                 540

Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr
545                 550                 555                 560

Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser
                565                 570                 575

Lys Val Pro Tyr Ile Val Arg Gln Cys Val Glu Glu Val Glu Lys Arg
            580                 585                 590

Gly Ile Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp
        595                 600                 605

Ile Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu
    610                 615                 620

Leu Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys
625                 630                 635                 640

Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr
                645                 650                 655

Pro Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu
            660                 665                 670

Asn Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile
        675                 680                 685

Thr Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu
    690                 695                 700

Pro Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro
```

705 710 715 720

Thr Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser
725 730 735

Ala Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Val Gln Val Leu
740 745 750

Leu Tyr Tyr Leu Gln His Pro Pro Ile Ser Phe Ala Glu Leu Lys Arg
755 760 765

Asn Thr Leu Tyr Phe Ser Thr Asp Val
770 775

<210> 1751
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486946"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1751
Xaa Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
1 5 10 15

Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
20 25 30

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile

```
        35                  40                  45

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
    50                  55                  60

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
65                  70                  75                  80

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
                85                  90                  95

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
            100                 105                 110

Trp Pro Val Trp Ile
        115


<210> 1752
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487120"

<400> 1752
Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu Val Leu Ser Gly
1               5                   10                  15

Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu Glu Ala Leu Leu
            20                  25                  30

Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr Ser Gln Pro Val
        35                  40                  45
```

Leu Thr Ile Gln
50

<210> 1753
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487341"

<400> 1753
Met Thr Asp Val Leu Pro Gln Pro Asp Cys Ser Pro Lys Ala Gly Arg
1 5 10 15

Glu Pro Leu Ala Leu Glu Glu Ser Gly Ser Lys Arg Pro Pro Asn Thr
20 25 30

Gly Ala Arg Leu Trp Gly Arg Val Arg Asn Lys Leu Leu Arg Asn Lys
35 40 45

Leu Asp Pro Gln Thr Val Glu Thr Lys Asn Trp His Thr Asp Val Ile
50 55 60

Glu Met Asn Gly Ile Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg
65 70 75 80

Asp Met Ser Leu Lys Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe
85 90 95

Gly Val Lys Ile Ser Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
100 105 110

Tyr Ile Val Arg Gln Cys Val Glu Glu Ala Val Arg Leu Leu Arg Lys

115 120 125

His His Arg Leu Asn Gly Gly Gly Met His Met Pro Arg Trp Val Ser
130 135 140

Arg Val Ala Gly Arg Gln Leu Ser Ser
145 150

<210> 1754
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487381"

<400> 1754
Met Glu Ile Leu Leu Ile Ile Arg Phe Cys Cys Asn Cys Thr Tyr Gly
1 5 10 15

Asn Pro Ala Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr
20 25 30

Leu Val Leu His Asp Leu Leu Lys His Thr Pro Val Asp His Pro Asp
35 40 45

Tyr Pro Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser
50 55 60

Ser Ile Asn Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr Thr Pro
65 70 75 80

Lys Gly Glu Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val Glu Val
85 90 95

```
Ser Glu Ser Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Val
            100                 105                 110

Leu Leu Cys Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His Gln Gln
        115                 120                 125

Tyr Asp Cys Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe Pro Ser
    130                 135                 140

Pro Glu Glu Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro Asp His
145                 150                 155                 160

Glu Leu Glu Asp Met
                165
```

<210> 1755
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487388"

<400> 1755

```
Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu
1               5                   10                  15

Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Gly Lys Phe Leu Pro
            20                  25                  30

Leu Pro Arg Ser Pro Met Met Ser Val Ala Leu Met Gly Leu Leu Tyr
        35                  40                  45

Phe
```

<210> 1756
<211> 641
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487391"

<400> 1756
Met Glu Ile Leu Leu Ile Ile Arg Phe Cys Cys Asn Cys Thr Tyr Ala
1 5 10 15

Leu Leu Tyr Lys Pro Ile Asp Arg Val Thr Arg Ser Thr Leu Val Leu
20 25 30

His Asp Leu Leu Lys His Thr Pro Val Asp His Pro Asp Tyr Pro Leu
35 40 45

Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn
50 55 60

Glu Asp Ile Asp Pro Arg Arg Thr Ala Val Thr Thr Pro Lys Gly Glu
65 70 75 80

Thr Arg Gln Leu Val Lys Asp Gly Phe Leu Val Glu Val Ser Glu Ser
85 90 95

Ser Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Val Leu Leu Cys
100 105 110

Ala Lys Leu Lys Lys Thr Ser Ala Gly Lys His Gln Gln Tyr Asp Cys
115 120 125

```
Lys Trp Tyr Ile Pro Leu Ala Asp Leu Val Phe Pro Ser Pro Glu Glu
    130                 135                 140

Ser Glu Ala Ser Pro Gln Val His Pro Phe Pro Asp His Glu Leu Glu
145                 150                 155                 160

Asp Met Lys Met Lys Ile Ser Ala Leu Lys Ser Glu Ile Gln Lys Glu
                165                 170                 175

Lys Ala Asn Lys Gly Gln Ser Arg Ala Ile Glu Arg Leu Lys Lys Lys
            180                 185                 190

Met Phe Glu Asn Glu Phe Leu Leu Leu Leu Asn Ser Pro Thr Ile Pro
        195                 200                 205

Phe Arg Ile His Asn Arg Asn Gly Lys Ser Tyr Leu Phe Leu Leu Ser
    210                 215                 220

Ser Asp Tyr Glu Arg Ser Glu Trp Arg Glu Ala Ile Gln Lys Leu Gln
225                 230                 235                 240

Lys Lys Asp Leu Gln Ala Phe Val Leu Ser Ser Val Glu Leu Gln Val
                245                 250                 255

Leu Thr Gly Ser Cys Phe Lys Leu Arg Thr Val His Asn Ile Pro Val
            260                 265                 270

Thr Ser Asn Lys Asp Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu
        275                 280                 285

His Val Ile Val His Ser Ala Lys Gly Phe Lys Gln Ser Ala Asn Leu
    290                 295                 300

Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe Val Ser Lys Ala
305                 310                 315                 320

Lys Thr Arg Val Phe Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu
                325                 330                 335

Phe Glu Ile Glu Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr
            340                 345                 350
```

```
Glu Lys Cys Tyr Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile
        355                 360                 365

Val Asp Lys Ile Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr
    370                 375                 380

Val Glu Thr Lys Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile
385                 390                 395                 400

Lys Val Glu Phe Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys
                405                 410                 415

Arg Thr Pro Ser Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser
            420                 425                 430

Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro Tyr Ile Val Arg Gln
        435                 440                 445

Cys Val Glu Glu Val Glu Lys Arg Gly Ile Glu Glu Val Gly Ile Tyr
    450                 455                 460

Arg Ile Ser Gly Val Ala Thr Asp Ile Gln Ala Leu Lys Ala Val Phe
465                 470                 475                 480

Asp Ala Asn Asn Lys Asp Ile Leu Leu Met Leu Ser Asp Met Asp Ile
                485                 490                 495

Asn Ala Ile Ala Gly Thr Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu
            500                 505                 510

Pro Leu Leu Thr Asp Arg Leu Tyr Pro Ala Phe Met Glu Gly Ile Ala
        515                 520                 525

Leu Ser Asp Pro Ala Ala Lys Glu Asn Cys Met Met His Leu Leu Arg
    530                 535                 540

Ser Leu Pro Asp Pro Asn Leu Ile Thr Phe Leu Phe Leu Leu Glu His
545                 550                 555                 560

Leu Lys Arg Val Ala Glu Lys Glu Pro Ile Asn Lys Met Ser Leu His
                565                 570                 575

Asn Leu Ala Thr Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Val
```

580 585 590

Glu Ser Lys Ala His Leu Thr Ser Ala Ala Asp Ile Trp Ser His Asp
595 600 605

Val Met Ala Gln Val Gln Val Leu Leu Tyr Tyr Leu Gln His Pro Pro
610 615 620

Ile Ser Phe Ala Glu Leu Lys Arg Asn Thr Leu Tyr Phe Ser Thr Asp
625 630 635 640

Val

<210> 1757
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487433"

<400> 1757
Met Pro Tyr Ile Asp Glu Ser Pro Thr Met Ser Pro Gln Leu Ser Ala
1 5 10 15

Arg Ser Gln Gly Gly Gly Asp Gly Val Ser Pro Thr Pro Pro Glu Gly
20 25 30

Leu Ala Pro Gly Val Glu Ala Gly Lys Gly Leu Glu Met Arg Lys Leu
35 40 45

Val Leu Ser Gly Phe Leu Ala Ser Glu Glu Ile Tyr Ile Asn Gln Leu
50 55 60

Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys Ala Thr Ala Thr Thr
65 70 75 80

Ser Gln Pro Val Leu Thr Ile Gln
85

<210> 1758
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487454"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1758
Xaa Glu Glu Val Gly Ile Tyr Arg Ile Ser Gly Val Ala Thr Asp Ile
1 5 10 15

Gln Ala Leu Lys Ala Val Phe Asp Ala Asn Asn Lys Asp Ile Leu Leu
20 25 30

Met Leu Ser Asp Met Asp Ile Asn Ala Ile Ala Gly Thr Leu Lys Leu
35 40 45

Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Asp Arg Leu Tyr Pro
50 55 60

Ala Phe Met Glu Gly Ile Ala Leu Ser Asp Pro Ala Ala Lys Glu Asn
65 70 75 80

```
Cys Met Met His Leu Leu Arg Ser Leu Pro Asp Pro Asn Leu Ile Thr
                85                  90                  95

Phe Leu Phe Leu Leu Glu His Leu Lys Arg Val Ala Glu Lys Glu Pro
            100                 105                 110

Ile Asn Lys Met Ser Leu His Asn Leu Ala Thr Val Phe Gly Pro Thr
        115                 120                 125

Leu Leu Arg Pro Ser Glu Val Glu Ser Lys Ala His Leu Thr Ser Ala
    130                 135                 140

Ala Asp Ile Trp Ser His Asp Val Met Ala Gln Asn Ser Ser Gly Thr
145                 150                 155                 160

His Cys Thr Ser Pro Pro Thr Cys Ser Pro Arg Gln Gly Gly Cys Gly
                165                 170                 175

Arg Val Val Glu Pro Ala Pro Pro Ala Trp Gly Pro Thr Gln Thr
            180                 185                 190


<210> 1759
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487459"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid
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<400> 1759
Xaa Arg Asp Thr Ala Glu Pro Lys Trp Asp Glu Glu Phe Glu Ile Glu
1   5   10   15

Leu Glu Gly Ser Gln Ser Leu Arg Ile Leu Cys Tyr Glu Lys Cys Tyr
            20   25   30

Asp Lys Thr Lys Val Asn Lys Asp Asn Asn Glu Ile Val Asp Lys Ile
        35   40   45

Met Gly Lys Gly Gln Ile Gln Leu Asp Pro Gln Thr Val Glu Thr Lys
    50   55   60

Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Ile Lys Val Glu Phe
65   70   75   80

Ser Met Lys Phe Thr Ser Arg Asp Met Ser Leu Lys Arg Thr Pro Ser
                85   90   95

Lys Lys Gln Thr Gly Val Phe Gly Val Lys Ile Ser Val Val Thr Lys
            100   105   110

Trp Pro Val Trp Ile
        115

<210> 1760
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
      active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487515"

<400> 1760
Glu Thr Lys Asn Trp His Thr Asp Val Ile Glu Met Asn Gly Val Ser

1 5 10 15

Arg Gly Trp Glu
20

<210> 1761
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 472; "

<220>
<221> source
<223> /note="Gene Symbol: ABR; "

<220>
<221> source
<223> /note="Gene Name:
active BCR-related; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487565"

<400> 1761
Gly Lys Ser Tyr Leu Phe Leu Leu Ser Ser Asp Tyr Glu Arg Ser Glu
1 5 10 15

Trp Arg Glu Ala Ile Gln Lys Leu Gln Lys Lys Gly Lys Phe Leu Pro
20 25 30

Leu Pro Arg Ser Pro Met Met Ser Val Ala Leu Met Gly Leu Leu Phe
35 40 45

Phe

<210> 1762
<211> 503
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 473; "

<220>
<221> source

<223> /note="Gene Symbol: ACVRL1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor type II-like
1; "

<220>
<221> source
<223> /note="Uniprot ID: P37023; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000373574"

<400> 1762
Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
1   5   10   15

Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
            20   25   30

Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
        35   40   45

Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
    50   55   60

Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
65   70   75   80

Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
                85   90   95

His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
            100   105   110

Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
        115   120   125

Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
    130   135   140

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
145   150   155   160

```
Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Ser Met Leu Gly Asp
                165                 170                 175

Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
            180                 185                 190

Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
        195                 200                 205

Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
    210                 215                 220

Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
225                 230                 235                 240

Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
                245                 250                 255

Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
            260                 265                 270

Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
        275                 280                 285

Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
    290                 295                 300

Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
305                 310                 315                 320

Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
                325                 330                 335

Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
            340                 345                 350

Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
        355                 360                 365

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
    370                 375                 380

Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
```

385 390 395 400

Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
405 410 415

Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
420 425 430

Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
435 440 445

Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
450 455 460

Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
465 470 475 480

Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
485 490 495

Glu Lys Pro Lys Val Ile Gln
500

<210> 1763
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 473; "

<220>
<221> source
<223> /note="Gene Symbol: ACVRL1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor type II-like
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000392492"

<400> 1763
Met Ala Leu Thr Pro Pro Leu Leu Leu Leu Ser Ala Gly Thr Met Thr
1 5 10 15

```
Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val
            20                  25                  30

Thr Gln Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His
        35                  40                  45

Gly Glu Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser
    50                  55                  60

Trp Phe Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp
65                  70                  75                  80

Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser
                85                  90                  95

Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr
            100                 105                 110

Asp Phe Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu
        115                 120                 125

Ala Val Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe
    130                 135                 140

Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg
145                 150                 155                 160

Asn Val Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly
                165                 170                 175

Leu Ala Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn
            180                 185                 190

Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp
        195                 200                 205

Glu Gln Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile
    210                 215                 220

Trp Ala Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val
225                 230                 235                 240
```

```
Asn Gly Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro
                245                 250                 255

Asn Asp Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln
            260                 265                 270

Gln Thr Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser
        275                 280                 285

Gly Leu Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala
    290                 295                 300

Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn
305                 310                 315                 320

Ser Pro Glu Lys Pro Lys Val Ile Gln
                325
```

<210> 1764
<211> 159
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 473; "

<220>
<221> source
<223> /note="Gene Symbol: ACVRL1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor type II-like
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446724"

<400> 1764

```
Met Ala Leu Thr Pro Pro Leu Leu Leu Leu Ser Ala Gly Thr Met Thr
1               5                   10                  15

Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val
            20                  25                  30
```

```
Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys
        35                  40                  45

Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp
    50                  55                  60

Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His
65                  70                  75                  80

Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr
                85                  90                  95

Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn
            100                 105                 110

Val Ser Leu Val Leu Glu Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
        115                 120                 125

Gly Leu Trp His Gly Glu Ser Val Ala Val Lys Ile Phe Ser Ser Arg
    130                 135                 140

Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu Ile Tyr Asn Thr Val
145                 150                 155


<210> 1765
<211> 517
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 473; "

<220>
<221> source
<223> /note="Gene Symbol: ACVRL1; "

<220>
<221> source
<223> /note="Gene Name:
      activin A receptor type II-like
      1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000447884"

<400> 1765
Met Ala Leu Thr Pro Pro Leu Leu Leu Leu Ser Ala Gly Thr Met Thr
```

```
1               5                   10                  15

Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val
            20                  25                  30

Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys
        35                  40                  45

Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp
    50                  55                  60

Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His
65                  70                  75                  80

Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr
                85                  90                  95

Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn
            100                 105                 110

Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly
        115                 120                 125

Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu
    130                 135                 140

Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg
145                 150                 155                 160

Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu
                165                 170                 175

Ile Leu Lys Ala Ser Glu Gln Gly Asp Ser Met Leu Gly Asp Leu Leu
            180                 185                 190

Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val
        195                 200                 205

Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys
    210                 215                 220

Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val
225                 230                 235                 240
```

```
Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu
                245                 250                 255

Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly
            260                 265                 270

Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp
        275                 280                 285

Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln
    290                 295                 300

Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala
305                 310                 315                 320

Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly
                325                 330                 335

Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val
            340                 345                 350

Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met
        355                 360                 365

His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val
    370                 375                 380

Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg
385                 390                 395                 400

Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly
                405                 410                 415

Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val
            420                 425                 430

Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser
        435                 440                 445

Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr
    450                 455                 460
```

```
Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln
465                 470                 475                 480


Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala
                485                 490                 495


Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys
            500                 505                 510


Pro Lys Val Ile Gln
        515


<210> 1766
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 473; "

<220>
<221> source
<223> /note="Gene Symbol: ACVRL1; "

<220>
<221> source
<223> /note="Gene Name:
      activin A receptor type II-like
      1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455848"

<400> 1766
Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
1               5                   10                  15


Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
            20                  25                  30


Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
        35                  40                  45


Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
    50                  55                  60
```

```
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
65                  70                  75                  80


Pro Thr Glu Phe Val Asn His Tyr Cys
                85


<210> 1767
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 473; "

<220>
<221> source
<223> /note="Gene Symbol: ACVRL1; "

<220>
<221> source
<223> /note="Gene Name:
      activin A receptor type II-like
      1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457394"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1767
Xaa Ser Arg Asn Val Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala
1               5                   10                  15


Asp Leu Gly Leu Ala Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp
            20                  25                  30


Ile Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
        35                  40                  45


Val Leu Asp Glu Gln Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp
    50                  55                  60


Thr Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg
65                  70                  75                  80
```

```
Thr Ile Val Asn Gly Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp
                85                  90                  95

Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys
            100                 105                 110

Val Asp Gln Gln Thr Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro
        115                 120                 125

Val Arg Pro Leu Leu Gly Leu Gly Trp Arg Gly Val Val Ala His Gly
    130                 135                 140

Trp Asp Phe Trp Ala Gln Glu Leu Val Ser Glu Ala Ser Ala Ser Ser
145                 150                 155                 160

His Arg Tyr
```

<210> 1768
<211> 509
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 474; "

<220>
<221> source
<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor, type I; "

<220>
<221> source
<223> /note="Uniprot ID: Q04771; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000263640"

<400> 1768

```
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1               5                  10                  15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
```

```
            20                  25                  30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
        35                  40                  45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
    50                  55                  60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65                  70                  75                  80

Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
                85                  90                  95

Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
            100                 105                 110

Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
        115                 120                 125

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
    130                 135                 140

Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
145                 150                 155                 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
                165                 170                 175

Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
            180                 185                 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
        195                 200                 205

Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
    210                 215                 220

Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225                 230                 235                 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
                245                 250                 255
```

```
Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
            260                 265                 270

Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
        275                 280                 285

Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
    290                 295                 300

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
305                 310                 315                 320

Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
                325                 330                 335

Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
            340                 345                 350

Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
        355                 360                 365

Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
    370                 375                 380

Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
385                 390                 395                 400

Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
                405                 410                 415

Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
            420                 425                 430

Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
        435                 440                 445

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
    450                 455                 460

Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
465                 470                 475                 480
```

Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
485 490 495

Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
500 505

<210> 1769
<211> 509
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 474; "

<220>
<221> source
<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor, type I; "

<220>
<221> source
<223> /note="Uniprot ID: Q04771; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387127"

<400> 1769
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1 5 10 15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
20 25 30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
35 40 45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
50 55 60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65 70 75 80

Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly

```
                85                  90                  95

Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
            100                 105                 110

Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
        115                 120                 125

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
    130                 135                 140

Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
145                 150                 155                 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
                165                 170                 175

Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
            180                 185                 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
        195                 200                 205

Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
    210                 215                 220

Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225                 230                 235                 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
                245                 250                 255

Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
            260                 265                 270

Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
        275                 280                 285

Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
    290                 295                 300

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
305                 310                 315                 320
```

```
Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
                325                 330                 335

Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
            340                 345                 350

Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
        355                 360                 365

Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
    370                 375                 380

Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
385                 390                 395                 400

Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
                405                 410                 415

Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
            420                 425                 430

Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
        435                 440                 445

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
    450                 455                 460

Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
465                 470                 475                 480

Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
                485                 490                 495

Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
            500                 505
```

<210> 1770
<211> 509
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 474; "

<220>
<221> source
<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor, type I; "

<220>
<221> source
<223> /note="Uniprot ID: Q04771; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387273"

<400> 1770

```
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1               5                  10                  15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
            20                  25                  30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
        35                  40                  45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
    50                  55                  60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65                  70                  75                  80

Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
                85                  90                  95

Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
            100                 105                 110

Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
        115                 120                 125

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
    130                 135                 140

Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
```

145 150 155 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
165 170 175

Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
180 185 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
195 200 205

Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
210 215 220

Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225 230 235 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
245 250 255

Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
260 265 270

Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
275 280 285

Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
290 295 300

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
305 310 315 320

Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
325 330 335

Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
340 345 350

Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
355 360 365

Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
370 375 380

```
Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
385                 390                 395                 400

Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
                405                 410                 415

Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
            420                 425                 430

Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
        435                 440                 445

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
    450                 455                 460

Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
465                 470                 475                 480

Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
                485                 490                 495

Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
            500                 505


<210> 1771
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 474; "

<220>
<221> source
<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:
      activin A receptor, type I; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000399322"

<400> 1771
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```
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1               5                  10                  15


Pro Ser Pro Ser Met
            20


<210> 1772
<211> 71
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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      activin A receptor, type I; "

<220>
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<223> /note="ENSP ID: ENSP00000400767"

<400> 1772
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1               5                  10                  15


Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
            20                  25                  30


Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
        35                  40                  45


Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
    50                  55                  60


Val Tyr Gln Lys Gly Cys Phe
65                  70


<210> 1773
<211> 86
<212> PRT
<213> Homo sapiens

<220>
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<221> source
<223> /note="Payload ID: 474; "

<220>
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<220>
<221> source
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000401189"

<400> 1773
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1 5 10 15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
20 25 30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
35 40 45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
50 55 60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65 70 75 80

Cys Lys Thr Pro Pro Ser
85

<210> 1774
<211> 87
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:

activin A receptor, type I; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403006"

<400> 1774
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1   5   10   15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
            20   25   30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
        35   40   45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
    50   55   60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65   70   75   80

Cys Lys Thr Pro Pro Ser Pro
                85

<210> 1775
<211> 509
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 474; "

<220>
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<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor, type I; "

<220>
<221> source
<223> /note="Uniprot ID: Q04771; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405004"

<400> 1775
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1 5 10 15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
20 25 30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
35 40 45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
50 55 60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65 70 75 80

Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
85 90 95

Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
100 105 110

Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
115 120 125

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
130 135 140

Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
145 150 155 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
165 170 175

Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
180 185 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
195 200 205

Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
210 215 220

```
Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225                 230                 235                 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
                245                 250                 255

Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
            260                 265                 270

Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
        275                 280                 285

Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
    290                 295                 300

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
305                 310                 315                 320

Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
                325                 330                 335

Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
            340                 345                 350

Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
        355                 360                 365

Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
    370                 375                 380

Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
385                 390                 395                 400

Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
                405                 410                 415

Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
            420                 425                 430

Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
        435                 440                 445

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
```

```
    450                 455                 460

Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
465                 470                 475                 480

Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
                485                 490                 495

Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
            500                 505


<210> 1776
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 474; "

<220>
<221> source
<223> /note="Gene Symbol: ACVR1; "

<220>
<221> source
<223> /note="Gene Name:
      activin A receptor, type I; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000440091"

<400> 1776
Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1               5                   10                  15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
            20                  25                  30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
        35                  40                  45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
    50                  55                  60

Val Tyr Gln Lys Gly Cys Phe Gln
65                  70
```

<210> 1777
<211> 505
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 475; "

<220>
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<223> /note="Gene Symbol: ACVR1B; "

<220>
<221> source
<223> /note="Gene Name:
activin A receptor, type IB; "

<220>
<221> source
<223> /note="Uniprot ID: P36896; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000257963"

<400> 1777
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1   5   10   15

Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
            20   25   30

Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
        35   40   45

Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Met Glu His
    50   55   60

His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65   70   75   80

Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
                85   90   95

Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
            100   105   110

Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val

```
        115                 120                 125

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
    130                 135                 140

Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145                 150                 155                 160

Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
                165                 170                 175

Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
            180                 185                 190

Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
        195                 200                 205

Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
    210                 215                 220

Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225                 230                 235                 240

Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
                245                 250                 255

Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
            260                 265                 270

Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
        275                 280                 285

Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
    290                 295                 300

Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
305                 310                 315                 320

Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
                325                 330                 335

Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
            340                 345                 350
```

```
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
        355                 360                 365

Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
    370                 375                 380

Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
385                 390                 395                 400

Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
                405                 410                 415

Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp
            420                 425                 430

Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
        435                 440                 445

Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu
    450                 455                 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
465                 470                 475                 480

Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
                485                 490                 495

Leu Ser Val Gln Glu Asp Val Lys Ile
            500                 505


<210> 1778
<211> 476
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 475; "

<220>
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<223> /note="Gene Symbol: ACVR1B; "

<220>
<221> source
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<223> /note="Gene Name:
activin A receptor, type IB; "

<220>
<221> source
<223> /note="Uniprot ID: P36896; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000390477"

<400> 1778

```
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1               5                  10                  15

Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
            20                  25                  30

Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
        35                  40                  45

Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Met Glu His
    50                  55                  60

His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65                  70                  75                  80

Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
                85                  90                  95

Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
            100                 105                 110

Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
        115                 120                 125

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
    130                 135                 140

Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145                 150                 155                 160

Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
                165                 170                 175

Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
```

```
            180                 185                 190

Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
        195                 200                 205

Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
    210                 215                 220

Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225                 230                 235                 240

Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
                245                 250                 255

Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
            260                 265                 270

Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
        275                 280                 285

Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
    290                 295                 300

Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
305                 310                 315                 320

Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
                325                 330                 335

Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
            340                 345                 350

Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
        355                 360                 365

Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
    370                 375                 380

Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
385                 390                 395                 400

Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
                405                 410                 415
```

```
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp
            420                 425                 430

Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
        435                 440                 445

Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu
    450                 455                 460

Val Arg Ser Trp Pro Pro Ala Ala Phe Pro Ser Ala
465                 470                 475


<210> 1779
<211> 487
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 475; "

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  P36896; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397550"

<400> 1779
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1               5                   10                  15

Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
            20                  25                  30

Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
        35                  40                  45
```

```
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Met Glu His
     50                  55                  60

His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65                  70                  75                  80

Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
                85                  90                  95

Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
            100                 105                 110

Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
        115                 120                 125

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
    130                 135                 140

Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145                 150                 155                 160

Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
                165                 170                 175

Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
            180                 185                 190

Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
        195                 200                 205

Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
    210                 215                 220

Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225                 230                 235                 240

Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
                245                 250                 255

Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
            260                 265                 270

Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
```

275 280 285

Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
290 295 300

Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
305 310 315 320

Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
325 330 335

Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
340 345 350

Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
355 360 365

Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
370 375 380

Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
385 390 395 400

Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
405 410 415

Cys Asn Ser Gly Gly Thr Phe Leu Phe Cys Leu Cys Ser Tyr Leu Pro
420 425 430

Phe Gln Asp Ala Gly Ser Pro Lys Ala Val Leu Leu Pro Pro Phe Phe
435 440 445

Leu Gln Pro Val Gly Cys Leu Leu Pro Glu Pro Glu Ser Ser Phe Lys
450 455 460

Val Ala Ile Lys Gly Val Glu Val Ala Val Leu Arg Val Arg Leu Phe
465 470 475 480

Phe Arg Asp Gln Phe Val Glu
485

<210> 1780
<211> 546

<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACVR1B; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID: P36896; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442656"

<400> 1780

```
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1               5                  10                  15


Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
            20                  25                  30


Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
        35                  40                  45


Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Met Glu His
    50                  55                  60


His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65                  70                  75                  80


Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
                85                  90                  95


Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
            100                 105                 110


Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
        115                 120                 125
```

```
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
    130                 135                 140

Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145                 150                 155                 160

Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
                165                 170                 175

Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
            180                 185                 190

Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
        195                 200                 205

Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
    210                 215                 220

Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225                 230                 235                 240

Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
                245                 250                 255

Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Ala Asp
            260                 265                 270

Cys Ser Phe Leu Thr Leu Pro Trp Glu Val Val Met Val Ser Ala Ala
        275                 280                 285

Pro Lys Leu Arg Ser Leu Arg Leu Gln Tyr Lys Gly Gly Arg Gly Arg
    290                 295                 300

Ala Arg Phe Leu Phe Pro Leu Asn Asn Gly Thr Trp Thr Gln Leu Trp
305                 310                 315                 320

Leu Val Ser Asp Tyr His Glu His Gly Ser Leu Phe Asp Tyr Leu Asn
                325                 330                 335

Arg Tyr Thr Val Thr Ile Glu Gly Met Ile Lys Leu Ala Leu Ser Ala
            340                 345                 350

Ala Ser Gly Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly
```

355 360 365

Lys Pro Gly Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Val
370 375 380

Lys Lys Asn Gly Met Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Arg
385 390 395 400

His Asp Ala Val Thr Asp Thr Ile Asp Ile Ala Pro Asn Gln Arg Val
405 410 415

Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Thr Ile Asn
420 425 430

Met Lys His Phe Asp Ser Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly
435 440 445

Leu Val Tyr Trp Glu Ile Ala Arg Arg Cys Asn Ser Gly Gly Val His
450 455 460

Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser
465 470 475 480

Ile Glu Glu Met Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn
485 490 495

Ile Pro Asn Trp Trp Gln Ser Tyr Glu Ala Leu Arg Val Met Gly Lys
500 505 510

Met Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala
515 520 525

Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser Val Gln Glu Asp Val
530 535 540

Lys Ile
545

<210> 1781
<211> 453
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 475; "

<220>
<221> source
<223> /note="Gene Symbol: ACVR1B; "

<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="Uniprot ID: P36896; "

<220>
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<223> /note="ENSP ID: ENSP00000442885"

<400> 1781

```
Met Val Ser Ile Phe Asn Leu Asp Gly Met Glu His His Val Arg Thr
1               5                  10                  15

Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys Pro Phe Tyr Cys
            20                  25                  30

Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys Tyr Thr Asp Tyr
        35                  40                  45

Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His Leu Lys Glu Pro
    50                  55                  60

Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val Gly Ile Ile Ala
65                  70                  75                  80

Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile Val Phe Leu Val
                85                  90                  95

Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln Arg Leu Asp Met
            100                 105                 110

Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp Lys Thr Leu Gln
        115                 120                 125

Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly Ser Gly Leu Pro
    130                 135                 140
```

```
Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val Leu Gln Glu Ile
145                 150                 155                 160

Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Arg Trp Arg Gly
                165                 170                 175

Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg Ser Trp
            180                 185                 190

Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His Glu Asn
        195                 200                 205

Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr Trp Thr
    210                 215                 220

Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu Phe Asp
225                 230                 235                 240

Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met Ile Lys Leu Ala
                245                 250                 255

Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met Glu Ile Val Gly
            260                 265                 270

Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu Lys Ser Lys Asn
        275                 280                 285

Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala Asp Leu Gly Leu
    290                 295                 300

Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp Ile Ala Pro Asn
305                 310                 315                 320

Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu
                325                 330                 335

Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys Ala Asp Ile Tyr
            340                 345                 350

Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg Cys Asn Ser Gly
        355                 360                 365

Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp Leu Val Pro Ser
```

370 375 380

Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys Asp Gln Lys Leu
385 390 395 400

Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu Ala Leu Arg Val
405 410 415

Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg
420 425 430

Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser Val Gln
435 440 445

Glu Asp Val Lys Ile
450

<210> 1782
<211> 71
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 475; "

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<223> /note="Gene Symbol: ACVR1B; "

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<223> /note="Gene Name:
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<220>
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<400> 1782
Met Val Ser Ile Phe Asn Leu Asp Gly Met Glu His His Val Arg Thr
1 5 10 15

Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys Pro Phe Tyr Cys
20 25 30

Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys Tyr Thr Asp Tyr
35 40 45

Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His Leu Lys Glu Pro
    50   55   60

Glu His Pro Ser Met Trp Gly
65   70

<210> 1783
<211> 493
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ACVR1C; "

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<223> /note="Gene Name:
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<223> /note="Uniprot ID: Q8NER5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000243349"

<400> 1783
Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu
1   5   10   15

Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu
            20   25   30

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
        35   40   45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val
    50   55   60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
65   70   75   80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr

```
                85                  90                  95

Leu His Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met
            100                 105                 110

Glu Leu Ala Ile Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala
        115                 120                 125

Ala Met Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg
    130                 135                 140

Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu
145                 150                 155                 160

Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Val Thr Ala
                165                 170                 175

Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala
            180                 185                 190

Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu
        195                 200                 205

Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe
    210                 215                 220

Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln
225                 230                 235                 240

Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp
                245                 250                 255

Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr
            260                 265                 270

His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr
        275                 280                 285

Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala
    290                 295                 300

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
305                 310                 315                 320
```

```
His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr
                325                 330                 335

Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu
            340                 345                 350

Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
        355                 360                 365

Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
    370                 375                 380

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
385                 390                 395                 400

Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu
                405                 410                 415

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
            420                 425                 430

Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp
        435                 440                 445

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
    450                 455                 460

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys
465                 470                 475                 480

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
                485                 490
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<210> 1784
<211> 336
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACVR1C; "

<220>
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<223> /note="Gene Name:
activin A receptor, type IC; "

<220>
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<223> /note="Uniprot ID: Q8NER5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000335139"

<400> 1784

```
Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu
1               5                   10                  15

Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu
            20                  25                  30

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
        35                  40                  45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val
    50                  55                  60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
65                  70                  75                  80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr
                85                  90                  95

Leu His Leu Pro Thr Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val
            100                 105                 110

Ser Glu Tyr His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn
        115                 120                 125

Ile Val Thr Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser
    130                 135                 140

Gly Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro
145                 150                 155                 160

Ala Ile Ala His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys
```

```
                165                 170                 175

Cys Glu Thr Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp
            180                 185                 190

Ser Ile Leu Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr
        195                 200                 205

Lys Arg Tyr Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn
    210                 215                 220

Ile Phe Glu Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val
225                 230                 235                 240

Tyr Trp Glu Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu
                245                 250                 255

Tyr Gln Leu Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu
            260                 265                 270

Glu Met Arg Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro
        275                 280                 285

Asn Gln Trp Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met
    290                 295                 300

Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg
305                 310                 315                 320

Ile Lys Lys Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
                325                 330                 335


<210> 1785
<211> 413
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 476; "

<220>
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<221> source
<223> /note="Gene Name:
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<221> source
<223> /note="Uniprot ID: Q8NER5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000335178"

<400> 1785

```
Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu
1               5                   10                  15

Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu
            20                  25                  30

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
        35                  40                  45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val
    50                  55                  60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
65                  70                  75                  80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr
                85                  90                  95

Leu His Leu Pro Thr Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala
            100                 105                 110

Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu
        115                 120                 125

Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe
    130                 135                 140

Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln
145                 150                 155                 160

Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp
                165                 170                 175
```

```
Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr
            180                 185                 190

His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr
        195                 200                 205

Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala
    210                 215                 220

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
225                 230                 235                 240

His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr
                245                 250                 255

Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu
            260                 265                 270

Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
        275                 280                 285

Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
    290                 295                 300

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
305                 310                 315                 320

Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu
                325                 330                 335

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
            340                 345                 350

Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp
        355                 360                 365

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
    370                 375                 380

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys
385                 390                 395                 400

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
```

405 410

<210> 1786
<211> 443
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ACVR1C; "

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID: Q8NER5; "

<220>
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<223> /note="ENSP ID: ENSP00000387168"

<400> 1786
Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val Ser Leu
1 5 10 15

Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn Val Thr
20 25 30

Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr Leu His
35 40 45

Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met Glu Leu
50 55 60

Ala Ile Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala Ala Met
65 70 75 80

Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg Lys Lys
85 90 95

Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu Val Asn
100 105 110

```
Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Val Thr Ala Ser Gly
        115                 120                 125

Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr
    130                 135                 140

Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu Val Trp
145                 150                 155                 160

His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe Ser Ser
                165                 170                 175

Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val
            180                 185                 190

Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys
        195                 200                 205

Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr His Glu
    210                 215                 220

Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr Val Ala
225                 230                 235                 240

Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala His Leu
                245                 250                 255

His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg
            260                 265                 270

Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr Cys Ala
        275                 280                 285

Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu Asn Thr
    290                 295                 300

Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr Met Ala
305                 310                 315                 320

Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu Ser Phe
                325                 330                 335
```

```
Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu Ile Ala
            340                 345                 350

Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr
        355                 360                 365

Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val
    370                 375                 380

Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp Gln Ser
385                 390                 395                 400

Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys Trp Tyr
                405                 410                 415

Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Ile
            420                 425                 430

Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
        435                 440


<210> 1787
<211> 513
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 477; "

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<221> source
<223> /note="Gene Symbol: ACVR2A; "

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<221> source
<223> /note="Gene Name:
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<221> source
<223> /note="Uniprot ID:  P27037; "

<220>
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<223> /note="ENSP ID: ENSP00000241416"

<400> 1787
Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
1               5                   10                  15
```

```
Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
            20                  25                  30

Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
        35                  40                  45

Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
    50                  55                  60

Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
65                  70                  75                  80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
                85                  90                  95

Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
            100                 105                 110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
        115                 120                 125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
    130                 135                 140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
145                 150                 155                 160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
                165                 170                 175

Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
            180                 185                 190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
        195                 200                 205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
    210                 215                 220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
225                 230                 235                 240
```

```
Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
                245                 250                 255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
            260                 265                 270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
        275                 280                 285

Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
    290                 295                 300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
305                 310                 315                 320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
                325                 330                 335

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
            340                 345                 350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
        355                 360                 365

Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
    370                 375                 380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
385                 390                 395                 400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
                405                 410                 415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
            420                 425                 430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
        435                 440                 445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
    450                 455                 460
```

```
Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
465                 470                 475                 480


Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
                485                 490                 495


Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
            500                 505                 510


Leu



<210> 1788
<211> 513
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 477; "

<220>
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<220>
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<223> /note="Uniprot ID:  P27037; "

<220>
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<223> /note="ENSP ID: ENSP00000384338"

<400> 1788
Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
1               5                   10                  15


Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
            20                  25                  30


Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
        35                  40                  45


Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
    50                  55                  60
```

```
Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
65                  70                  75                  80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
                85                  90                  95

Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
            100                 105                 110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
        115                 120                 125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
    130                 135                 140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
145                 150                 155                 160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
                165                 170                 175

Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
            180                 185                 190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
        195                 200                 205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
    210                 215                 220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
225                 230                 235                 240

Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
                245                 250                 255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
            260                 265                 270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
        275                 280                 285
```

```
Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
    290                 295                 300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
305                 310                 315                 320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
                325                 330                 335

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
            340                 345                 350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
        355                 360                 365

Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
    370                 375                 380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
385                 390                 395                 400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
                405                 410                 415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
            420                 425                 430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
        435                 440                 445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
    450                 455                 460

Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
465                 470                 475                 480

Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
                485                 490                 495

Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
            500                 505                 510
```

Leu

<210> 1789
<211> 405
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 477; "

<220>
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<220>
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<220>
<221> source
<223> /note="Uniprot ID: P27037; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439988"

<400> 1789
Met Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln
1 5 10 15

Pro Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu
20 25 30

Leu Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys
35 40 45

Ala Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu
50 55 60

Val Pro Thr Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly
65 70 75 80

Leu Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly
85 90 95

Cys Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile
100 105 110

```
Phe Pro Ile Gln Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr
        115                 120                 125

Ser Leu Pro Gly Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala
    130                 135                 140

Glu Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala
145                 150                 155                 160

Phe His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val
                165                 170                 175

Ser Trp Asn Glu Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu
            180                 185                 190

Ala Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro
        195                 200                 205

Ala Ile Ser His Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn
    210                 215                 220

Asn Leu Thr Ala Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu
225                 230                 235                 240

Ala Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg
                245                 250                 255

Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp
            260                 265                 270

Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu
        275                 280                 285

Leu Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met
    290                 295                 300

Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met
305                 310                 315                 320

Gln Glu Val Val Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr
                325                 330                 335
```

```
Trp Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu
            340                 345                 350

Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly
        355                 360                 365

Glu Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu
    370                 375                 380

Asp Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro
385                 390                 395                 400

Lys Glu Ser Ser Leu
                405
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<210> 1790
<211> 512
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 478; "

<220>
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<223> /note="Gene Symbol: ACVR2B; "

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<223> /note="Gene Name:
activin A receptor, type IIB; "

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<223> /note="Uniprot ID: Q13705; "

<220>
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<400> 1790

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Met Thr Ala Pro Trp Val Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
1               5                   10                  15

Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
            20                  25                  30

Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
```

```
        35                  40                  45

Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
    50                  55                  60

Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
65                  70                  75                  80

Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
                85                  90                  95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
            100                 105                 110

Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val Thr Tyr Glu Pro
        115                 120                 125

Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
    130                 135                 140

Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
145                 150                 155                 160

Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Asp Pro
                165                 170                 175

Gly Pro Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu
            180                 185                 190

Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Gln
        195                 200                 205

Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp Lys
    210                 215                 220

Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met Lys
225                 230                 235                 240

His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn
                245                 250                 255

Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser
            260                 265                 270
```

```
Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu Cys
        275                 280                 285

His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu Asp
    290                 295                 300

Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His Arg
305                 310                 315                 320

Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala Val
                325                 330                 335

Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro
            340                 345                 350

Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu
        355                 360                 365

Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg Ile
    370                 375                 380

Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Val Ser Arg Cys
385                 390                 395                 400

Lys Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu Glu
                405                 410                 415

Glu Ile Gly Gln His Pro Ser Leu Glu Glu Leu Gln Glu Val Val Val
            420                 425                 430

His Lys Lys Met Arg Pro Thr Ile Lys Asp His Trp Leu Lys His Pro
        435                 440                 445

Gly Leu Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp
    450                 455                 460

Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Val Ser Leu
465                 470                 475                 480

Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu
                485                 490                 495
```

Val Thr Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
500 505 510

<210> 1791
<211> 1102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 479; "

<220>
<221> source
<223> /note="Gene Symbol: ADNP; "

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<223> /note="Gene Name:
activity-dependent neuroprotector homeobox; "

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000342905"

<400> 1791
Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1 5 10 15

Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
20 25 30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
35 40 45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
50 55 60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65 70 75 80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
85 90 95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys

```
            100                 105                 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
        115                 120                 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
    130                 135                 140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145                 150                 155                 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
                165                 170                 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
            180                 185                 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
        195                 200                 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
    210                 215                 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225                 230                 235                 240

Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
                245                 250                 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
            260                 265                 270

Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
        275                 280                 285

Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
    290                 295                 300

Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
305                 310                 315                 320

Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
                325                 330                 335
```

```
Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
            340                 345                 350

Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
        355                 360                 365

Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
    370                 375                 380

Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385                 390                 395                 400

Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
                405                 410                 415

Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
            420                 425                 430

Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
        435                 440                 445

Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
    450                 455                 460

Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
465                 470                 475                 480

Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
                485                 490                 495

Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
            500                 505                 510

Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
        515                 520                 525

Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
    530                 535                 540

Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
545                 550                 555                 560
```

```
Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
                565                 570                 575

Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
            580                 585                 590

Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
        595                 600                 605

Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
    610                 615                 620

Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
625                 630                 635                 640

His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
                645                 650                 655

Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
            660                 665                 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
        675                 680                 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
    690                 695                 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705                 710                 715                 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
                725                 730                 735

Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
            740                 745                 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
        755                 760                 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
    770                 775                 780
```

```
Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785                 790                 795                 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
                805                 810                 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
            820                 825                 830

Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
        835                 840                 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
    850                 855                 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865                 870                 875                 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
                885                 890                 895

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
            900                 905                 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
        915                 920                 925

Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
    930                 935                 940

Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945                 950                 955                 960

Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
                965                 970                 975

Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
            980                 985                 990

Pro Gly Thr Trp Ser Asp Glu Ser  Ser Gln Ser Glu Asp  Ala Arg
Ser
        995                 1000                1005
```

```
Ser Lys  Pro Ala Ala Lys Lys  Lys Ala Thr Met Gln  Gly Asp Arg
    1010                1015                1020

Glu Gln  Leu Lys Trp Lys Asn  Ser Ser Tyr Gly Lys  Val Glu Gly
    1025                1030                1035

Phe Trp  Ser Lys Asp Gln Ser  Gln Trp Lys Asn Ala  Ser Glu Asn
    1040                1045                1050

Asp Glu  Arg Leu Ser Asn Pro  Gln Ile Glu Trp Gln  Asn Ser Thr
    1055                1060                1065

Ile Asp  Ser Glu Asp Gly Glu  Gln Phe Asp Asn Met  Thr Asp Gly
    1070                1075                1080

Val Ala  Glu Pro Met His Gly  Ser Leu Ala Gly Val  Lys Leu Ser
    1085                1090                1095

Ser Gln  Gln Ala
    1100
```

<210> 1792
<211> 1102
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 479; "

<220>
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<223> /note="Gene Symbol: ADNP; "

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<223> /note="Gene Name:
activity-dependent neuroprotector homeobox; "

<220>
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<223> /note="Uniprot ID: Q9H2P0; "

<220>
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<223> /note="ENSP ID: ENSP00000360662"

<400> 1792

```
Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1               5                  10                  15
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```
Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
            20                  25                  30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
        35                  40                  45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
    50                  55                  60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65                  70                  75                  80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
                85                  90                  95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
            100                 105                 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
        115                 120                 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
    130                 135                 140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145                 150                 155                 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
                165                 170                 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
            180                 185                 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
        195                 200                 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
    210                 215                 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225                 230                 235                 240
```

```
Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
                245                 250                 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
            260                 265                 270

Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
        275                 280                 285

Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
    290                 295                 300

Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
305                 310                 315                 320

Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
                325                 330                 335

Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
            340                 345                 350

Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
        355                 360                 365

Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
    370                 375                 380

Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385                 390                 395                 400

Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
                405                 410                 415

Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
            420                 425                 430

Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
        435                 440                 445

Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
    450                 455                 460
```

```
Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
465                 470                 475                 480

Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
                485                 490                 495

Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
            500                 505                 510

Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
        515                 520                 525

Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
    530                 535                 540

Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
545                 550                 555                 560

Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
                565                 570                 575

Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
            580                 585                 590

Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
        595                 600                 605

Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
    610                 615                 620

Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
625                 630                 635                 640

His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
                645                 650                 655

Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
            660                 665                 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
        675                 680                 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
```

690 695 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705 710 715 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
725 730 735

Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
740 745 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
755 760 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
770 775 780

Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785 790 795 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
805 810 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
820 825 830

Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
835 840 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
850 855 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865 870 875 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
885 890 895

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
900 905 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
915 920 925

```
Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
    930                 935                 940

Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945                 950                 955                 960

Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
                965                 970                 975

Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
            980                 985                 990

Pro Gly Thr Trp Ser Asp Glu Ser  Ser Gln Ser Glu Asp  Ala Arg
Ser
        995                 1000                1005

Ser Lys  Pro Ala Ala Lys Lys  Lys Ala Thr Met Gln  Gly Asp Arg
    1010                1015                1020

Glu Gln  Leu Lys Trp Lys Asn  Ser Ser Tyr Gly Lys  Val Glu Gly
    1025                1030                1035

Phe Trp  Ser Lys Asp Gln Ser  Gln Trp Lys Asn Ala  Ser Glu Asn
    1040                1045                1050

Asp Glu  Arg Leu Ser Asn Pro  Gln Ile Glu Trp Gln  Asn Ser Thr
    1055                1060                1065

Ile Asp  Ser Glu Asp Gly Glu  Gln Phe Asp Asn Met  Thr Asp Gly
    1070                1075                1080

Val Ala  Glu Pro Met His Gly  Ser Leu Ala Gly Val  Lys Leu Ser
    1085                1090                1095

Ser Gln  Gln Ala
    1100
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<210> 1793
<211> 1102
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 479; "

<220>
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<223> /note="Gene Symbol: ADNP; "

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<223> /note="Gene Name:
activity-dependent neuroprotector homeobox; "

<220>
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<223> /note="Uniprot ID: Q9H2P0; "

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<223> /note="ENSP ID: ENSP00000379346"

<400> 1793

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Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1               5                  10                  15

Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
            20                  25                  30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
        35                  40                  45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
    50                  55                  60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65                  70                  75                  80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
                85                  90                  95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
            100                 105                 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
        115                 120                 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
    130                 135                 140
```

```
Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145                 150                 155                 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
                165                 170                 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
            180                 185                 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
        195                 200                 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
    210                 215                 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225                 230                 235                 240

Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
                245                 250                 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
            260                 265                 270

Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
        275                 280                 285

Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
    290                 295                 300

Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
305                 310                 315                 320

Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
                325                 330                 335

Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
            340                 345                 350

Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
        355                 360                 365

Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
```

370 375 380

Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385 390 395 400

Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
405 410 415

Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
420 425 430

Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
435 440 445

Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
450 455 460

Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
465 470 475 480

Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
485 490 495

Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
500 505 510

Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
515 520 525

Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
530 535 540

Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
545 550 555 560

Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
565 570 575

Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
580 585 590

Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
595 600 605

```
Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
    610                 615                 620

Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
625                 630                 635                 640

His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
                645                 650                 655

Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
            660                 665                 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
        675                 680                 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
    690                 695                 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705                 710                 715                 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
                725                 730                 735

Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
            740                 745                 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
        755                 760                 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
    770                 775                 780

Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785                 790                 795                 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
                805                 810                 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
            820                 825                 830
```

```
Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
        835                 840                 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
    850                 855                 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865                 870                 875                 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
                885                 890                 895

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
            900                 905                 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
        915                 920                 925

Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
    930                 935                 940

Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945                 950                 955                 960

Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
                965                 970                 975

Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
            980                 985                 990

Pro Gly Thr Trp Ser Asp Glu Ser  Ser Gln Ser Glu Asp  Ala Arg
Ser
        995                 1000                1005

Ser Lys  Pro Ala Ala Lys Lys  Lys Ala Thr Met Gln  Gly Asp Arg
    1010                1015                1020

Glu Gln  Leu Lys Trp Lys Asn  Ser Ser Tyr Gly Lys  Val Glu Gly
    1025                1030                1035

Phe Trp  Ser Lys Asp Gln Ser  Gln Trp Lys Asn Ala  Ser Glu Asn
    1040                1045                1050
```

```
Asp Glu  Arg Leu Ser Asn Pro  Gln Ile Glu Trp Gln  Asn Ser Thr
    1055                 1060                 1065


Ile Asp  Ser Glu Asp Gly Glu  Gln Phe Asp Asn Met  Thr Asp Gly
    1070                 1075                 1080


Val Ala  Glu Pro Met His Gly  Ser Leu Ala Gly Val  Lys Leu Ser
    1085                 1090                 1095


Ser Gln  Gln Ala
    1100


<210> 1794
<211> 1102
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 479; "

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<223> /note="Gene Symbol: ADNP; "

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<223> /note="Gene Name:
      activity-dependent neuroprotector homeobox; "

<220>
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<223> /note="Uniprot ID:  Q9H2P0; "

<220>
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<223> /note="ENSP ID: ENSP00000379349"

<400> 1794
Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1               5                  10                  15


Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
            20                  25                  30


Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
        35                  40                  45


Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
```

```
    50                  55                  60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65                  70                  75                  80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
                85                  90                  95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
            100                 105                 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
        115                 120                 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
    130                 135                 140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145                 150                 155                 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
                165                 170                 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
            180                 185                 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
        195                 200                 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
    210                 215                 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225                 230                 235                 240

Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
                245                 250                 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
            260                 265                 270

Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
        275                 280                 285
```

```
Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
    290                 295                 300

Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
305                 310                 315                 320

Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
                325                 330                 335

Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
            340                 345                 350

Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
        355                 360                 365

Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
    370                 375                 380

Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385                 390                 395                 400

Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
                405                 410                 415

Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
            420                 425                 430

Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
        435                 440                 445

Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
    450                 455                 460

Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
465                 470                 475                 480

Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
                485                 490                 495

Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
            500                 505                 510
```

```
Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
        515                 520                 525

Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
    530                 535                 540

Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
545                 550                 555                 560

Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
                565                 570                 575

Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
            580                 585                 590

Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
        595                 600                 605

Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
    610                 615                 620

Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
625                 630                 635                 640

His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
                645                 650                 655

Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
            660                 665                 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
        675                 680                 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
    690                 695                 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705                 710                 715                 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
                725                 730                 735
```

```
Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
            740                 745                 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
        755                 760                 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
    770                 775                 780

Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785                 790                 795                 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
                805                 810                 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
            820                 825                 830

Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
        835                 840                 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
    850                 855                 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865                 870                 875                 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
                885                 890                 895

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
            900                 905                 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
        915                 920                 925

Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
    930                 935                 940

Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945                 950                 955                 960

Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
```

965 970 975

Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
980 985 990

Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg
Ser
995 1000 1005

Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg
1010 1015 1020

Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly
1025 1030 1035

Phe Trp Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn
1040 1045 1050

Asp Glu Arg Leu Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr
1055 1060 1065

Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Asn Met Thr Asp Gly
1070 1075 1080

Val Ala Glu Pro Met His Gly Ser Leu Ala Gly Val Lys Leu Ser
1085 1090 1095

Ser Gln Gln Ala
1100

<210> 1795
<211> 172
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 479; "

<220>
<221> source
<223> /note="Gene Symbol: ADNP; "

<220>
<221> source
<223> /note="Gene Name:
activity-dependent neuroprotector homeobox; "

<220>
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<223> /note="ENSP ID: ENSP00000436181"

<400> 1795
Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1   5   10   15

Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
            20   25   30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
        35   40   45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
    50   55   60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65   70   75   80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
                85   90   95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
            100   105   110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
        115   120   125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
    130   135   140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145   150   155   160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr
                165   170

<210> 1796
<211> 1102
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 479; "

<220>
<221> source
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<220>
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<223> /note="Gene Name:
activity-dependent neuroprotector homeobox; "

<220>
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<223> /note="Uniprot ID: Q9H2P0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483881"

<400> 1796

```
Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1               5                  10                  15

Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
            20                  25                  30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
        35                  40                  45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
    50                  55                  60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65                  70                  75                  80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
                85                  90                  95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
            100                 105                 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
        115                 120                 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
    130                 135                 140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
```

145 150 155 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
165 170 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
180 185 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
195 200 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
210 215 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225 230 235 240

Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
245 250 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
260 265 270

Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
275 280 285

Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
290 295 300

Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
305 310 315 320

Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
325 330 335

Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
340 345 350

Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
355 360 365

Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
370 375 380

```
Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385                 390                 395                 400

Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
                405                 410                 415

Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
            420                 425                 430

Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
        435                 440                 445

Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
    450                 455                 460

Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
465                 470                 475                 480

Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
                485                 490                 495

Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
            500                 505                 510

Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
        515                 520                 525

Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
    530                 535                 540

Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
545                 550                 555                 560

Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
                565                 570                 575

Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
            580                 585                 590

Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
        595                 600                 605
```

```
Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
    610                 615                 620

Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
625                 630                 635                 640

His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
                645                 650                 655

Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
            660                 665                 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
        675                 680                 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
    690                 695                 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705                 710                 715                 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
                725                 730                 735

Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
            740                 745                 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
        755                 760                 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
    770                 775                 780

Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785                 790                 795                 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
                805                 810                 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
            820                 825                 830
```

```
Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
        835                 840                 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
    850                 855                 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865                 870                 875                 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
                885                 890                 895

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
            900                 905                 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
        915                 920                 925

Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
    930                 935                 940

Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945                 950                 955                 960

Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
                965                 970                 975

Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
            980                 985                 990

Pro Gly Thr Trp Ser Asp Glu Ser  Ser Gln Ser Glu Asp  Ala Arg
Ser
        995                 1000                1005

Ser Lys  Pro Ala Ala Lys Lys  Lys Ala Thr Met Gln  Gly Asp Arg
    1010                1015                1020

Glu Gln  Leu Lys Trp Lys Asn  Ser Ser Tyr Gly Lys  Val Glu Gly
    1025                1030                1035

Phe Trp  Ser Lys Asp Gln Ser  Gln Trp Lys Asn Ala  Ser Glu Asn
    1040                1045                1050
```

```
Asp Glu  Arg Leu Ser Asn Pro  Gln Ile Glu Trp Gln  Asn Ser Thr
    1055                 1060                 1065


Ile Asp  Ser Glu Asp Gly Glu  Gln Phe Asp Asn Met  Thr Asp Gly
    1070                 1075                 1080


Val Ala  Glu Pro Met His Gly  Ser Leu Ala Gly Val  Lys Leu Ser
    1085                 1090                 1095


Ser Gln  Gln Ala
    1100


<210> 1797
<211> 396
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 480; "

<220>
<221> source
<223> /note="Gene Symbol: ARC; "

<220>
<221> source
<223> /note="Gene Name:
      activity-regulated cytoskeleton-associated prt; "

<220>
<221> source
<223> /note="Uniprot ID:  Q7LC44; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000349022"

<400> 1797
Met Glu Leu Asp His Arg Thr Ser Gly Gly Leu His Ala Tyr Pro Gly
1               5                  10                  15


Pro Arg Gly Gly Gln Val Ala Lys Pro Asn Val Ile Leu Gln Ile Gly
            20                  25                  30


Lys Cys Arg Ala Glu Met Leu Glu His Val Arg Arg Thr His Arg His
        35                  40                  45


Leu Leu Ala Glu Val Ser Lys Gln Val Glu Arg Glu Leu Lys Gly Leu
    50                  55                  60
```

```
His Arg Ser Val Gly Lys Leu Glu Ser Asn Leu Asp Gly Tyr Val Pro
65                  70                  75                  80

Thr Ser Asp Ser Gln Arg Trp Lys Lys Ser Ile Lys Ala Cys Leu Cys
                85                  90                  95

Arg Cys Gln Glu Thr Ile Ala Asn Leu Glu Arg Trp Val Lys Arg Glu
            100                 105                 110

Met His Val Trp Arg Glu Val Phe Tyr Arg Leu Glu Arg Trp Ala Asp
        115                 120                 125

Arg Leu Glu Ser Thr Gly Gly Lys Tyr Pro Val Gly Ser Glu Ser Ala
    130                 135                 140

Arg His Thr Val Ser Val Gly Val Gly Gly Pro Glu Ser Tyr Cys His
145                 150                 155                 160

Glu Ala Asp Gly Tyr Asp Tyr Thr Val Ser Pro Tyr Ala Ile Thr Pro
                165                 170                 175

Pro Pro Ala Ala Gly Glu Leu Pro Gly Gln Glu Pro Ala Glu Ala Gln
            180                 185                 190

Gln Tyr Gln Pro Trp Val Pro Gly Glu Asp Gly Gln Pro Ser Pro Gly
        195                 200                 205

Val Asp Thr Gln Ile Phe Glu Asp Pro Arg Glu Phe Leu Ser His Leu
    210                 215                 220

Glu Glu Tyr Leu Arg Gln Val Gly Gly Ser Glu Glu Tyr Trp Leu Ser
225                 230                 235                 240

Gln Ile Gln Asn His Met Asn Gly Pro Ala Lys Lys Trp Trp Glu Phe
                245                 250                 255

Lys Gln Gly Ser Val Lys Asn Trp Val Glu Phe Lys Lys Glu Phe Leu
            260                 265                 270

Gln Tyr Ser Glu Gly Thr Leu Ser Arg Glu Ala Ile Gln Arg Glu Leu
        275                 280                 285
```

```
Asp Leu Pro Gln Lys Gln Gly Glu Pro Leu Asp Gln Phe Leu Trp Arg
    290                 295                 300

Lys Arg Asp Leu Tyr Gln Thr Leu Tyr Val Asp Ala Asp Glu Glu Glu
305                 310                 315                 320

Ile Ile Gln Tyr Val Val Gly Thr Leu Gln Pro Lys Leu Lys Arg Phe
                325                 330                 335

Leu Arg His Pro Leu Pro Lys Thr Leu Glu Gln Leu Ile Gln Arg Gly
            340                 345                 350

Met Glu Val Gln Asp Asp Leu Glu Gln Ala Ala Glu Pro Ala Gly Pro
        355                 360                 365

His Leu Pro Val Glu Asp Glu Ala Glu Thr Leu Thr Pro Ala Pro Asn
    370                 375                 380

Ser Glu Ser Val Ala Ser Asp Arg Thr Gln Pro Glu
385                 390                 395


<210> 1798
<211> 732
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 481; "

<220>
<221> source
<223> /note="Gene Symbol: APEH; "

<220>
<221> source
<223> /note="Gene Name:
      acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="Uniprot ID:  P13798; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000296456"

<400> 1798
Met Glu Arg Gln Val Leu Leu Ser Glu Pro Glu Glu Ala Ala Ala Leu
```

```
1               5                   10                  15

Tyr Arg Gly Leu Ser Arg Gln Pro Ala Leu Ser Ala Ala Cys Leu Gly
            20                  25                  30

Pro Glu Val Thr Thr Gln Tyr Gly Gly Gln Tyr Arg Thr Val His Thr
        35                  40                  45

Glu Trp Thr Gln Arg Asp Leu Glu Arg Met Glu Asn Ile Arg Phe Cys
    50                  55                  60

Arg Gln Tyr Leu Val Phe His Asp Gly Asp Ser Val Val Phe Ala Gly
65                  70                  75                  80

Pro Ala Gly Asn Ser Val Glu Thr Arg Gly Glu Leu Leu Ser Arg Glu
                85                  90                  95

Ser Pro Ser Gly Thr Met Lys Ala Val Leu Arg Lys Ala Gly Gly Thr
            100                 105                 110

Gly Pro Gly Glu Glu Lys Gln Phe Leu Glu Val Trp Glu Lys Asn Arg
        115                 120                 125

Lys Leu Lys Ser Phe Asn Leu Ser Ala Leu Glu Lys His Gly Pro Val
    130                 135                 140

Tyr Glu Asp Asp Cys Phe Gly Cys Leu Ser Trp Ser His Ser Glu Thr
145                 150                 155                 160

His Leu Leu Tyr Val Ala Glu Lys Lys Arg Pro Lys Ala Glu Ser Phe
                165                 170                 175

Phe Gln Thr Lys Ala Leu Asp Val Ser Ala Ser Asp Asp Glu Ile Ala
            180                 185                 190

Arg Leu Lys Lys Pro Asp Gln Ala Ile Lys Gly Asp Gln Phe Val Phe
        195                 200                 205

Tyr Glu Asp Trp Gly Glu Asn Met Val Ser Lys Ser Ile Pro Val Leu
    210                 215                 220

Cys Val Leu Asp Val Glu Ser Gly Asn Ile Ser Val Leu Glu Gly Val
225                 230                 235                 240
```

```
Pro Glu Asn Val Ser Pro Gly Gln Ala Phe Trp Ala Pro Gly Asp Ala
                245                 250                 255

Gly Val Val Phe Val Gly Trp Trp His Glu Pro Phe Arg Leu Gly Ile
            260                 265                 270

Arg Phe Cys Thr Asn Arg Arg Ser Ala Leu Tyr Tyr Val Asp Leu Ile
        275                 280                 285

Gly Gly Lys Cys Glu Leu Leu Ser Asp Asp Ser Leu Ala Val Ser Ser
    290                 295                 300

Pro Arg Leu Ser Pro Asp Gln Cys Arg Ile Val Tyr Leu Gln Tyr Pro
305                 310                 315                 320

Ser Leu Ile Pro His His Gln Cys Ser Gln Leu Cys Leu Tyr Asp Trp
                325                 330                 335

Tyr Thr Lys Val Thr Ser Val Val Val Asp Val Val Pro Arg Gln Leu
            340                 345                 350

Gly Glu Asn Phe Ser Gly Ile Tyr Cys Ser Leu Leu Pro Leu Gly Cys
        355                 360                 365

Trp Ser Ala Asp Ser Gln Arg Val Val Phe Asp Ser Ala Gln Arg Ser
    370                 375                 380

Arg Gln Asp Leu Phe Ala Val Asp Thr Gln Val Gly Thr Val Thr Ser
385                 390                 395                 400

Leu Thr Ala Gly Gly Ser Gly Gly Ser Trp Lys Leu Leu Thr Ile Asp
                405                 410                 415

Gln Asp Leu Met Val Ala Gln Phe Ser Thr Pro Ser Leu Pro Pro Thr
            420                 425                 430

Leu Lys Val Gly Phe Leu Pro Ser Ala Gly Lys Glu Gln Ser Val Leu
        435                 440                 445

Trp Val Ser Leu Glu Glu Ala Glu Pro Ile Pro Asp Ile His Trp Gly
    450                 455                 460
```

```
Ile Arg Val Leu Gln Pro Pro Pro Glu Gln Glu Asn Val Gln Tyr Ala
465                 470                 475                 480

Gly Leu Asp Phe Glu Ala Ile Leu Leu Gln Pro Gly Ser Pro Pro Asp
                485                 490                 495

Lys Thr Gln Val Pro Met Val Val Met Pro His Gly Gly Pro His Ser
            500                 505                 510

Ser Phe Val Thr Ala Trp Met Leu Phe Pro Ala Met Leu Cys Lys Met
        515                 520                 525

Gly Phe Ala Val Leu Leu Val Asn Tyr Arg Gly Ser Thr Gly Phe Gly
    530                 535                 540

Gln Asp Ser Ile Leu Ser Leu Pro Gly Asn Val Gly His Gln Asp Val
545                 550                 555                 560

Lys Asp Val Gln Phe Ala Val Glu Gln Val Leu Gln Glu Glu His Phe
                565                 570                 575

Asp Ala Ser His Val Ala Leu Met Gly Gly Ser His Gly Gly Phe Ile
            580                 585                 590

Ser Cys His Leu Ile Gly Gln Tyr Pro Glu Thr Tyr Arg Ala Cys Val
        595                 600                 605

Ala Arg Asn Pro Val Ile Asn Ile Ala Ser Met Leu Gly Ser Thr Asp
    610                 615                 620

Ile Pro Asp Trp Cys Val Val Glu Ala Gly Phe Pro Phe Ser Ser Asp
625                 630                 635                 640

Cys Leu Pro Asp Leu Ser Val Trp Ala Glu Met Leu Asp Lys Ser Pro
                645                 650                 655

Ile Arg Tyr Ile Pro Gln Val Lys Thr Pro Leu Leu Leu Met Leu Gly
            660                 665                 670

Gln Glu Asp Arg Arg Val Pro Phe Lys Gln Gly Met Glu Tyr Tyr Arg
        675                 680                 685
```

```
Ala Leu Lys Thr Arg Asn Val Pro Val Arg Leu Leu Leu Tyr Pro Lys
    690                 695                 700

Ser Thr His Ala Leu Ser Glu Val Glu Val Glu Ser Asp Ser Phe Met
705                 710                 715                 720

Asn Ala Val Leu Trp Leu Arg Thr His Leu Gly Ser
                725                 730
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<210> 1799
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 481; "

<220>
<221> source
<223> /note="Gene Symbol: APEH; "

<220>
<221> source
<223> /note="Gene Name:
acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401871"

<400> 1799

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Met Glu Arg Gln Val Leu Leu Ser Glu Pro Glu Glu Ala Ala Ala Leu
1               5                   10                  15

Tyr Arg Gly Leu Ser Arg Gln Pro Ala Leu Ser Ala Ala Cys Leu Gly
            20                  25                  30

Pro Glu Val Thr Thr Gln Tyr Gly Gly Gln Tyr Arg Thr Val His Thr
        35                  40                  45

Asp Cys
    50
```

<210> 1800
<211> 308
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 481; "

<220>
<221> source
<223> /note="Gene Symbol: APEH; "

<220>
<221> source
<223> /note="Gene Name:
acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402365"

<400> 1800
Thr Pro Arg Leu Ala Pro Ala Ala Glu Arg Arg Leu Trp Asn Val Arg
1 5 10 15

Leu Leu Ser Arg Glu Ser Pro Ser Gly Thr Met Lys Ala Val Leu Arg
20 25 30

Lys Ala Gly Gly Thr Gly Pro Gly Glu Glu Lys Gln Phe Leu Glu Val
35 40 45

Trp Glu Lys Asn Arg Lys Leu Lys Ser Phe Asn Leu Ser Ala Leu Glu
50 55 60

Lys His Gly Pro Val Tyr Glu Asp Asp Cys Phe Gly Cys Leu Ser Trp
65 70 75 80

Ser His Ser Glu Thr His Leu Leu Tyr Val Ala Glu Lys Lys Arg Pro
85 90 95

Lys Ala Glu Ser Phe Phe Gln Thr Lys Ala Leu Asp Val Ser Ala Ser
100 105 110

Asp Asp Glu Ile Ala Arg Leu Lys Lys Pro Asp Gln Ala Ile Lys Gly
115 120 125

Asp Gln Phe Val Phe Tyr Glu Asp Trp Gly Glu Asn Met Val Ser Lys
130 135 140

Ser Ile Pro Val Leu Cys Val Leu Asp Val Glu Ser Gly Asn Ile Ser
145 150 155 160

```
Val Leu Glu Gly Val Pro Glu Asn Val Ser Pro Gly Gln Ala Phe Trp
                165                 170                 175

Ala Pro Gly Asp Ala Gly Val Val Phe Val Gly Trp Trp His Glu Pro
            180                 185                 190

Phe Arg Leu Gly Ile Arg Phe Cys Thr Asn Arg Arg Ser Ala Leu Tyr
        195                 200                 205

Tyr Val Asp Leu Ile Gly Gly Lys Cys Glu Leu Leu Ser Asp Asp Ser
    210                 215                 220

Leu Ala Val Ser Ser Pro Arg Leu Ser Pro Asp Gln Cys Arg Ile Val
225                 230                 235                 240

Tyr Leu Gln Tyr Pro Ser Leu Ile Pro His His Gln Cys Ser Gln Leu
                245                 250                 255

Cys Leu Tyr Asp Trp Tyr Thr Lys Val Thr Ser Val Val Val Asp Val
            260                 265                 270

Val Pro Arg Gln Leu Gly Glu Asn Phe Ser Gly Ile Tyr Cys Ser Leu
        275                 280                 285

Leu Pro Leu Gly Cys Trp Ser Ala Asp Ser Gln Arg Val Val Phe Asp
    290                 295                 300

Ser Ala Gln Arg
305


<210> 1801
<211> 54
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 481; "

<220>
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<223> /note="Gene Symbol: APEH; "

<220>
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<223> /note="Gene Name:
      acylaminoacyl-peptide hydrolase; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000404353"

<400> 1801
Thr Ala Glu Gln Arg Val Ser Phe Arg His His Glu Ser Cys Ala Ala
1   5   10   15

Gln Gly Trp Arg His Gly Pro Trp Gly Arg Glu Ala Val Pro Gly Gly
            20   25   30

Leu Gly Glu Glu Pro Glu Ala Gln Glu Leu Gln Pro Val Ser Ala Gly
        35   40   45

Glu Thr Trp Ala Cys Leu
    50

<210> 1802
<211> 58
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 481; "

<220>
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<223> /note="Gene Symbol: APEH; "

<220>
<221> source
<223> /note="Gene Name:
      acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410149"

<400> 1802
Met Glu Arg Gln Thr Ala Glu Gln Arg Val Ser Phe Arg His His Glu
1   5   10   15

Ser Cys Ala Ala Gln Gly Trp Arg His Gly Pro Trp Gly Arg Glu Ala
            20   25   30

Val Pro Gly Gly Leu Gly Glu Glu Pro Glu Ala Gln Glu Leu Gln Pro
        35   40   45

Val Ser Ala Gly Glu Thr Trp Ala Cys Leu
50 55

<210> 1803
<211> 284
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410366"

<400> 1803
Gln Val Leu Leu Ser Glu Pro Glu Glu Ala Ala Ala Leu Tyr Arg Gly
1 5 10 15

Leu Ser Arg Gln Pro Ala Leu Ser Ala Ala Cys Leu Gly Pro Glu Val
20 25 30

Thr Thr Gln Tyr Gly Gly Gln Tyr Arg Thr Val His Thr Glu Trp Thr
35 40 45

Gln Arg Asp Leu Glu Arg Met Glu Asn Ile Arg Phe Cys Arg Gln Tyr
50 55 60

Leu Val Phe His Asp Gly Asp Ser Val Val Phe Ala Gly Pro Ala Gly
65 70 75 80

Asn Ser Val Glu Thr Arg Gly Glu Leu Leu Ser Arg Glu Ser Pro Ser
85 90 95

Gly Thr Met Lys Ala Val Leu Arg Lys Ala Gly Gly Thr Gly Pro Gly
100 105 110

Glu Glu Lys Gln Phe Leu Glu Val Trp Glu Lys Asn Arg Lys Leu Lys
115 120 125

```
Ser Phe Asn Leu Ser Ala Leu Glu Lys His Gly Pro Val Tyr Glu Asp
    130                 135                 140

Asp Cys Phe Gly Cys Leu Ser Trp Ser His Ser Glu Thr His Leu Leu
145                 150                 155                 160

Tyr Val Ala Glu Lys Lys Arg Pro Lys Ala Glu Ser Phe Phe Gln Thr
                165                 170                 175

Lys Ala Leu Asp Val Ser Ala Ser Asp Asp Glu Ile Ala Arg Leu Lys
            180                 185                 190

Lys Pro Asp Gln Ala Ile Lys Ala Phe Trp Ala Pro Gly Asp Ala Gly
        195                 200                 205

Val Val Phe Val Gly Trp Trp His Glu Pro Phe Arg Leu Gly Ile Arg
    210                 215                 220

Phe Cys Thr Asn Arg Arg Ser Ala Leu Tyr Tyr Val Asp Leu Ile Gly
225                 230                 235                 240

Gly Lys Cys Glu Leu Leu Ser Asp Asp Ser Leu Ala Val Ser Ser Pro
                245                 250                 255

Arg Leu Ser Pro Asp Gln Cys Arg Ile Val Tyr Leu Gln Tyr Pro Ser
            260                 265                 270

Leu Ile Pro His His Gln Cys Ser Gln Leu Cys Leu
        275                 280


<210> 1804
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<223> /note="Gene Symbol: APEH; "

<220>
<221> source
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<223> /note="Gene Name:
acylaminoacyl-peptide hydrolase; "

<220>
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<223> /note="ENSP ID: ENSP00000414369"

<400> 1804

```
Met Lys Ala Val Leu Arg Lys Ala Gly Gly Thr Gly Pro Gly Glu Glu
1               5                  10                  15

Lys Gln Phe Leu Glu Val Trp Glu Lys Asn Arg Lys Leu Lys Ser Phe
            20                  25                  30

Asn Leu Ser Ala Leu Glu Lys His Gly Pro Val Tyr Glu Asp Asp Cys
        35                  40                  45

Phe Gly Cys Leu Ser Trp Ser His Ser Glu Thr His Leu Leu Tyr Val
    50                  55                  60

Ala Glu Lys Lys Arg Pro Lys Ala Glu Ser Phe Phe Gln Thr Lys Ala
65                  70                  75                  80

Leu Asp Val Ser Ala Ser Asp Asp Glu Ile Ala Arg Leu Lys Lys Pro
                85                  90                  95

Asp Gln Ala Ile Lys Gly Asp Gln Phe Val Phe Tyr Glu Asp Trp Gly
            100                 105                 110

Glu Asn Met Val Ser Lys Ser Ile Pro Val Leu Cys Val Leu Asp Val
        115                 120                 125

Glu Ser Gly Asn Ile Ser Val Leu Glu Gly Val Pro Glu Asn Val Ser
    130                 135                 140

Pro Gly Gln Ala Phe Trp Ala Pro Gly Asp Ala Gly Val Val Phe Val
145                 150                 155                 160

Gly Trp Trp His Glu Pro Phe Arg Leu Gly Ile Arg Phe Cys Thr Asn
                165                 170                 175

Arg Arg Ser Ala Leu Tyr Tyr Val Asp Leu Ile Gly Gly Lys Cys Glu
            180                 185                 190

Leu Leu Ser Asp Asp Ser Leu Ala Val Ser Ser Pro Arg Leu Ser Pro
```

195 200 205

Asp Gln Cys Arg Ile Val Tyr Leu Gln Tyr Pro Ser Leu Ile Pro His
210 215 220

His Gln Cys Ser Gln Leu Cys Leu
225 230

<210> 1805
<211> 737
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 481; "

<220>
<221> source
<223> /note="Gene Symbol: APEH; "

<220>
<221> source
<223> /note="Gene Name:
acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000415862"

<400> 1805
Met Glu Arg Gln Val Leu Leu Ser Glu Pro Glu Glu Ala Ala Ala Leu
1 5 10 15

Tyr Arg Gly Leu Ser Arg Gln Pro Ala Leu Ser Ala Ala Cys Leu Gly
20 25 30

Pro Glu Val Thr Thr Gln Tyr Gly Gly Gln Tyr Arg Thr Val His Thr
35 40 45

Glu Trp Thr Gln Arg Asp Leu Glu Arg Met Glu Asn Ile Arg Phe Cys
50 55 60

Arg Gln Tyr Leu Val Phe His Asp Gly Asp Ser Val Val Phe Ala Gly
65 70 75 80

Pro Ala Gly Asn Ser Val Glu Thr Arg Gly Glu Leu Leu Ser Arg Glu
85 90 95

```
Ser Pro Ser Gly Thr Met Lys Ala Val Leu Arg Lys Ala Gly Gly Thr
            100                 105                 110

Gly Pro Gly Glu Glu Lys Gln Phe Leu Glu Val Trp Glu Lys Asn Arg
        115                 120                 125

Lys Leu Lys Ser Phe Asn Leu Ser Ala Leu Glu Lys His Gly Pro Val
    130                 135                 140

Tyr Glu Asp Asp Cys Phe Gly Cys Leu Ser Trp Ser His Ser Glu Thr
145                 150                 155                 160

His Leu Leu Tyr Val Ala Glu Lys Lys Arg Pro Lys Ala Glu Ser Phe
                165                 170                 175

Phe Gln Thr Lys Ala Leu Asp Val Ser Ala Ser Asp Asp Glu Ile Ala
            180                 185                 190

Arg Leu Lys Lys Pro Asp Gln Ala Ile Lys Gly Asp Gln Phe Val Phe
        195                 200                 205

Tyr Glu Asp Trp Gly Glu Asn Met Val Ser Lys Ser Ile Pro Val Leu
    210                 215                 220

Cys Val Leu Asp Val Glu Ser Gly Asn Ile Ser Val Leu Glu Gly Val
225                 230                 235                 240

Pro Glu Asn Val Ser Pro Gly Gln Ala Phe Trp Ala Pro Gly Asp Ala
                245                 250                 255

Gly Val Val Phe Val Gly Trp Trp His Glu Pro Phe Arg Leu Gly Ile
            260                 265                 270

Arg Phe Cys Thr Asn Arg Arg Ser Ala Leu Tyr Tyr Val Asp Leu Ile
        275                 280                 285

Gly Gly Lys Cys Glu Leu Leu Ser Asp Asp Ser Leu Ala Val Ser Ser
    290                 295                 300

Pro Arg Leu Ser Pro Asp Gln Cys Arg Ile Val Tyr Leu Gln Tyr Pro
305                 310                 315                 320
```

```
Ser Leu Ile Pro His His Gln Cys Ser Gln Leu Cys Leu Tyr Asp Trp
                325                 330                 335

Tyr Thr Lys Val Thr Ser Val Val Val Asp Val Val Pro Arg Gln Leu
            340                 345                 350

Gly Glu Asn Phe Ser Gly Ile Tyr Cys Ser Leu Leu Pro Leu Gly Cys
        355                 360                 365

Trp Ser Ala Asp Ser Gln Arg Val Val Phe Asp Ser Ala Gln Arg Ser
    370                 375                 380

Arg Gln Asp Leu Phe Ala Val Asp Thr Gln Val Gly Thr Val Thr Ser
385                 390                 395                 400

Leu Thr Ala Gly Gly Ser Gly Gly Ser Trp Lys Leu Leu Thr Ile Asp
                405                 410                 415

Gln Asp Leu Met Val Ala Gln Phe Ser Thr Pro Ser Leu Pro Pro Thr
            420                 425                 430

Leu Lys Val Gly Phe Leu Pro Ser Ala Gly Lys Glu Gln Ser Val Leu
        435                 440                 445

Trp Val Ser Leu Glu Glu Ala Glu Pro Ile Pro Asp Ile His Trp Gly
    450                 455                 460

Ile Arg Val Leu Gln Pro Pro Pro Glu Gln Glu Asn Val Gln Tyr Ala
465                 470                 475                 480

Gly Leu Asp Phe Glu Ala Ile Leu Leu Gln Pro Gly Ser Pro Pro Asp
                485                 490                 495

Lys Thr Gln Val Pro Met Val Val Met Pro His Gly Gly Pro His Ser
            500                 505                 510

Ser Phe Val Thr Ala Trp Met Leu Phe Pro Ala Met Leu Cys Lys Met
        515                 520                 525

Gly Phe Ala Val Leu Leu Val Asn Tyr Arg Gly Ser Thr Gly Phe Gly
    530                 535                 540

Gln Asp Ser Ile Leu Ser Leu Pro Gly Asn Val Gly His Gln Asp Val
```

545 550 555 560

Lys Asp Val Gln Phe Ala Val Glu Gln Val Leu Gln Glu Glu His Phe
565 570 575

Asp Ala Ser His Val Ala Leu Met Gly Gly Ser His Gly Gly Phe Ile
580 585 590

Ser Cys His Leu Ile Gly Gln Tyr Pro Glu Thr Tyr Arg Ala Cys Val
595 600 605

Ala Arg Asn Pro Val Ile Asn Ile Ala Ser Met Leu Gly Ser Thr Asp
610 615 620

Ile Pro Asp Cys Ser Val Ser Cys Arg Cys Val Val Glu Ala Gly Phe
625 630 635 640

Pro Phe Ser Ser Asp Cys Leu Pro Asp Leu Ser Val Trp Ala Glu Met
645 650 655

Leu Asp Lys Ser Pro Ile Arg Tyr Ile Pro Gln Val Lys Thr Pro Leu
660 665 670

Leu Leu Met Leu Gly Gln Glu Asp Arg Arg Val Pro Phe Lys Gln Gly
675 680 685

Met Glu Tyr Tyr Arg Ala Leu Lys Thr Arg Asn Val Pro Val Arg Leu
690 695 700

Leu Leu Tyr Pro Lys Ser Thr His Ala Leu Ser Glu Val Glu Val Glu
705 710 715 720

Ser Asp Ser Phe Met Asn Ala Val Leu Trp Leu Arg Thr His Leu Gly
725 730 735

Ser

<210> 1806
<211> 47
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 481; "

<220>
<221> source
<223> /note="Gene Symbol: APEH; "

<220>
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<223> /note="Gene Name:
acylaminoacyl-peptide hydrolase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438180"

<400> 1806
Gln Arg Val Val Phe Asp Ser Ala Gln Arg Ser Arg Gln Asp Leu Phe
1 5 10 15

Ala Val Asp Thr Gln Val Gly Ala Gly Ser Cys Ser Gln Leu Thr Arg
20 25 30

Thr Ser Trp Trp His Ser Phe Pro His Pro Ala Tyr Leu Gln Pro
35 40 45

<210> 1807
<211> 528
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 482; "

<220>
<221> source
<223> /note="Gene Symbol: ACBD3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA binding
domain containing 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H3P7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000355777"

<400> 1807

```
Met Ala Ala Val Leu Asn Ala Glu Arg Leu Glu Val Ser Val Asp Gly
1               5                  10                  15

Leu Thr Leu Ser Pro Asp Pro Glu Glu Arg Pro Gly Ala Glu Gly Ala
            20                  25                  30

Pro Leu Leu Pro Pro Pro Leu Pro Pro Pro Ser Pro Pro Gly Ser Gly
        35                  40                  45

Arg Gly Pro Gly Ala Ser Gly Glu Gln Pro Glu Pro Gly Glu Ala Ala
    50                  55                  60

Ala Gly Gly Ala Ala Glu Glu Ala Arg Arg Leu Glu Gln Arg Trp Gly
65                  70                  75                  80

Phe Gly Leu Glu Glu Leu Tyr Gly Leu Ala Leu Arg Phe Phe Lys Glu
                85                  90                  95

Lys Asp Gly Lys Ala Phe His Pro Thr Tyr Glu Glu Lys Leu Lys Leu
            100                 105                 110

Val Ala Leu His Lys Gln Val Leu Met Gly Pro Tyr Asn Pro Asp Thr
        115                 120                 125

Cys Pro Glu Val Gly Phe Phe Asp Val Leu Gly Asn Asp Arg Arg Arg
    130                 135                 140

Glu Trp Ala Ala Leu Gly Asn Met Ser Lys Glu Asp Ala Met Val Glu
145                 150                 155                 160

Phe Val Lys Leu Leu Asn Arg Cys Cys His Leu Phe Ser Thr Tyr Val
                165                 170                 175

Ala Ser His Lys Ile Glu Lys Glu Glu Gln Glu Lys Lys Arg Lys Glu
            180                 185                 190

Glu Glu Glu Arg Arg Arg Arg Glu Glu Glu Glu Arg Glu Arg Leu Gln
        195                 200                 205

Lys Glu Glu Glu Lys Arg Arg Arg Glu Glu Glu Glu Arg Leu Arg Arg
    210                 215                 220

Glu Glu Glu Glu Arg Arg Arg Ile Glu Glu Glu Arg Leu Arg Leu Glu
```

225 230 235 240

Gln Gln Lys Gln Gln Ile Met Ala Ala Leu Asn Ser Gln Thr Ala Val
245 250 255

Gln Phe Gln Gln Tyr Ala Ala Gln Gln Tyr Pro Gly Asn Tyr Glu Gln
260 265 270

Gln Gln Ile Leu Ile Arg Gln Leu Gln Glu Gln His Tyr Gln Gln Tyr
275 280 285

Met Gln Gln Leu Tyr Gln Val Gln Leu Ala Gln Gln Gln Ala Ala Leu
290 295 300

Gln Lys Gln Gln Glu Val Val Val Ala Gly Ser Ser Leu Pro Thr Ser
305 310 315 320

Ser Lys Val Asn Ala Thr Val Pro Ser Asn Met Met Ser Val Asn Gly
325 330 335

Gln Ala Lys Thr His Thr Asp Ser Ser Glu Lys Glu Leu Glu Pro Glu
340 345 350

Ala Ala Glu Glu Ala Leu Glu Asn Gly Pro Lys Glu Ser Leu Pro Val
355 360 365

Ile Ala Ala Pro Ser Met Trp Thr Arg Pro Gln Ile Lys Asp Phe Lys
370 375 380

Glu Lys Ile Gln Gln Asp Ala Asp Ser Val Ile Thr Val Gly Arg Gly
385 390 395 400

Glu Val Val Thr Val Arg Val Pro Thr His Glu Glu Gly Ser Tyr Leu
405 410 415

Phe Trp Glu Phe Ala Thr Asp Asn Tyr Asp Ile Gly Phe Gly Val Tyr
420 425 430

Phe Glu Trp Thr Asp Ser Pro Asn Thr Ala Val Ser Val His Val Ser
435 440 445

Glu Ser Ser Asp Asp Asp Glu Glu Glu Glu Glu Asn Ile Gly Cys Glu
450 455 460

```
Glu Lys Ala Lys Lys Asn Ala Asn Lys Pro Leu Leu Asp Glu Ile Val
465                 470                 475                 480


Pro Val Tyr Arg Arg Asp Cys His Glu Glu Val Tyr Ala Gly Ser His
                485                 490                 495


Gln Tyr Pro Gly Arg Gly Val Tyr Leu Leu Lys Phe Asp Asn Ser Tyr
            500                 505                 510


Ser Leu Trp Arg Ser Lys Ser Val Tyr Tyr Arg Val Tyr Tyr Thr Arg
        515                 520                 525


<210> 1808
<211> 305
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 483; "

<220>
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<223> /note="Gene Symbol: ACBD4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA binding
      domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8NC06; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000314440"

<400> 1808
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1               5                   10                  15


Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
            20                  25                  30


Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
        35                  40                  45
```

```
Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
    50                  55                  60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
65                  70                  75                  80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala
                85                  90                  95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
            100                 105                 110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
        115                 120                 125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
    130                 135                 140

Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys
145                 150                 155                 160

Glu Pro Ala Pro Pro Ser Pro Glu Ser His Ser Pro Arg Asp Leu Asp
                165                 170                 175

Ser Glu Val Phe Cys Asp Ser Leu Glu Gln Leu Glu Pro Glu Leu Val
            180                 185                 190

Trp Thr Glu Gln Arg Ala Ala Ser Gly Gly Lys Arg Asp Pro Arg Asn
        195                 200                 205

Ser Pro Val Pro Pro Thr Lys Lys Glu Gly Leu Arg Gly Ser Pro Pro
    210                 215                 220

Gly Pro Gln Glu Leu Asp Val Trp Leu Leu Gly Thr Val Arg Ala Leu
225                 230                 235                 240

Gln Glu Ser Met Gln Glu Val Gln Ala Arg Val Gln Ser Leu Glu Ser
                245                 250                 255

Met Pro Arg Pro Pro Glu Gln Arg Pro Gln Pro Arg Pro Ser Ala Arg
            260                 265                 270
```

```
Pro Trp Pro Leu Gly Leu Pro Gly Pro Ala Leu Leu Phe Phe Leu Leu
        275                 280                 285

Trp Pro Phe Val Val Gln Trp Leu Phe Arg Met Phe Arg Thr Gln Lys
    290                 295                 300

Arg
305


<210> 1809
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 483; "

<220>
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<223> /note="Gene Name:
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      domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8NC06; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000366154"

<400> 1809
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1               5                   10                  15

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
            20                  25                  30

Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
        35                  40                  45

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
    50                  55                  60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
```

65 70 75 80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala
85 90 95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
100 105 110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
115 120 125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
130 135 140

Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys
145 150 155 160

Glu Pro Ala Pro Pro Ser Pro Glu Ser His Ser Pro Arg Asp Leu Asp
165 170 175

Ser Glu Val Phe Cys Asp Ser Leu Glu Gln Leu Glu Pro Glu Leu Ser
180 185 190

Ser Gly Gln His Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys
195 200 205

Pro Pro Gln Arg Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg
210 215 220

Ser Trp Thr Cys Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala
225 230 235 240

Cys Arg Arg Cys Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly
245 250 255

Pro Leu Ser Ser Leu Thr Leu Ser Val Arg Leu Glu
260 265

<210> 1810
<211> 305
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 483; "

<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA binding
domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q8NC06; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000381367"

<400> 1810

```
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1               5                  10                  15

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
            20                  25                  30

Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
        35                  40                  45

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
    50                  55                  60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
65                  70                  75                  80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala
                85                  90                  95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
            100                 105                 110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
        115                 120                 125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
    130                 135                 140
```

```
Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys
145                 150                 155                 160

Glu Pro Ala Pro Pro Ser Pro Glu Ser His Ser Pro Arg Asp Leu Asp
                165                 170                 175

Ser Glu Val Phe Cys Asp Ser Leu Glu Gln Leu Glu Pro Glu Leu Val
            180                 185                 190

Trp Thr Glu Gln Arg Ala Ala Ser Gly Gly Lys Arg Asp Pro Arg Asn
        195                 200                 205

Ser Pro Val Pro Pro Thr Lys Lys Glu Gly Leu Arg Gly Ser Pro Pro
    210                 215                 220

Gly Pro Gln Glu Leu Asp Val Trp Leu Leu Gly Thr Val Arg Ala Leu
225                 230                 235                 240

Gln Glu Ser Met Gln Glu Val Gln Ala Arg Val Gln Ser Leu Glu Ser
                245                 250                 255

Met Pro Arg Pro Pro Glu Gln Arg Pro Gln Pro Arg Pro Ser Ala Arg
            260                 265                 270

Pro Trp Pro Leu Gly Leu Pro Gly Pro Ala Leu Leu Phe Phe Leu Leu
        275                 280                 285

Trp Pro Phe Val Val Gln Trp Leu Phe Arg Met Phe Arg Thr Gln Lys
    290                 295                 300

Arg
305
```

<210> 1811
<211> 341
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 483; "

<220>
<221> source
<223> /note="Gene Symbol: ACBD4; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA binding
domain containing 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q8NC06; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000405969"

<400> 1811
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1 5 10 15

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
20 25 30

Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
35 40 45

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
50 55 60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
65 70 75 80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala
85 90 95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
100 105 110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
115 120 125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
130 135 140

Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys
145 150 155 160

Glu Pro Ala Pro Pro Ser Pro Ala Ser Leu Trp Ala Val Thr Leu Pro

```
                165                 170                 175

Thr Pro Pro Gln Ser Pro Ile His Pro Gly Thr Trp Thr Pro Arg Phe
            180                 185                 190

Ser Val Ile Pro Trp Ser Ser Trp Ser Leu Ser Trp Phe Gly Gln Ser
        195                 200                 205

Ser Gly Gln His Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys
    210                 215                 220

Pro Pro Gln Arg Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg
225                 230                 235                 240

Ser Trp Thr Cys Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala
                245                 250                 255

Cys Arg Arg Cys Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly
            260                 265                 270

Pro Leu Ser Arg Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro
        275                 280                 285

Leu Gly Ser Arg Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser
    290                 295                 300

Ser Ser Ser Gly Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys
305                 310                 315                 320

Gln Trp Arg Gly Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu
                325                 330                 335

Ser Leu Pro Arg Val
            340


<210> 1812
<211> 341
<212> PRT
<213> Homo sapiens

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<400> 1812

Met	Gly	Thr	Glu	Lys	Glu	Ser	Pro	Glu	Pro	Asp	Cys	Gln	Lys	Gln	Phe
1				5				10					15		
Gln	Ala	Ala	Val	Ser	Val	Ile	Gln	Asn	Leu	Pro	Lys	Asn	Gly	Ser	Tyr
		20					25					30			
Arg	Pro	Ser	Tyr	Glu	Glu	Met	Leu	Arg	Phe	Tyr	Ser	Tyr	Tyr	Lys	Gln
	35					40					45				
Ala	Thr	Met	Gly	Pro	Cys	Leu	Val	Pro	Arg	Pro	Gly	Phe	Trp	Asp	Pro
50					55					60					
Ile	Gly	Arg	Tyr	Lys	Trp	Asp	Ala	Trp	Asn	Ser	Leu	Gly	Lys	Met	Ser
65				70					75					80	
Arg	Glu	Glu	Ala	Met	Ser	Ala	Tyr	Ile	Thr	Glu	Met	Lys	Leu	Val	Ala
			85					90					95		
Gln	Lys	Val	Ile	Asp	Thr	Val	Pro	Leu	Gly	Glu	Val	Ala	Glu	Asp	Met
		100					105					110			
Phe	Gly	Tyr	Phe	Glu	Pro	Leu	Tyr	Gln	Val	Ile	Pro	Asp	Met	Pro	Arg
	115					120					125				
Pro	Pro	Glu	Thr	Phe	Leu	Arg	Arg	Val	Thr	Gly	Trp	Lys	Glu	Gln	Val
130					135					140					
Val	Asn	Gly	Asp	Val	Gly	Ala	Val	Ser	Glu	Pro	Pro	Cys	Leu	Pro	Lys
145				150					155					160	

```
Glu Pro Ala Pro Pro Ser Pro Ala Ser Leu Trp Ala Val Thr Leu Pro
                165                 170                 175

Thr Pro Pro Gln Ser Pro Ile His Pro Gly Thr Trp Thr Pro Arg Phe
            180                 185                 190

Ser Val Ile Pro Trp Ser Ser Trp Ser Leu Ser Trp Phe Gly Gln Ser
        195                 200                 205

Ser Gly Gln His Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys
    210                 215                 220

Pro Pro Gln Arg Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg
225                 230                 235                 240

Ser Trp Thr Cys Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala
                245                 250                 255

Cys Arg Arg Cys Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly
            260                 265                 270

Pro Leu Ser Arg Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro
        275                 280                 285

Leu Gly Ser Arg Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser
    290                 295                 300

Ser Ser Ser Gly Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys
305                 310                 315                 320

Gln Trp Arg Gly Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu
                325                 330                 335

Ser Leu Pro Arg Val
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<210> 1813
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<400> 1813
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1   5   10   15

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
            20   25   30

Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
        35   40   45

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
    50   55   60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
65   70   75   80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala
                85   90   95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
            100   105   110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
        115   120   125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
    130   135   140

Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys

145 150 155 160

Glu Pro Ala Pro Pro Ser Pro Ala Ser Leu Trp Ala Val Thr Leu Pro
165 170 175

Thr Pro Pro Gln Ser Pro Ile His Pro Gly Thr Trp Thr Pro Arg Phe
180 185 190

Ser Val Ile Pro Trp Ser Ser Trp Ser Leu Ser Trp Phe Gly Gln Ser
195 200 205

Ser Gly Gln His Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys
210 215 220

Pro Pro Gln Arg Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg
225 230 235 240

Ser Trp Thr Cys Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala
245 250 255

Cys Arg Arg Cys Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly
260 265 270

Pro Leu Ser Arg Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro
275 280 285

Leu Gly Ser Arg Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser
290 295 300

Ser Ser Ser Gly Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys
305 310 315 320

Gln Trp Arg Gly Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu
325 330 335

Ser Leu Pro Arg Val
340

<210> 1814
<211> 269
<212> PRT
<213> Homo sapiens

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<400> 1814

```
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1               5                  10                  15

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
            20                  25                  30

Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
        35                  40                  45

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
    50                  55                  60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
65                  70                  75                  80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala
                85                  90                  95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
            100                 105                 110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
        115                 120                 125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
    130                 135                 140

Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys
145                 150                 155                 160
```

```
Glu Pro Ala Pro Pro Ser Pro Glu Ser His Ser Pro Arg Asp Leu Asp
                165                 170                 175

Ser Glu Val Phe Cys Asp Ser Leu Glu Gln Leu Glu Pro Glu Leu Val
            180                 185                 190

Trp Thr Glu Gln Arg Ala Ala Ser Gly Gly Lys Arg Asp Pro Arg Asn
        195                 200                 205

Ser Pro Val Pro Pro Thr Lys Lys Glu Ala Ala Ala Gln Ala Gln Cys
    210                 215                 220

Ser Ala Met Ala Pro Trp Ala Pro Gly Ala Arg Ala Ala Leu Leu Pro
225                 230                 235                 240

Pro Val Ala Leu Arg Arg Pro Val Ala Leu Pro Asn Val Ser Asp Pro
                245                 250                 255

Lys Glu Val Thr Val Ser Gly Gly Val Ser Ala Ala Asn
            260                 265


<210> 1815
<211> 38
<212> PRT
<213> Homo sapiens

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<400> 1815
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1               5                  10                  15
```

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Thr Pro
            20   25   30

Gly Thr Val Trp Ala Arg
        35

<210> 1816
<211> 268
<212> PRT
<213> Homo sapiens

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<400> 1816
Met Gly Thr Glu Lys Glu Ser Pro Glu Pro Asp Cys Gln Lys Gln Phe
1   5   10   15

Gln Ala Ala Val Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr
            20   25   30

Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
        35   40   45

Ala Thr Met Gly Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro
    50   55   60

Ile Gly Arg Tyr Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser
65   70   75   80

Arg Glu Glu Ala Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala

```
                85                  90                  95

Gln Lys Val Ile Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met
            100                 105                 110

Phe Gly Tyr Phe Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg
        115                 120                 125

Pro Pro Glu Thr Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val
    130                 135                 140

Val Asn Gly Asp Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys
145                 150                 155                 160

Glu Pro Ala Pro Pro Ser Pro Glu Ser His Ser Pro Arg Asp Leu Asp
                165                 170                 175

Ser Glu Val Phe Cys Asp Ser Leu Glu Gln Leu Glu Pro Glu Leu Ser
            180                 185                 190

Ser Gly Gln His Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys
        195                 200                 205

Pro Pro Gln Arg Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg
    210                 215                 220

Ser Trp Thr Cys Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala
225                 230                 235                 240

Cys Arg Arg Cys Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly
                245                 250                 255

Pro Leu Ser Ser Leu Thr Leu Ser Val Arg Leu Glu
            260                 265


<210> 1817
<211> 534
<212> PRT
<213> Homo sapiens

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domain containing 5; "

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<223> /note="Uniprot ID: Q5T8D3; "

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<223> /note="ENSP ID: ENSP00000365049"

<400> 1817

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Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys
1               5                   10                  15


Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu
            20                  25                  30


Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
        35                  40                  45


Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr
    50                  55                  60


Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
65                  70                  75                  80


Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
                85                  90                  95


Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
            100                 105                 110


Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
        115                 120                 125


Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
    130                 135                 140


Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
145                 150                 155                 160
```

```
Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn
                165                 170                 175

Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu
            180                 185                 190

Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu
        195                 200                 205

Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys
    210                 215                 220

Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp
225                 230                 235                 240

Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser
                245                 250                 255

Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn
            260                 265                 270

Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp Ile Asn
        275                 280                 285

Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr Ser Asp
    290                 295                 300

Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln Glu
305                 310                 315                 320

Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr
                325                 330                 335

Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg Glu
            340                 345                 350

Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln Val
        355                 360                 365

Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp Gly
    370                 375                 380
```

```
Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu Thr
385                 390                 395                 400

Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln His
                405                 410                 415

Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp Gly
            420                 425                 430

Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln
        435                 440                 445

Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn Val Leu
    450                 455                 460

Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys Ser
465                 470                 475                 480

Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro
                485                 490                 495

Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala Ile
            500                 505                 510

Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln Arg
        515                 520                 525

Arg Arg Arg Lys Leu Asn
    530


<210> 1818
<211> 523
<212> PRT
<213> Homo sapiens

<220>
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<400> 1818

```
Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys
1               5                  10                  15

Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu
            20                  25                  30

Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
        35                  40                  45

Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr
    50                  55                  60

Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
65                  70                  75                  80

Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
                85                  90                  95

Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
            100                 105                 110

Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
        115                 120                 125

Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
    130                 135                 140

Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
145                 150                 155                 160

Ser Asp Leu Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val
                165                 170                 175

Asn Gly Lys Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu
            180                 185                 190

Glu Ala Gln Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys
        195                 200                 205
```

```
Lys Met Met Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val
    210                 215                 220

Thr Asn Gly Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp
225                 230                 235                 240

Ile His Ala Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys
                245                 250                 255

Pro Ile Asp Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile
            260                 265                 270

His Gln Asp Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln
        275                 280                 285

His Leu Thr Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu
    290                 295                 300

Gln Phe Gly Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly
305                 310                 315                 320

Pro Phe Gln Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn
                325                 330                 335

Ser Gly Phe Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile
            340                 345                 350

Gly Asn Met Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His
        355                 360                 365

Gly Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys
    370                 375                 380

Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly
385                 390                 395                 400

His Arg Met Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly
                405                 410                 415

Ser Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly
            420                 425                 430
```

```
Ser Leu Asn Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp
        435                 440                 445

Met Gln Asn Val Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala
    450                 455                 460

Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro
465                 470                 475                 480

Thr Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val
                485                 490                 495

Leu Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr
            500                 505                 510

Leu Tyr Tyr Gln Arg Arg Arg Arg Lys Leu Asn
        515                 520


<210> 1819
<211> 416
<212> PRT
<213> Homo sapiens

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<400> 1819
Met Thr Lys Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys
1               5                   10                  15
```

```
Ile Ile Glu Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg
            20                  25                  30

Val Ile Gly Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg
        35                  40                  45

Ser Ser Asp Ile Thr Ser Asp Leu Gly Asn Val Leu Thr Ser Thr Pro
    50                  55                  60

Asn Ala Lys Thr Val Asn Gly Lys Ala Glu Ser Ser Asp Ser Gly Ala
65                  70                  75                  80

Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu Val Lys Gly Ala Glu Gln
                85                  90                  95

Ser Asp Asn Asp Lys Lys Met Met Lys Lys Ser Ala Asp His Lys Asn
            100                 105                 110

Leu Glu Val Ile Val Thr Asn Gly Tyr Asp Lys Asp Gly Phe Val Gln
        115                 120                 125

Asp Ile Gln Asn Asp Ile His Ala Ser Ser Ser Leu Asn Gly Arg Ser
    130                 135                 140

Thr Glu Glu Val Lys Pro Ile Asp Glu Asn Leu Gly Gln Thr Gly Lys
145                 150                 155                 160

Ser Ala Val Cys Ile His Gln Asp Ile Asn Asp Asp His Val Glu Asp
                165                 170                 175

Val Thr Gly Ile Gln His Leu Thr Ser Asp Ser Asp Ser Glu Val Tyr
            180                 185                 190

Cys Asp Ser Met Glu Gln Phe Gly Gln Glu Glu Ser Leu Asp Ser Phe
        195                 200                 205

Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr Leu Gly Gly His Ser Ser
    210                 215                 220

Gln Pro Met Glu Asn Ser Gly Phe Arg Glu Asp Ile Gln Val Pro Pro
225                 230                 235                 240

Gly Asn Gly Asn Ile Gly Asn Met Gln Val Val Ala Val Glu Gly Lys
```

```
                245                 250                 255

Gly Glu Val Lys His Gly Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala
            260                 265                 270

Pro His Arg Glu Lys Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val
        275                 280                 285

Arg Arg Gly Arg Gly His Arg Met Gln His Leu Ser Glu Gly Thr Lys
    290                 295                 300

Gly Arg Gln Val Gly Ser Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp
305                 310                 315                 320

Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln Ile Ala Leu Val Leu Met
                325                 330                 335

Arg Leu Gln Glu Asp Met Gln Asn Val Leu Gln Arg Leu Gln Lys Leu
            340                 345                 350

Glu Thr Leu Thr Ala Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln
        355                 360                 365

Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu
    370                 375                 380

Met Ser Pro Gly Val Leu Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala
385                 390                 395                 400

Gln Trp Leu Val Tyr Leu Tyr Tyr Gln Arg Arg Arg Arg Lys Leu Asn
                405                 410                 415


<210> 1820
<211> 490
<212> PRT
<213> Homo sapiens

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<223> /note="ENSP ID: ENSP00000365070"

<400> 1820

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Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala Val
1               5                  10                  15

Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr Asn
            20                  25                  30

Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu Gly
        35                  40                  45

Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr
    50                  55                  60

Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu Ala
65                  70                  75                  80

Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met Pro
                85                  90                  95

Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe Tyr
            100                 105                 110

Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr Ser
        115                 120                 125

Asp Leu Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn
    130                 135                 140

Gly Lys Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu
145                 150                 155                 160

Ala Gln Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys
                165                 170                 175
```

```
Met Met Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr
            180                 185                 190

Asn Gly Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile
        195                 200                 205

His Ala Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro
    210                 215                 220

Ile Asp Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His
225                 230                 235                 240

Gln Asp Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His
                245                 250                 255

Leu Thr Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln
            260                 265                 270

Phe Gly Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro
        275                 280                 285

Phe Gln Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser
    290                 295                 300

Gly Phe Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly
305                 310                 315                 320

Asn Met Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly
                325                 330                 335

Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg
            340                 345                 350

Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His
        355                 360                 365

Arg Met Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser
    370                 375                 380

Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser
385                 390                 395                 400
```

```
Leu Asn Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met
                405                 410                 415

Gln Asn Val Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu
            420                 425                 430

Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr
        435                 440                 445

Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu
    450                 455                 460

Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu
465                 470                 475                 480

Tyr Tyr Gln Arg Arg Arg Arg Lys Leu Asn
                485                 490


<210> 1821
<211> 525
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID:  Q5T8D3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000379568"

<400> 1821
Met Leu Phe Leu Ser Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys
1               5                   10                  15

Cys Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp
```

```
            20                  25                  30

Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu
        35                  40                  45

Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln
    50                  55                  60

Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala
65                  70                  75                  80

Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile
                85                  90                  95

Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys
            100                 105                 110

Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu
        115                 120                 125

Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly
    130                 135                 140

Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp
145                 150                 155                 160

Ile Thr Ser Asp Leu Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys
                165                 170                 175

Thr Val Asn Gly Lys Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu
            180                 185                 190

Glu Glu Glu Ala Gln Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn
        195                 200                 205

Asp Lys Lys Met Met Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val
    210                 215                 220

Ile Val Thr Asn Gly Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln
225                 230                 235                 240

Asn Asp Ile His Ala Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu
                245                 250                 255
```

```
Val Lys Pro Ile Asp Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val
            260                 265                 270

Cys Ile His Gln Asp Ile Asn Asp Asp His Val Glu Asp Val Thr Gly
        275                 280                 285

Ile Gln His Leu Thr Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser
    290                 295                 300

Met Glu Gln Phe Gly Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn
305                 310                 315                 320

Asn Gly Pro Phe Gln Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met
                325                 330                 335

Glu Asn Ser Gly Phe Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly
            340                 345                 350

Asn Ile Gly Asn Met Gln Val Val Ala Val Glu Gly Lys Gly Glu Val
        355                 360                 365

Lys His Gly Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg
    370                 375                 380

Glu Lys Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly
385                 390                 395                 400

Arg Gly His Arg Met Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln
                405                 410                 415

Val Gly Ser Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser
            420                 425                 430

Arg Gly Ser Leu Asn Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln
        435                 440                 445

Glu Asp Met Gln Asn Val Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu
    450                 455                 460

Thr Ala Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro
465                 470                 475                 480
```

```
Gln Pro Thr Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro
                485                 490                 495


Gly Val Leu Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu
            500                 505                 510


Val Tyr Leu Tyr Tyr Gln Arg Arg Arg Arg Lys Leu Asn
        515                 520                 525


<210> 1822
<211> 251
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 484; "

<220>
<221> source
<223> /note="Gene Symbol: ACBD5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA binding
      domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393398"

<400> 1822
Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala Val
1               5                   10                  15


Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr Asn
            20                  25                  30


Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu Gly
        35                  40                  45


Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr
    50                  55                  60


Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu Ala
65                  70                  75                  80
```

```
Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met Pro
                85                  90                  95

Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe Tyr
            100                 105                 110

Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr Ser
        115                 120                 125

Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn Val
    130                 135                 140

Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu Ser
145                 150                 155                 160

Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu Val
                165                 170                 175

Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys Ser
            180                 185                 190

Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp Lys
        195                 200                 205

Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser Ser
    210                 215                 220

Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn Leu
225                 230                 235                 240

Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His
                245                 250
```

<210> 1823
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 484; "

<220>
<221> source
<223> /note="Gene Symbol: ACBD5; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA binding
domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401591"

<400> 1823
Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala Val
1 5 10 15

Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr Asn
20 25 30

Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu Gly
35 40 45

Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr
50 55 60

Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu Ala
65 70 75 80

Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met Pro
85 90 95

Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe Tyr
100 105 110

Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr Ser
115 120 125

Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn Val
130 135 140

Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu Ser
145 150 155 160

Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu Val
165 170 175

Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys Ser
180 185 190

```
Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp Lys
        195                 200                 205

Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser Ser
    210                 215                 220

Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn Leu
225                 230                 235                 240

Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln
                245                 250


<210> 1824
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 484; "

<220>
<221> source
<223> /note="Gene Symbol: ACBD5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA binding
      domain containing 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483256"

<400> 1824
Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys
1               5                   10                  15

Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu
            20                  25                  30

Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
        35                  40                  45

Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Met Leu Gly Val His
    50                  55                  60
```

Trp Val Ile
65

<210> 1825
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 485; "

<220>
<221> source
<223> /note="Gene Symbol: ACBD6; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA binding
domain containing 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BR61; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356567"

<400> 1825
Met Ala Ser Ser Phe Leu Pro Ala Gly Ala Ile Thr Gly Asp Ser Gly
1 5 10 15

Gly Glu Leu Ser Ser Gly Asp Asp Ser Gly Glu Val Glu Phe Pro His
20 25 30

Ser Pro Glu Ile Glu Glu Thr Ser Cys Leu Ala Glu Leu Phe Glu Lys
35 40 45

Ala Ala Ala His Leu Gln Gly Leu Ile Gln Val Ala Ser Arg Glu Gln
50 55 60

Leu Leu Tyr Leu Tyr Ala Arg Tyr Lys Gln Val Lys Val Gly Asn Cys
65 70 75 80

Asn Thr Pro Lys Pro Ser Phe Phe Asp Phe Glu Gly Lys Gln Lys Trp
85 90 95

```
Glu Ala Trp Lys Ala Leu Gly Asp Ser Ser Pro Ser Gln Ala Met Gln
            100                 105                 110

Glu Tyr Ile Ala Val Val Lys Lys Leu Asp Pro Gly Trp Asn Pro Gln
        115                 120                 125

Ile Pro Glu Lys Lys Gly Lys Glu Ala Asn Thr Gly Phe Gly Gly Pro
    130                 135                 140

Val Ile Ser Ser Leu Tyr His Glu Glu Thr Ile Arg Glu Glu Asp Lys
145                 150                 155                 160

Asn Ile Phe Asp Tyr Cys Arg Glu Asn Asn Ile Asp His Ile Thr Lys
                165                 170                 175

Ala Ile Lys Ser Lys Asn Val Asp Val Asn Val Lys Asp Glu Glu Gly
            180                 185                 190

Arg Ala Leu Leu His Trp Ala Cys Asp Arg Gly His Lys Glu Leu Val
        195                 200                 205

Thr Val Leu Leu Gln His Arg Ala Asp Ile Asn Cys Gln Asp Asn Glu
    210                 215                 220

Gly Gln Thr Ala Leu His Tyr Ala Ser Ala Cys Glu Phe Leu Asp Ile
225                 230                 235                 240

Val Glu Leu Leu Leu Gln Ser Gly Ala Asp Pro Thr Leu Arg Asp Gln
                245                 250                 255

Asp Gly Cys Leu Pro Glu Glu Val Thr Gly Cys Lys Thr Val Ser Leu
            260                 265                 270

Val Leu Gln Arg His Thr Thr Gly Lys Ala
        275                 280


<210> 1826
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 486; "
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<220>
<221> source
<223> /note="Gene Symbol: ACBD7; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA binding
domain containing 7; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N6N7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000367453"

<400> 1826
Met Ala Leu Gln Ala Asp Phe Asp Arg Ala Ala Glu Asp Val Arg Lys
1   5   10   15

Leu Lys Ala Arg Pro Asp Asp Gly Glu Leu Lys Glu Leu Tyr Gly Leu
            20   25   30

Tyr Lys Gln Ala Ile Val Gly Asp Ile Asn Ile Ala Cys Pro Gly Met
        35   40   45

Leu Asp Leu Lys Gly Lys Ala Lys Trp Glu Ala Trp Asn Leu Lys Lys
    50   55   60

Gly Leu Ser Thr Glu Asp Ala Thr Ser Ala Tyr Ile Ser Lys Ala Lys
65   70   75   80

Glu Leu Ile Glu Lys Tyr Gly Ile
                85

<210> 1827
<211> 1059
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 487; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD10; "

<220>

<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 10; "

<220>
<221> source
<223> /note="Uniprot ID: Q6JQN1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000325137"

<400> 1827

```
Met Cys Val Arg Ser Cys Phe Gln Ser Pro Arg Leu Gln Trp Val Trp
1               5                  10                  15

Arg Thr Ala Phe Leu Lys His Thr Gln Arg Arg His Gln Gly Ser His
            20                  25                  30

Arg Trp Thr His Leu Gly Gly Ser Thr Tyr Arg Ala Val Ile Phe Asp
        35                  40                  45

Met Gly Gly Val Leu Ile Pro Ser Pro Gly Arg Val Ala Ala Glu Trp
    50                  55                  60

Glu Val Gln Asn Arg Ile Pro Ser Gly Thr Ile Leu Lys Ala Leu Met
65                  70                  75                  80

Glu Gly Gly Glu Asn Gly Pro Trp Met Arg Phe Met Arg Ala Glu Ile
                85                  90                  95

Thr Ala Glu Gly Phe Leu Arg Glu Phe Gly Arg Leu Cys Ser Glu Met
            100                 105                 110

Leu Lys Thr Ser Val Pro Val Asp Ser Phe Phe Ser Leu Leu Thr Ser
        115                 120                 125

Glu Arg Val Ala Lys Gln Phe Pro Val Met Thr Glu Ala Ile Thr Gln
    130                 135                 140

Ile Arg Ala Lys Gly Leu Gln Thr Ala Val Leu Ser Asn Asn Phe Tyr
145                 150                 155                 160

Leu Pro Asn Gln Lys Ser Phe Leu Pro Leu Asp Arg Lys Gln Phe Asp
                165                 170                 175
```

```
Val Ile Val Glu Ser Cys Met Glu Gly Ile Cys Lys Pro Asp Pro Arg
            180                 185                 190

Ile Tyr Lys Leu Cys Leu Glu Gln Leu Gly Leu Gln Pro Ser Glu Ser
        195                 200                 205

Ile Phe Leu Asp Asp Leu Gly Thr Asn Leu Lys Glu Ala Ala Arg Leu
    210                 215                 220

Gly Ile His Thr Ile Lys Val Asn Asp Pro Glu Thr Ala Val Lys Glu
225                 230                 235                 240

Leu Glu Ala Leu Leu Gly Phe Thr Leu Arg Val Gly Val Pro Asn Thr
                245                 250                 255

Arg Pro Val Lys Lys Thr Met Glu Ile Pro Lys Asp Ser Leu Gln Lys
            260                 265                 270

Tyr Leu Lys Asp Leu Leu Gly Ile Gln Thr Thr Gly Pro Leu Glu Leu
        275                 280                 285

Leu Gln Phe Asp His Gly Gln Ser Asn Pro Thr Tyr Tyr Ile Arg Leu
    290                 295                 300

Ala Asn Arg Asp Leu Val Leu Arg Lys Lys Pro Pro Gly Thr Leu Leu
305                 310                 315                 320

Pro Ser Ala His Ala Ile Glu Arg Glu Phe Arg Ile Met Lys Ala Leu
                325                 330                 335

Ala Asn Ala Gly Val Pro Val Pro Asn Val Leu Asp Leu Cys Glu Asp
            340                 345                 350

Ser Ser Val Ile Gly Thr Pro Phe Tyr Val Met Glu Tyr Cys Pro Gly
        355                 360                 365

Leu Ile Tyr Lys Asp Pro Ser Leu Pro Gly Leu Glu Pro Ser His Arg
    370                 375                 380

Arg Ala Ile Tyr Thr Ala Met Asn Thr Val Leu Cys Lys Ile His Ser
385                 390                 395                 400
```

```
Val Asp Leu Gln Ala Val Gly Leu Glu Asp Tyr Gly Lys Gln Gly Asp
                405                 410                 415

Tyr Ile Pro Arg Gln Val Arg Thr Trp Val Lys Gln Tyr Arg Ala Ser
            420                 425                 430

Glu Thr Ser Thr Ile Pro Ala Met Glu Arg Leu Ile Glu Trp Leu Pro
        435                 440                 445

Leu His Leu Pro Arg Gln Gln Arg Thr Thr Val Val His Gly Asp Phe
    450                 455                 460

Arg Leu Asp Asn Leu Val Phe His Pro Glu Glu Pro Glu Val Leu Ala
465                 470                 475                 480

Val Leu Asp Trp Glu Leu Ser Thr Leu Gly Asp Pro Leu Ala Asp Val
                485                 490                 495

Ala Tyr Ser Cys Leu Ala His Tyr Leu Pro Ser Ser Phe Pro Val Leu
            500                 505                 510

Arg Gly Ile Asn Asp Cys Asp Leu Thr Gln Leu Gly Ile Pro Ala Ala
        515                 520                 525

Glu Glu Tyr Phe Arg Met Tyr Cys Leu Gln Met Gly Leu Pro Pro Thr
    530                 535                 540

Glu Asn Trp Asn Phe Tyr Met Ala Phe Ser Phe Phe Arg Val Ala Ala
545                 550                 555                 560

Ile Leu Gln Gly Val Tyr Lys Arg Ser Leu Thr Gly Gln Ala Ser Ser
                565                 570                 575

Thr Tyr Ala Glu Gln Thr Gly Lys Leu Thr Glu Phe Val Ser Asn Leu
            580                 585                 590

Ala Trp Asp Phe Ala Val Lys Glu Gly Phe Arg Val Phe Lys Glu Met
        595                 600                 605

Pro Phe Thr Asn Pro Leu Thr Arg Ser Tyr His Thr Trp Ala Arg Pro
    610                 615                 620

Gln Ser Gln Trp Cys Pro Thr Gly Ser Arg Ser Tyr Ser Ser Val Pro
```

625 630 635 640

Glu Ala Ser Pro Ala His Thr Ser Arg Gly Gly Leu Val Ile Ser Pro
645 650 655

Glu Ser Leu Ser Pro Pro Val Arg Glu Leu Tyr His Arg Leu Lys His
660 665 670

Phe Met Glu Gln Arg Val Tyr Pro Ala Glu Pro Glu Leu Gln Ser His
675 680 685

Gln Ala Ser Ala Ala Arg Trp Ser Pro Ser Pro Leu Ile Glu Asp Leu
690 695 700

Lys Glu Lys Ala Lys Ala Glu Gly Leu Trp Asn Leu Phe Leu Pro Leu
705 710 715 720

Glu Ala Asp Pro Glu Lys Lys Tyr Gly Ala Gly Leu Thr Asn Val Glu
725 730 735

Tyr Ala His Leu Cys Glu Leu Met Gly Thr Ser Leu Tyr Ala Pro Glu
740 745 750

Val Cys Asn Cys Ser Ala Pro Asp Thr Gly Asn Met Glu Leu Leu Val
755 760 765

Arg Tyr Gly Thr Glu Ala Gln Lys Ala Arg Trp Leu Ile Pro Leu Leu
770 775 780

Glu Gly Lys Ala Arg Ser Cys Phe Ala Met Thr Glu Pro Gln Val Ala
785 790 795 800

Ser Ser Asp Ala Thr Asn Ile Glu Ala Ser Ile Arg Glu Glu Asp Ser
805 810 815

Phe Tyr Val Ile Asn Gly His Lys Trp Trp Ile Thr Gly Ile Leu Asp
820 825 830

Pro Arg Cys Gln Leu Cys Val Phe Met Gly Lys Thr Asp Pro His Ala
835 840 845

Pro Arg His Arg Gln Gln Ser Val Leu Leu Val Pro Met Asp Thr Pro
850 855 860

```
Gly Ile Lys Ile Ile Arg Pro Leu Thr Val Tyr Gly Leu Glu Asp Ala
865                 870                 875                 880

Pro Gly Gly His Gly Glu Val Arg Phe Glu His Val Arg Val Pro Lys
                885                 890                 895

Glu Asn Met Val Leu Gly Pro Gly Arg Gly Phe Glu Ile Ala Gln Gly
            900                 905                 910

Arg Leu Gly Pro Gly Arg Ile His His Cys Met Arg Leu Ile Gly Phe
        915                 920                 925

Ser Glu Arg Ala Leu Ala Leu Met Lys Ala Arg Val Lys Ser Arg Leu
    930                 935                 940

Ala Phe Gly Lys Pro Leu Val Glu Gln Gly Thr Val Leu Ala Asp Ile
945                 950                 955                 960

Ala Gln Ser Arg Val Glu Ile Glu Gln Ala Arg Leu Leu Val Leu Arg
                965                 970                 975

Ala Ala His Leu Met Asp Leu Ala Gly Asn Lys Ala Ala Ala Leu Asp
            980                 985                 990

Ile Ala Met Ile Lys Met Val Ala  Pro Ser Met Ala Ser  Arg Val
Ile
        995                 1000                1005

Asp Arg  Ala Ile Gln Ala Phe  Gly Ala Ala Gly Leu  Ser Ser Asp
    1010                1015                1020

Tyr Pro  Leu Ala Gln Phe Phe  Thr Trp Ala Arg Ala  Leu Arg Phe
    1025                1030                1035

Ala Asp  Gly Pro Asp Glu Val  His Arg Ala Thr Val  Ala Lys Leu
    1040                1045                1050

Glu Leu  Lys His Arg Ile
    1055

<210> 1828
<211> 1090
```

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 487; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD10; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 10; "

<220>
<221> source
<223> /note="Uniprot ID: Q6JQN1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389813"

<400> 1828

Met	Cys	Val	Arg	Ser	Cys	Phe	Gln	Ser	Pro	Arg	Leu	Gln	Trp	Val	Trp
1				5				10						15	
Arg	Thr	Ala	Phe	Leu	Lys	His	Thr	Gln	Arg	Arg	His	Gln	Gly	Ser	His
			20					25					30		
Arg	Trp	Thr	His	Leu	Gly	Gly	Ser	Thr	Tyr	Arg	Ala	Val	Ile	Phe	Asp
		35					40					45			
Met	Gly	Gly	Val	Leu	Ile	Pro	Ser	Pro	Gly	Arg	Val	Ala	Ala	Glu	Trp
	50					55					60				
Glu	Val	Gln	Asn	Arg	Ile	Pro	Ser	Gly	Thr	Ile	Leu	Lys	Ala	Leu	Met
65					70					75					80
Glu	Gly	Gly	Glu	Asn	Gly	Pro	Trp	Met	Arg	Phe	Met	Arg	Ala	Glu	Ile
				85					90					95	
Thr	Ala	Glu	Gly	Phe	Leu	Arg	Glu	Phe	Gly	Arg	Leu	Cys	Ser	Glu	Met
			100					105					110		
Leu	Lys	Thr	Ser	Val	Pro	Val	Asp	Ser	Phe	Phe	Ser	Leu	Leu	Thr	Ser
		115					120					125			

```
Glu Arg Val Ala Lys Gln Phe Pro Val Met Thr Glu Ala Ile Thr Gln
    130                 135                 140

Ile Arg Ala Lys Gly Leu Gln Thr Ala Val Leu Ser Asn Asn Phe Tyr
145                 150                 155                 160

Leu Pro Asn Gln Lys Ser Phe Leu Pro Leu Asp Arg Lys Gln Phe Asp
                165                 170                 175

Val Ile Val Glu Ser Cys Met Glu Gly Ile Cys Lys Pro Asp Pro Arg
            180                 185                 190

Ile Tyr Lys Leu Cys Leu Glu Gln Leu Gly Leu Gln Pro Ser Glu Ser
        195                 200                 205

Ile Phe Leu Asp Asp Leu Gly Thr Asn Leu Lys Glu Ala Ala Arg Leu
    210                 215                 220

Gly Ile His Thr Ile Lys Arg Gln Gly Phe Ala Val Leu Pro Lys Leu
225                 230                 235                 240

Val Ser Asn Ser Trp Ala Gln Ala Ile Tyr Pro Pro Tyr Pro Pro Lys
                245                 250                 255

Val Val Arg Leu Gln Val Asn Asp Pro Glu Thr Ala Val Lys Glu Leu
            260                 265                 270

Glu Ala Leu Leu Gly Phe Thr Leu Arg Val Gly Val Pro Asn Thr Arg
        275                 280                 285

Pro Val Lys Lys Thr Met Glu Ile Pro Lys Asp Ser Leu Gln Lys Tyr
    290                 295                 300

Leu Lys Asp Leu Leu Gly Ile Gln Thr Thr Gly Pro Leu Glu Leu Leu
305                 310                 315                 320

Gln Phe Asp His Gly Gln Ser Asn Pro Thr Tyr Tyr Ile Arg Leu Ala
                325                 330                 335

Asn Arg Asp Leu Val Leu Arg Lys Lys Pro Pro Gly Thr Leu Leu Pro
            340                 345                 350
```

```
Ser Ala His Ala Ile Glu Arg Glu Phe Arg Ile Met Lys Ala Leu Ala
        355                 360                 365

Asn Ala Gly Val Pro Val Pro Asn Val Leu Asp Leu Cys Glu Asp Ser
    370                 375                 380

Ser Val Ile Gly Thr Pro Phe Tyr Val Met Glu Tyr Cys Pro Gly Leu
385                 390                 395                 400

Ile Tyr Lys Asp Pro Ser Leu Pro Gly Leu Glu Pro Ser His Arg Arg
                405                 410                 415

Ala Ile Tyr Thr Ala Met Asn Thr Val Leu Cys Lys Ile His Ser Val
            420                 425                 430

Asp Leu Gln Ala Val Gly Leu Glu Asp Tyr Gly Lys Gln Gly Asp Tyr
        435                 440                 445

Ile Pro Arg Gln Val Arg Thr Trp Val Lys Gln Tyr Arg Ala Ser Glu
    450                 455                 460

Thr Ser Thr Ile Pro Ala Met Glu Arg Leu Ile Glu Trp Leu Pro Leu
465                 470                 475                 480

His Leu Pro Arg Gln Gln Arg Thr Thr Val Val His Gly Asp Phe Arg
                485                 490                 495

Leu Asp Asn Leu Val Phe His Pro Glu Glu Pro Glu Val Leu Ala Val
            500                 505                 510

Leu Asp Trp Glu Leu Ser Thr Leu Gly Asp Pro Leu Ala Asp Val Ala
        515                 520                 525

Tyr Ser Cys Leu Ala His Tyr Leu Pro Ser Ser Phe Pro Val Leu Arg
    530                 535                 540

Gly Ile Asn Asp Cys Asp Leu Thr Gln Leu Gly Ile Pro Ala Ala Glu
545                 550                 555                 560

Glu Tyr Phe Arg Met Tyr Cys Leu Gln Met Gly Leu Pro Pro Thr Glu
                565                 570                 575

Asn Trp Asn Phe Tyr Met Ala Phe Ser Phe Phe Arg Val Ala Ala Ile
```

580 585 590

Leu Gln Gly Val Tyr Lys Arg Ser Leu Thr Gly Gln Ala Ser Ser Thr
595 600 605

Tyr Ala Glu Gln Thr Gly Lys Leu Thr Glu Phe Val Ser Asn Leu Ala
610 615 620

Trp Asp Phe Ala Val Lys Glu Gly Phe Arg Val Phe Lys Glu Met Pro
625 630 635 640

Phe Thr Asn Pro Leu Thr Arg Ser Tyr His Thr Trp Ala Arg Pro Gln
645 650 655

Ser Gln Trp Cys Pro Thr Gly Ser Arg Ser Tyr Ser Ser Val Pro Glu
660 665 670

Ala Ser Pro Ala His Thr Ser Arg Gly Gly Leu Val Ile Ser Pro Glu
675 680 685

Ser Leu Ser Pro Pro Val Arg Glu Leu Tyr His Arg Leu Lys His Phe
690 695 700

Met Glu Gln Arg Val Tyr Pro Ala Glu Pro Glu Leu Gln Ser His Gln
705 710 715 720

Ala Ser Ala Ala Arg Trp Ser Pro Ser Pro Leu Ile Glu Asp Leu Lys
725 730 735

Glu Lys Ala Lys Ala Glu Gly Leu Trp Asn Leu Phe Leu Pro Leu Glu
740 745 750

Ala Asp Pro Glu Lys Lys Tyr Gly Ala Gly Leu Thr Asn Val Glu Tyr
755 760 765

Ala His Leu Cys Glu Leu Met Gly Thr Ser Leu Tyr Ala Pro Glu Val
770 775 780

Cys Asn Cys Ser Ala Pro Asp Thr Gly Asn Met Glu Leu Leu Val Arg
785 790 795 800

Tyr Gly Thr Glu Ala Gln Lys Ala Arg Trp Leu Ile Pro Leu Leu Glu
805 810 815

```
Gly Lys Ala Arg Ser Cys Phe Ala Met Thr Glu Pro Gln Val Ala Ser
            820                 825                 830

Ser Asp Ala Thr Asn Ile Glu Ala Ser Ile Arg Glu Glu Asp Ser Phe
        835                 840                 845

Tyr Val Ile Asn Gly His Lys Trp Trp Ile Thr Gly Ile Leu Asp Pro
    850                 855                 860

Arg Cys Gln Leu Cys Val Phe Met Gly Lys Thr Asp Pro His Ala Pro
865                 870                 875                 880

Arg His Arg Gln Gln Ser Val Leu Leu Val Pro Met Asp Thr Pro Gly
                885                 890                 895

Ile Lys Ile Ile Arg Pro Leu Thr Val Tyr Gly Leu Glu Asp Ala Pro
            900                 905                 910

Gly Gly His Gly Glu Val Arg Phe Glu His Val Arg Val Pro Lys Glu
        915                 920                 925

Asn Met Val Leu Gly Pro Gly Arg Gly Phe Glu Ile Ala Gln Gly Arg
    930                 935                 940

Leu Gly Pro Gly Arg Ile His His Cys Met Arg Leu Ile Gly Phe Ser
945                 950                 955                 960

Glu Arg Ala Leu Ala Leu Met Lys Ala Arg Val Lys Ser Arg Leu Ala
                965                 970                 975

Phe Gly Lys Pro Leu Val Glu Gln Gly Thr Val Leu Ala Asp Ile Ala
            980                 985                 990

Gln Ser Arg Val Glu Ile Glu Gln  Ala Arg Leu Leu Val  Leu Arg
Ala
        995                 1000                1005

Ala His  Leu Met Asp Leu Ala  Gly Asn Lys Ala Ala  Ala Leu Asp
    1010                1015                1020

Ile Ala  Met Ile Lys Met Val  Ala Pro Ser Met Ala  Ser Arg Val
    1025                1030                1035
```

```
Ile Asp  Arg Ala Ile Gln Ala  Phe Gly Ala Ala Gly  Leu Ser Ser
    1040                1045                1050

Asp Tyr  Pro Leu Ala Gln Phe  Phe Thr Trp Ala Arg  Ala Leu Arg
    1055                1060                1065

Phe Ala  Asp Gly Pro Asp Glu  Val His Arg Ala Thr  Val Ala Lys
    1070                1075                1080

Leu Glu  Leu Lys His Arg Ile
    1085                1090


<210> 1829
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 487; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD10; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421527"

<400> 1829
Met Cys Val Arg Ser Cys Phe Gln Ser Pro Arg Leu Gln Trp Val Trp
1               5                  10                  15

Arg Thr Ala Phe Leu Lys His Thr Gln Arg Arg His Gln Gly Ser His
            20                  25                  30

Arg Trp Thr His Leu Gly Gly Ser Thr Tyr Arg Ala Val Ile Phe Asp
        35                  40                  45

Met Gly Gly Val Leu Ile Pro Ser Pro Gly Arg Val Ala Ala Glu Trp
    50                  55                  60
```

```
Glu Val Gln Asn Arg Ile Pro Ser Gly Thr Ile Leu Lys Ala Leu Met
65                  70                  75                  80


Glu Gly Gly Glu Asn Gly Pro Trp Met Arg Phe Met Arg Ala Glu Ile
                85                  90                  95


<210> 1830
<211> 278
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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      family, member 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446711"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1830
Xaa Glu Leu Glu Ala Leu Leu Gly Phe Thr Leu Arg Val Gly Val Pro
1               5                   10                  15


Asn Thr Arg Pro Val Lys Lys Thr Met Glu Ile Pro Lys Asp Ser Leu
            20                  25                  30


Gln Lys Tyr Leu Lys Asp Leu Leu Gly Ile Gln Thr Thr Gly Pro Leu
        35                  40                  45


Glu Leu Leu Gln Phe Asp His Gly Gln Ser Asn Pro Thr Tyr Tyr Ile
    50                  55                  60


Arg Leu Ala Asn Arg Asp Leu Val Leu Arg Lys Lys Pro Pro Gly Thr
65                  70                  75                  80
```

```
Leu Leu Pro Ser Ala His Ala Ile Glu Arg Glu Phe Arg Ile Met Lys
                85                  90                  95

Ala Leu Ala Asn Ala Gly Val Pro Val Pro Asn Val Leu Asp Leu Cys
            100                 105                 110

Glu Asp Ser Ser Val Ile Gly Thr Pro Phe Tyr Val Met Glu Tyr Cys
        115                 120                 125

Pro Gly Leu Ile Tyr Lys Asp Pro Ser Leu Pro Gly Leu Glu Pro Ser
    130                 135                 140

His Arg Arg Ala Ile Tyr Thr Ala Met Asn Thr Val Leu Cys Lys Ile
145                 150                 155                 160

His Ser Val Asp Leu Gln Ala Val Gly Leu Glu Asp Tyr Gly Lys Gln
                165                 170                 175

Gly Gln Ala Ser Ser Thr Tyr Ala Glu Gln Thr Gly Lys Leu Thr Glu
            180                 185                 190

Phe Val Ser Asn Leu Ala Trp Asp Phe Ala Val Lys Glu Gly Phe Arg
        195                 200                 205

Val Phe Lys Glu Met Pro Phe Thr Asn Pro Leu Thr Arg Ser Tyr His
    210                 215                 220

Thr Trp Ala Arg Pro Gln Ser Gln Trp Cys Pro Thr Gly Ser Arg Ser
225                 230                 235                 240

Tyr Ser Ser Val Pro Glu Ala Ser Pro Ala His Thr Ser Arg Gly Gly
                245                 250                 255

Leu Val Ile Ser Pro Glu Ser Leu Ser Pro Pro Val Arg Glu Leu Tyr
            260                 265                 270

His Arg Leu Lys His Phe
        275
```

<210> 1831
<211> 710
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Payload ID: 487; "

<220>
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<223> /note="Gene Symbol: ACAD10; "

<220>
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<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446959"

<400> 1831
Met Cys Val Arg Ser Cys Phe Gln Ser Pro Arg Leu Gln Trp Val Trp
1 5 10 15

Arg Thr Ala Phe Leu Lys His Thr Gln Arg Arg His Gln Gly Ser His
20 25 30

Arg Trp Thr His Leu Gly Gly Ser Thr Tyr Arg Ala Val Ile Phe Asp
35 40 45

Met Gly Gly Val Leu Ile Pro Ser Pro Gly Arg Val Ala Ala Glu Trp
50 55 60

Glu Val Gln Asn Arg Ile Pro Ser Gly Thr Ile Leu Lys Ala Leu Met
65 70 75 80

Glu Gly Gly Glu Asn Gly Pro Trp Met Arg Phe Met Arg Ala Glu Ile
85 90 95

Thr Ala Glu Gly Phe Leu Arg Glu Phe Gly Arg Leu Cys Ser Glu Met
100 105 110

Leu Lys Thr Ser Val Pro Val Asp Ser Phe Phe Ser Leu Leu Thr Ser
115 120 125

Glu Arg Val Ala Lys Gln Phe Pro Val Met Thr Glu Ala Ile Thr Gln
130 135 140

```
Ile Arg Ala Lys Gly Leu Gln Thr Ala Val Leu Ser Asn Asn Phe Tyr
145                 150                 155                 160

Leu Pro Asn Gln Lys Ser Phe Leu Pro Leu Asp Arg Lys Gln Phe Asp
                165                 170                 175

Val Ile Val Glu Ser Cys Met Glu Gly Ile Cys Lys Pro Asp Pro Arg
            180                 185                 190

Ile Tyr Lys Leu Cys Leu Glu Gln Leu Gly Leu Gln Pro Ser Glu Ser
        195                 200                 205

Ile Phe Leu Asp Asp Leu Gly Thr Asn Leu Lys Glu Ala Ala Arg Leu
    210                 215                 220

Gly Ile His Thr Ile Lys Val Asn Asp Pro Glu Thr Ala Val Lys Glu
225                 230                 235                 240

Leu Glu Ala Leu Leu Gly Phe Thr Leu Arg Val Gly Val Pro Asn Thr
                245                 250                 255

Arg Pro Val Lys Lys Thr Met Glu Ile Pro Lys Asp Ser Leu Gln Lys
            260                 265                 270

Tyr Leu Lys Asp Leu Leu Gly Ile Gln Thr Thr Gly Pro Leu Glu Leu
        275                 280                 285

Leu Gln Phe Asp His Gly Gln Ser Asn Pro Thr Tyr Tyr Ile Arg Leu
    290                 295                 300

Ala Asn Arg Asp Leu Val Leu Arg Lys Lys Pro Pro Gly Thr Leu Leu
305                 310                 315                 320

Pro Ser Ala His Ala Ile Glu Arg Glu Phe Arg Ile Met Lys Ala Leu
                325                 330                 335

Ala Asn Ala Gly Val Pro Val Pro Asn Val Leu Asp Leu Cys Glu Asp
            340                 345                 350

Ser Ser Val Ile Gly Thr Pro Phe Tyr Val Met Glu Tyr Cys Pro Gly
        355                 360                 365

Leu Ile Tyr Lys Asp Pro Ser Leu Pro Gly Leu Glu Pro Ser His Arg
```

```
    370                 375                 380

Arg Ala Ile Tyr Thr Ala Met Asn Thr Val Leu Cys Lys Ile His Ser
385                 390                 395                 400

Val Asp Leu Gln Ala Val Gly Leu Glu Asp Tyr Gly Lys Gln Gly Asp
                405                 410                 415

Tyr Ile Pro Arg Gln Val Arg Thr Trp Val Lys Gln Tyr Arg Ala Ser
            420                 425                 430

Glu Thr Ser Thr Ile Pro Ala Met Glu Arg Leu Ile Glu Trp Leu Pro
        435                 440                 445

Leu His Leu Pro Arg Gln Gln Arg Thr Thr Val Val His Gly Asp Phe
    450                 455                 460

Arg Leu Asp Asn Leu Val Phe His Pro Glu Glu Pro Glu Val Leu Ala
465                 470                 475                 480

Val Leu Asp Trp Glu Leu Ser Thr Leu Gly Asp Pro Leu Ala Asp Val
                485                 490                 495

Ala Tyr Ser Cys Leu Ala His Tyr Leu Pro Ser Ser Phe Pro Val Leu
            500                 505                 510

Arg Gly Ile Asn Asp Cys Asp Leu Thr Gln Leu Gly Ile Pro Ala Ala
        515                 520                 525

Glu Glu Tyr Phe Arg Met Tyr Cys Leu Gln Met Gly Leu Pro Pro Thr
    530                 535                 540

Glu Asn Trp Asn Phe Tyr Met Ala Phe Ser Phe Phe Arg Val Ala Ala
545                 550                 555                 560

Ile Leu Gln Gly Val Tyr Lys Arg Ser Leu Thr Gly Gln Ala Ser Ser
                565                 570                 575

Thr Tyr Ala Glu Gln Thr Gly Lys Leu Thr Glu Phe Val Ser Asn Leu
            580                 585                 590

Ala Trp Asp Phe Ala Val Lys Glu Gly Phe Arg Val Phe Lys Glu Met
        595                 600                 605
```

```
Pro Phe Thr Asn Pro Leu Thr Arg Ser Tyr His Thr Trp Ala Arg Pro
    610                 615                 620

Gln Ser Gln Trp Cys Pro Thr Gly Ser Arg Ser Tyr Ser Ser Val Pro
625                 630                 635                 640

Glu Ala Ser Pro Ala His Thr Ser Arg Gly Gly Leu Val Ile Ser Pro
                645                 650                 655

Glu Ser Leu Ser Pro Pro Val Arg Glu Leu Tyr His Arg Leu Lys His
            660                 665                 670

Phe Met Glu Gln Arg Val Tyr Pro Ala Glu Pro Glu Leu Gln Ser His
        675                 680                 685

Gln Ala Ser Ala Ala Arg Trp Ser Pro Ser Pro Leu Ile Glu Asp Leu
    690                 695                 700

Lys Val Lys Gln Pro Trp
705                 710


<210> 1832
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 487; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD10; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446998"

<400> 1832
Met Cys Val Arg Ser Cys Phe Gln Ser Pro Arg Leu Gln
1               5                   10
```

<210> 1833
<211> 226
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACAD10; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000447561"

<400> 1833
Val Asn Asp Pro Glu Thr Ala Val Lys Glu Leu Glu Ala Leu Leu Gly
1 5 10 15

Phe Thr Leu Arg Val Gly Val Pro Asn Thr Arg Pro Val Lys Lys Thr
20 25 30

Met Glu Ile Pro Lys Asp Ser Leu Gln Lys Tyr Leu Lys Asp Leu Leu
35 40 45

Gly Ile Gln Thr Thr Gly Pro Leu Glu Leu Leu Gln Phe Asp His Gly
50 55 60

Gln Ser Asn Pro Thr Tyr Tyr Ile Arg Leu Ala Asn Arg Asp Leu Val
65 70 75 80

Leu Arg Lys Lys Pro Pro Gly Thr Leu Leu Pro Ser Ala His Ala Ile
85 90 95

Glu Arg Glu Phe Arg Ile Met Lys Ala Leu Ala Asn Ala Gly Val Pro
100 105 110

Val Pro Asn Val Leu Asp Leu Cys Glu Asp Ser Ser Val Ile Gly Thr
115 120 125

```
Pro Phe Tyr Val Met Glu Tyr Cys Pro Gly Leu Ile Tyr Lys Asp Pro
    130                 135                 140

Ser Leu Pro Gly Leu Glu Pro Ser His Arg Arg Ala Ile Tyr Thr Ala
145                 150                 155                 160

Met Asn Thr Val Leu Cys Lys Ile His Ser Val Asp Leu Gln Ala Val
                165                 170                 175

Gly Leu Glu Asp Tyr Gly Lys Gln Gly Ser Thr Thr Trp Cys Phe Ile
            180                 185                 190

Gln Lys Ser Gln Arg Cys Leu Leu Ser Leu Thr Gly Asn Phe Leu Pro
        195                 200                 205

Trp Ala Thr Pro Leu Leu Met Trp Pro Thr Ala Ala Trp Leu Ile Thr
    210                 215                 220

Cys His
225
```

<210> 1834
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 487; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD10; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000449097"

<400> 1834

```
Met Pro Phe Thr Asn Pro Leu Thr Arg Ser Tyr His Thr Trp Ala Arg
1               5                   10                  15

Pro Gln Ser Gln Trp Cys Pro Thr Gly Ser Arg Ser Tyr Ser Ser Val
```

```
            20                  25                  30

Pro Glu Ala Ser Pro Ala His Thr Ser Arg Gly Gly Leu Val Ile Ser
        35                  40                  45

Pro Glu Ser Leu Ser Pro Pro Val Arg Glu Leu Tyr His Arg Leu Lys
    50                  55                  60

His Phe Met Glu Gln Arg Val Tyr Pro Ala Glu Pro Glu Leu Gln Ser
65                  70                  75                  80

His Gln Ala Ser Ala Ala Arg Trp Ser Pro Ser Pro Leu Ile Glu Asp
                85                  90                  95

Leu Lys Glu Lys Ala Lys Ala Glu Gly Leu Trp Asn Leu Phe Leu Pro
            100                 105                 110

Leu Glu Ala Asp Pro Glu Lys Lys Tyr Gly Ala Gly Leu Thr Asn Val
        115                 120                 125

Glu Tyr Ala His Leu Cys Glu Leu Met Gly Thr Ser Leu Tyr Ala Pro
    130                 135                 140

Glu Val
145


<210> 1835
<211> 780
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 488; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD11; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 11; "

<220>
<221> source
<223> /note="Uniprot ID:  Q709F0; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000264990"

<400> 1835
Met Lys Pro Gly Ala Thr Gly Glu Ser Asp Leu Ala Glu Val Leu Pro
1   5   10   15

Gln His Lys Phe Asp Ser Lys Ser Leu Glu Ala Tyr Leu Asn Gln His
            20   25   30

Leu Ser Gly Phe Gly Ala Glu Arg Glu Ala Thr Leu Thr Ile Ala Gln
        35   40   45

Tyr Arg Ala Gly Lys Ser Asn Pro Thr Phe Tyr Leu Gln Lys Gly Phe
    50   55   60

Gln Thr Tyr Val Leu Arg Lys Lys Pro Pro Gly Ser Leu Leu Pro Lys
65   70   75   80

Ala His Gln Ile Asp Arg Glu Phe Lys Val Gln Lys Ala Leu Phe Ser
                85   90   95

Ile Gly Phe Pro Val Pro Lys Pro Ile Leu Tyr Cys Ser Asp Thr Ser
            100   105   110

Val Ile Gly Thr Glu Phe Tyr Val Met Glu His Val Gln Gly Arg Ile
        115   120   125

Phe Arg Asp Leu Thr Ile Pro Gly Leu Ser Pro Ala Glu Arg Ser Ala
    130   135   140

Ile Tyr Val Ala Thr Val Glu Thr Leu Ala Gln Leu His Ser Leu Asn
145   150   155   160

Ile Gln Ser Leu Gln Leu Glu Gly Tyr Gly Ile Gly Ala Gly Tyr Cys
                165   170   175

Lys Arg Gln Val Ser Thr Trp Thr Lys Gln Tyr Gln Ala Ala Ala His
            180   185   190

Gln Asp Ile Pro Ala Met Gln Gln Leu Ser Glu Trp Leu Met Lys Asn
        195   200   205

```
Leu Pro Asp Asn Asp Asn Glu Glu Asn Leu Ile His Gly Asp Phe Arg
    210                 215                 220

Leu Asp Asn Ile Val Phe His Pro Lys Glu Cys Arg Val Ile Ala Val
225                 230                 235                 240

Leu Asp Trp Glu Leu Ser Thr Ile Gly His Pro Leu Ser Asp Leu Ala
                245                 250                 255

His Phe Ser Leu Phe Tyr Phe Trp Pro Arg Thr Val Pro Met Ile Asn
            260                 265                 270

Gln Gly Ser Tyr Ser Glu Asn Ser Gly Ile Pro Ser Met Glu Glu Leu
        275                 280                 285

Ile Ser Ile Tyr Cys Arg Cys Arg Gly Ile Asn Ser Ile Leu Pro Asn
    290                 295                 300

Trp Asn Phe Phe Leu Ala Leu Ser Tyr Phe Lys Met Ala Gly Ile Ala
305                 310                 315                 320

Gln Gly Val Tyr Ser Arg Tyr Leu Leu Gly Asn Asn Ser Ser Glu Asp
                325                 330                 335

Ser Phe Leu Phe Ala Asn Ile Val Gln Pro Leu Ala Glu Thr Gly Leu
            340                 345                 350

Gln Leu Ser Lys Arg Thr Phe Ser Thr Val Leu Pro Gln Ile Asp Thr
        355                 360                 365

Thr Gly Gln Leu Phe Val Gln Thr Arg Lys Gly Gln Glu Val Leu Ile
    370                 375                 380

Lys Val Lys His Phe Met Lys Gln His Ile Leu Pro Ala Glu Lys Glu
385                 390                 395                 400

Val Thr Glu Phe Tyr Val Gln Asn Glu Asn Ser Val Asp Lys Trp Gly
                405                 410                 415

Lys Pro Leu Val Ile Asp Lys Leu Lys Glu Met Ala Lys Val Glu Gly
            420                 425                 430
```

```
Leu Trp Asn Leu Phe Leu Pro Ala Val Ser Gly Leu Ser His Val Asp
        435                 440                 445

Tyr Ala Leu Ile Ala Glu Glu Thr Gly Lys Cys Phe Phe Ala Pro Asp
    450                 455                 460

Val Phe Asn Cys Gln Ala Pro Asp Thr Gly Asn Met Glu Val Leu His
465                 470                 475                 480

Leu Tyr Gly Ser Glu Glu Gln Lys Lys Gln Trp Leu Glu Pro Leu Leu
                485                 490                 495

Gln Gly Asn Ile Thr Ser Cys Phe Cys Met Thr Glu Pro Asp Val Ala
            500                 505                 510

Ser Ser Asp Ala Thr Asn Ile Glu Cys Ser Ile Gln Arg Asp Glu Asp
        515                 520                 525

Ser Tyr Val Ile Asn Gly Lys Lys Trp Trp Ser Ser Gly Ala Gly Asn
    530                 535                 540

Pro Lys Cys Lys Ile Ala Ile Val Leu Gly Arg Thr Gln Asn Thr Ser
545                 550                 555                 560

Leu Ser Arg His Lys Gln His Ser Met Ile Leu Val Pro Met Asn Thr
                565                 570                 575

Pro Gly Val Lys Ile Ile Arg Pro Leu Ser Val Phe Gly Tyr Thr Asp
            580                 585                 590

Asn Phe His Gly Gly His Phe Glu Ile His Phe Asn Gln Val Arg Val
        595                 600                 605

Pro Ala Thr Asn Leu Ile Leu Gly Glu Gly Arg Gly Phe Glu Ile Ser
    610                 615                 620

Gln Gly Arg Leu Gly Pro Gly Arg Ile His His Cys Met Arg Thr Val
625                 630                 635                 640

Gly Leu Ala Glu Arg Ala Leu Gln Ile Met Cys Glu Arg Ala Thr Gln
                645                 650                 655

Arg Ile Ala Phe Lys Lys Lys Leu Tyr Ala His Glu Val Val Ala His
```

```
            660                 665                 670

Trp Ile Ala Glu Ser Arg Ile Ala Ile Glu Lys Ile Arg Leu Leu Thr
        675                 680                 685

Leu Lys Ala Ala His Ser Met Asp Thr Leu Gly Ser Ala Gly Ala Lys
    690                 695                 700

Lys Glu Ile Ala Met Ile Lys Val Ala Ala Pro Arg Ala Val Ser Lys
705                 710                 715                 720

Ile Val Asp Trp Ala Ile Gln Val Cys Gly Gly Ala Gly Val Ser Gln
                725                 730                 735

Asp Tyr Pro Leu Ala Asn Met Tyr Ala Ile Thr Arg Val Leu Arg Leu
            740                 745                 750

Ala Asp Gly Pro Asp Glu Val His Leu Ser Ala Ile Ala Thr Met Glu
        755                 760                 765

Leu Arg Asp Gln Ala Lys Arg Leu Thr Ala Lys Ile
    770                 775                 780


<210> 1836
<211> 433
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 488; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD11; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419973"

<400> 1836
Met Lys Pro Gly Ala Thr Gly Glu Ser Asp Leu Ala Glu Val Leu Pro
1               5                   10                  15
```

```
Gln His Lys Phe Asp Ser Lys Ser Leu Glu Ala Tyr Leu Asn Gln His
            20                  25                  30

Leu Ser Gly Phe Gly Ala Glu Arg Glu Ala Thr Leu Thr Ile Ala Gln
        35                  40                  45

Tyr Arg Ala Gly Lys Ser Asn Pro Thr Phe Tyr Leu Gln Lys Gly Phe
    50                  55                  60

Gln Thr Tyr Val Leu Arg Lys Lys Pro Pro Gly Ser Leu Leu Pro Lys
65                  70                  75                  80

Ala His Gln Ile Asp Arg Glu Phe Lys Val Gln Lys Ala Leu Phe Ser
                85                  90                  95

Ile Gly Phe Pro Val Pro Lys Pro Ile Leu Tyr Cys Ser Asp Thr Ser
            100                 105                 110

Val Ile Gly Thr Glu Phe Tyr Val Met Glu His Val Gln Gly Arg Ile
        115                 120                 125

Phe Arg Asp Leu Thr Ile Pro Gly Leu Ser Pro Ala Glu Arg Ser Ala
    130                 135                 140

Ile Tyr Val Ala Thr Val Glu Thr Leu Ala Gln Leu His Ser Leu Asn
145                 150                 155                 160

Ile Gln Ser Leu Gln Leu Glu Gly Tyr Gly Ile Gly Ala Gly Tyr Cys
                165                 170                 175

Lys Arg Gln Val Ser Thr Trp Thr Lys Gln Tyr Gln Ala Ala Ala His
            180                 185                 190

Gln Asp Ile Pro Ala Met Gln Gln Leu Ser Glu Trp Leu Met Lys Asn
        195                 200                 205

Leu Pro Asp Asn Asp Asn Glu Glu Asn Leu Ile His Gly Asp Phe Arg
    210                 215                 220

Leu Asp Asn Ile Val Phe His Pro Lys Glu Cys Arg Val Ile Ala Val
225                 230                 235                 240
```

```
Leu Asp Trp Glu Leu Ser Thr Ile Gly His Pro Leu Ser Asp Leu Ala
                245                 250                 255

His Phe Ser Leu Phe Tyr Phe Trp Pro Arg Thr Val Pro Met Ile Asn
            260                 265                 270

Gln Gly Ser Tyr Ser Glu Asn Ser Gly Ile Pro Ser Met Glu Glu Leu
        275                 280                 285

Ile Ser Ile Tyr Cys Arg Cys Arg Gly Ile Asn Ser Ile Leu Pro Asn
    290                 295                 300

Trp Asn Phe Phe Leu Ala Leu Ser Tyr Phe Lys Met Ala Gly Ile Ala
305                 310                 315                 320

Gln Gly Val Tyr Ser Arg Tyr Leu Leu Gly Asn Asn Ser Ser Glu Asp
                325                 330                 335

Ser Phe Leu Phe Ala Asn Ile Val Gln Pro Leu Ala Glu Thr Gly Leu
            340                 345                 350

Gln Leu Ser Lys Arg Thr Phe Ser Thr Val Leu Pro Gln Ile Asp Thr
        355                 360                 365

Thr Gly Gln Leu Phe Val Gln Thr Arg Lys Gly Gln Glu Val Leu Ile
    370                 375                 380

Lys Val Lys His Phe Met Lys Gln His Ile Leu Pro Ala Glu Lys Thr
385                 390                 395                 400

Gln Gly Ile Trp Arg Phe Cys Thr Cys Met Glu Val Arg Asn Arg Arg
                405                 410                 415

Asn Ser Gly Leu Ser Leu Phe Phe Lys Gly Thr Leu Pro Leu Ala Ser
            420                 425                 430

Val
```

<210> 1837
<211> 476
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 488; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD11; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420907"

<400> 1837
Met Lys Pro Gly Ala Thr Gly Glu Ser Asp Leu Ala Glu Val Leu Pro
1 5 10 15

Gln His Lys Phe Asp Ser Lys Ser Leu Glu Ala Tyr Leu Asn Gln His
20 25 30

Leu Ser Gly Phe Gly Ala Glu Arg Glu Ala Thr Leu Thr Ile Ala Gln
35 40 45

Tyr Arg Ala Gly Lys Ser Asn Pro Thr Phe Tyr Leu Gln Lys Gly Phe
50 55 60

Gln Thr Tyr Val Leu Arg Lys Lys Pro Pro Gly Ser Leu Leu Pro Lys
65 70 75 80

Ala His Gln Ile Asp Arg Glu Phe Lys Val Gln Lys Ala Leu Phe Ser
85 90 95

Ile Gly Phe Pro Val Pro Lys Pro Ile Leu Tyr Cys Ser Asp Thr Ser
100 105 110

Val Ile Gly Thr Glu Phe Tyr Val Met Glu His Val Gln Gly Arg Ile
115 120 125

Phe Arg Asp Leu Thr Ile Pro Gly Leu Ser Pro Ala Glu Arg Ser Ala
130 135 140

Ile Tyr Val Ala Thr Val Glu Thr Leu Ala Gln Leu His Ser Leu Asn

145 150 155 160

Ile Gln Ser Leu Gln Leu Glu Gly Tyr Gly Ile Gly Ala Gly Tyr Cys
165 170 175

Lys Arg Gln Val Ser Thr Trp Thr Lys Gln Tyr Gln Ala Ala Ala His
180 185 190

Gln Asp Ile Pro Ala Met Gln Gln Leu Ser Glu Trp Leu Met Lys Asn
195 200 205

Leu Pro Asp Asn Asp Asn Glu Glu Asn Leu Ile His Gly Asp Phe Arg
210 215 220

Leu Asp Asn Ile Val Phe His Pro Lys Glu Cys Arg Val Ile Ala Val
225 230 235 240

Leu Asp Trp Glu Leu Ser Thr Ile Gly His Pro Leu Ser Asp Leu Ala
245 250 255

His Phe Ser Leu Phe Tyr Phe Trp Pro Arg Thr Val Pro Met Ile Asn
260 265 270

Gln Gly Ser Tyr Ser Glu Asn Ser Gly Ile Pro Ser Met Glu Glu Leu
275 280 285

Ile Ser Ile Tyr Cys Arg Cys Arg Gly Ile Asn Ser Ile Leu Pro Asn
290 295 300

Trp Asn Phe Phe Leu Ala Leu Ser Tyr Phe Lys Met Ala Gly Ile Ala
305 310 315 320

Gln Gly Val Tyr Ser Arg Tyr Leu Leu Gly Asn Asn Ser Ser Glu Asp
325 330 335

Ser Phe Leu Phe Ala Asn Ile Val Gln Pro Leu Ala Glu Thr Gly Leu
340 345 350

Gln Leu Ser Lys Arg Thr Phe Ser Thr Val Leu Pro Gln Ile Asp Thr
355 360 365

Thr Gly Gln Leu Phe Val Gln Thr Arg Lys Gly Gln Glu Val Leu Ile
370 375 380

```
Lys Val Lys His Phe Met Lys Gln His Ile Leu Pro Ala Glu Lys Glu
385                 390                 395                 400

Val Thr Glu Phe Tyr Val Gln Asn Glu Asn Ser Val Asp Lys Trp Gly
                405                 410                 415

Lys Pro Leu Val Ile Asp Lys Leu Lys Glu Met Ala Lys Val Glu Gly
            420                 425                 430

Leu Trp Asn Leu Phe Leu Pro Ala Val Ser Gly Leu Ser His Val Asp
        435                 440                 445

Tyr Ala Leu Ile Ala Glu Glu Thr Gly Lys Cys Phe Phe Ala Pro Asp
    450                 455                 460

Val Phe Asn Cys Gln Ala Pro Gly Tyr Tyr Ile Asn
465                 470                 475


<210> 1838
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 488; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD11; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423796"

<400> 1838
Gly Leu Ser His Val Asp Tyr Ala Leu Ile Ala Glu Glu Thr Gly Lys
1               5                   10                  15

Cys Phe Phe Ala Pro Asp Val Phe Asn Cys Gln Ala Pro Asp Thr Gly
            20                  25                  30
```

```
Asn Met Glu Val Leu His Leu Tyr Gly Ser Glu Glu Gln Lys Lys Gln
        35                  40                  45

Trp Leu Glu Pro Leu Leu Gln Gly Asn Ile Thr Ser Cys Phe Cys Met
    50                  55                  60

Thr Glu Pro Asp Val Ala Ser Ser Asp Ala Thr Asn Ile Glu Cys Ser
65                  70                  75                  80

Ile Gln Arg Asp Glu Asp Ser Tyr Val Ile Asn Gly Lys Lys Trp Trp
                85                  90                  95

Ser Ser Gly Ala Gly Asn Pro Lys Cys Lys Ile Ala Ile Val Leu Gly
            100                 105                 110

Arg Thr Gln Asn Thr Ser Leu Ser Arg Ser Gln Pro Ala Ser Asp Tyr
        115                 120                 125

Val Gly Val Arg Leu Leu His Ser Ser His Ser Ser His His Cys Leu
    130                 135                 140

His Asp Tyr Met Lys Thr Ser Lys Arg Gln Leu
145                 150                 155


<210> 1839
<211> 415
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 489; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD8; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 8; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UKU7; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000281182"

<400> 1839
Met Leu Trp Ser Gly Cys Arg Arg Phe Gly Ala Arg Leu Gly Cys Leu
1 5 10 15

Pro Gly Gly Leu Arg Val Leu Val Gln Thr Gly His Arg Ser Leu Thr
20 25 30

Ser Cys Ile Asp Pro Ser Met Gly Leu Asn Glu Glu Gln Lys Glu Phe
35 40 45

Gln Lys Val Ala Phe Asp Phe Ala Ala Arg Glu Met Ala Pro Asn Met
50 55 60

Ala Glu Trp Asp Gln Lys Glu Leu Phe Pro Val Asp Val Met Arg Lys
65 70 75 80

Ala Ala Gln Leu Gly Phe Gly Gly Val Tyr Ile Gln Thr Asp Val Gly
85 90 95

Gly Ser Gly Leu Ser Arg Leu Asp Thr Ser Val Ile Phe Glu Ala Leu
100 105 110

Ala Thr Gly Cys Thr Ser Thr Thr Ala Tyr Ile Ser Ile His Asn Met
115 120 125

Cys Ala Trp Met Ile Asp Ser Phe Gly Asn Glu Glu Gln Arg His Lys
130 135 140

Phe Cys Pro Pro Leu Cys Thr Met Glu Lys Phe Ala Ser Tyr Cys Leu
145 150 155 160

Thr Glu Pro Gly Ser Gly Ser Asp Ala Ala Ser Leu Leu Thr Ser Ala
165 170 175

Lys Lys Gln Gly Asp His Tyr Ile Leu Asn Gly Ser Lys Ala Phe Ile
180 185 190

Ser Gly Ala Gly Glu Ser Asp Ile Tyr Val Val Met Cys Arg Thr Gly
195 200 205

Gly Pro Gly Pro Lys Gly Ile Ser Cys Ile Val Val Glu Lys Gly Thr

```
    210                 215                 220

Pro Gly Leu Ser Phe Gly Lys Lys Glu Lys Lys Val Gly Trp Asn Ser
225                 230                 235                 240

Gln Pro Thr Arg Ala Val Ile Phe Glu Asp Cys Ala Val Pro Val Ala
                245                 250                 255

Asn Arg Ile Gly Ser Glu Gly Gln Gly Phe Leu Ile Ala Val Arg Gly
            260                 265                 270

Leu Asn Gly Gly Arg Ile Asn Ile Ala Ser Cys Ser Leu Gly Ala Ala
        275                 280                 285

His Ala Ser Val Ile Leu Thr Arg Asp His Leu Asn Val Arg Lys Gln
    290                 295                 300

Phe Gly Glu Pro Leu Ala Ser Asn Gln Tyr Leu Gln Phe Thr Leu Ala
305                 310                 315                 320

Asp Met Ala Thr Arg Leu Val Ala Ala Arg Leu Met Val Arg Asn Ala
                325                 330                 335

Ala Val Ala Leu Gln Glu Glu Arg Lys Asp Ala Val Ala Leu Cys Ser
            340                 345                 350

Met Ala Lys Leu Phe Ala Thr Asp Glu Cys Phe Ala Ile Cys Asn Gln
        355                 360                 365

Ala Leu Gln Met His Gly Gly Tyr Gly Tyr Leu Lys Asp Tyr Ala Val
    370                 375                 380

Gln Gln Tyr Val Arg Asp Ser Arg Val His Gln Ile Leu Glu Gly Ser
385                 390                 395                 400

Asn Glu Val Met Arg Ile Leu Ile Ser Arg Ser Leu Leu Gln Glu
                405                 410                 415


<210> 1840
<211> 288
<212> PRT
<213> Homo sapiens

<220>
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<221> source
<223> /note="Payload ID: 489; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD8; "

<220>
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<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 8; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKU7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000363884"

<400> 1840

```
Met Leu Trp Ser Gly Cys Arg Arg Phe Gly Ala Arg Leu Gly Cys Leu
1               5                   10                  15

Pro Gly Gly Leu Arg Val Leu Val Gln Thr Gly His Arg Ser Leu Thr
            20                  25                  30

Ser Cys Ile Asp Arg Ser Gly Ser Asp Ala Ala Ser Leu Leu Thr Ser
        35                  40                  45

Ala Lys Lys Gln Gly Asp His Tyr Ile Leu Asn Gly Ser Lys Ala Phe
    50                  55                  60

Ile Ser Gly Ala Gly Glu Ser Asp Ile Tyr Val Val Met Cys Arg Thr
65                  70                  75                  80

Gly Gly Pro Gly Pro Lys Gly Ile Ser Cys Ile Val Val Glu Lys Gly
                85                  90                  95

Thr Pro Gly Leu Ser Phe Gly Lys Lys Glu Lys Lys Val Gly Trp Asn
            100                 105                 110

Ser Gln Pro Thr Arg Ala Val Ile Phe Glu Asp Cys Ala Val Pro Val
        115                 120                 125

Ala Asn Arg Ile Gly Ser Glu Gly Gln Gly Phe Leu Ile Ala Val Arg
    130                 135                 140
```

```
Gly Leu Asn Gly Gly Arg Ile Asn Ile Ala Ser Cys Ser Leu Gly Ala
145                 150                 155                 160

Ala His Ala Ser Val Ile Leu Thr Arg Asp His Leu Asn Val Arg Lys
                165                 170                 175

Gln Phe Gly Glu Pro Leu Ala Ser Asn Gln Tyr Leu Gln Phe Thr Leu
            180                 185                 190

Ala Asp Met Ala Thr Arg Leu Val Ala Ala Arg Leu Met Val Arg Asn
        195                 200                 205

Ala Ala Val Ala Leu Gln Glu Glu Arg Lys Asp Ala Val Ala Leu Cys
    210                 215                 220

Ser Met Ala Lys Leu Phe Ala Thr Asp Glu Cys Phe Ala Ile Cys Asn
225                 230                 235                 240

Gln Ala Leu Gln Met His Gly Gly Tyr Gly Tyr Leu Lys Asp Tyr Ala
                245                 250                 255

Val Gln Gln Tyr Val Arg Asp Ser Arg Val His Gln Ile Leu Glu Gly
            260                 265                 270

Ser Asn Glu Val Met Arg Ile Leu Ile Ser Arg Ser Leu Leu Gln Glu
        275                 280                 285


<210> 1841
<211> 76
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ACAD8; "

<220>
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<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 8; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000431310"

<400> 1841
Met Leu Trp Ser Gly Cys Arg Arg Phe Gly Ala Arg Leu Gly Cys Leu
1 5 10 15

Pro Gly Gly Leu Arg Val Leu Val Gln Thr Gly His Arg Ser Leu Thr
20 25 30

Ser Cys Ile Asp Pro Ser Met Gly Leu Asn Glu Glu Gln Lys Glu Phe
35 40 45

Gln Lys Val Ala Phe Asp Phe Ala Ala Arg Glu Met Ala Pro Asn Met
50 55 60

Ala Glu Trp Asp Gln Lys His Val Cys Leu Asp Asp
65 70 75

<210> 1842
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 489; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD8; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431532"

<400> 1842
Met Leu Trp Ser Gly Cys Arg Arg Phe Gly Ala Arg Leu Gly Cys Leu
1 5 10 15

Pro Gly Gly Leu Arg Val Leu Val Gln Thr Gly His Arg Ser Leu Thr
20 25 30

Ser Cys Ile Asp Arg Ala Val Pro Ser Gly Cys Asp Ala Glu Gly Ser

```
        35                  40                  45

Pro Ala Arg Leu Arg Arg Gly Leu His Thr Asn Arg Cys Gly Arg Val
    50                  55                  60

Trp Ala Val Thr Ser
65
```

<210> 1843
<211> 621
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 9; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H845; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000312618"

<400> 1843

```
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1               5                   10                  15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20                  25                  30

Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
        35                  40                  45

Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
    50                  55                  60

Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
65                  70                  75                  80
```

```
Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu
                85                  90                  95

Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro
            100                 105                 110

Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu
        115                 120                 125

Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala
    130                 135                 140

His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu
145                 150                 155                 160

Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala
                165                 170                 175

Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile
            180                 185                 190

Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn
        195                 200                 205

Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr
    210                 215                 220

Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp
225                 230                 235                 240

Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn
                245                 250                 255

Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu
            260                 265                 270

Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu
        275                 280                 285

Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg
    290                 295                 300
```

```
Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
305                 310                 315                 320

Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
                325                 330                 335

Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala Gln Lys
            340                 345                 350

Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met Leu Asp
        355                 360                 365

Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val Lys Val
    370                 375                 380

Phe Ser Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala Leu Gln Ile
385                 390                 395                 400

Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg Ile Leu
                405                 410                 415

Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu Ile Leu
            420                 425                 430

Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg Ile Leu
        435                 440                 445

Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr Val Met
    450                 455                 460

Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr Val Asp
465                 470                 475                 480

Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu Ala Asp
                485                 490                 495

Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg Thr Val
            500                 505                 510

Glu Thr Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu Gln Leu
        515                 520                 525
```

```
Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly Met Thr
    530                 535                 540

Ala Val Leu Ser Arg Ala Ser Arg Ser Ile Arg Ile Gly Leu Arg Asn
545                 550                 555                 560

His Asp His Glu Val Leu Leu Ala Asn Thr Phe Cys Val Glu Ala Tyr
                565                 570                 575

Leu Gln Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr Ala Pro Glu
            580                 585                 590

Asn Leu Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile Leu Glu Lys
        595                 600                 605

Arg Ala Tyr Ile Cys Ala His Pro Leu Asp Arg Thr Cys
    610                 615                 620
```

<210> 1844
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422020"

<400> 1844

```
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1               5                   10                  15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20                  25                  30

Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
```

35 40 45

Lys Lys Lys Phe Ser His Phe Gln Lys Leu Ala Lys Met Asn Leu Met
50 55 60

Lys Ser Ile Ser Ser Trp Asp Pro Trp Lys Asn Ser Ser Leu Lys Arg
65 70 75 80

Trp Thr Pro Glu Lys Leu Thr Arg Lys Gly Lys Ser Gln Met Lys Leu
85 90 95

Trp Arg Asn

<210> 1845
<211> 384
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422683"

<400> 1845
Val Lys Asp Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly
1 5 10 15

Val Thr Asn Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn
20 25 30

Thr Cys Glu Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile
35 40 45

Leu Gly Glu Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn
50 55 60

```
Ser Gly Arg Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg
65                  70                  75                  80

Leu Ile Glu Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn
                85                  90                  95

Lys Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met
            100                 105                 110

Ala Gln Lys Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly
        115                 120                 125

Met Leu Asp Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met
    130                 135                 140

Val Lys Val Phe Ser Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala
145                 150                 155                 160

Leu Gln Ile Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu
                165                 170                 175

Arg Ile Leu Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn
            180                 185                 190

Glu Ile Leu Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly
        195                 200                 205

Arg Ile Leu Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser
    210                 215                 220

Thr Val Met Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg
225                 230                 235                 240

Thr Val Asp Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser
                245                 250                 255

Leu Ala Asp Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly
            260                 265                 270

Arg Thr Val Glu Thr Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu
        275                 280                 285
```

```
Glu Gln Leu Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr
    290                 295                 300

Gly Met Thr Ala Val Leu Ser Arg Ala Ser Arg Ser Ile Arg Ile Gly
305                 310                 315                 320

Leu Arg Asn His Asp His Glu Val Leu Leu Ala Asn Thr Phe Cys Val
                325                 330                 335

Glu Ala Tyr Leu Gln Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr
            340                 345                 350

Ala Pro Glu Asn Leu Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile
        355                 360                 365

Leu Glu Lys Arg Ala Tyr Ile Cys Ala His Pro Leu Asp Arg Thr Cys
    370                 375                 380


<210> 1846
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423758"

<400> 1846
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1               5                   10                  15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20                  25                  30
```

```
Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
        35                  40                  45

Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
    50                  55                  60

Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
65                  70                  75                  80

Glu Ala Tyr Ile Cys Leu Ile Lys Ile Phe Leu Leu Ala Val Asp Ser
                85                  90                  95

Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu Thr Leu Glu Lys
            100                 105                 110

Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro Glu Glu Tyr Gly
        115                 120                 125

Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu Gly Glu Ile Ile
    130                 135                 140

Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala His Gln Ala Ile
145                 150                 155                 160

Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu Gln
                165                 170


<210> 1847
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 9; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000425226"

<400> 1847
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1   5   10   15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20   25   30

Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
        35   40   45

Lys Lys Val Thr Arg Ala Leu Gly Glu Pro Leu Leu Ser Gly Ser Arg
    50   55   60

Phe Ser Pro Ser Ala Ala Arg Leu Val Leu Asn Phe Val Arg Phe Pro
65   70   75   80

Lys Pro Ala Arg Glu Ile His Pro Ala Ala Glu Ala Cys
                85   90

<210> 1848
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425346"

<400> 1848
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1   5   10   15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20   25   30

```
Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
        35                  40                  45

Lys Lys Val Thr Arg Ala Leu Gly Glu Pro Leu Leu Ser Gly Ser Arg
    50                  55                  60

Phe Ser Pro Ser Ala Ala Arg Leu Val Leu Asn Phe Val Arg Phe Pro
65                  70                  75                  80

Lys Pro Ala Arg Glu Ile His Pro Ala Ala Glu Ala Cys
                85                  90


<210> 1849
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426189"

<400> 1849
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1               5                   10                  15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20                  25                  30

Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
        35                  40                  45

Lys Lys Val Thr Arg Ala Leu Gly Glu Pro Leu Leu Ser Gly Ser Arg
    50                  55                  60
```

```
Phe Ser Pro Ser Ala Ala Arg Leu Val Leu Asn Phe Val Arg Phe Pro
65                  70                  75                  80


Lys Pro Ala Arg Glu Ile His Pro Ala Ala Glu Ala Cys
                85                  90


<210> 1850
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase
      family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426277"

<400> 1850
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1               5                   10                  15


Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
            20                  25                  30


Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
        35                  40                  45


Lys Lys Trp Thr Pro Glu Lys Leu Thr Arg Lys Gly Lys Ser Gln Met
    50                  55                  60


Lys Leu Trp Arg Asn
65


<210> 1851
<211> 93
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427283"

<400> 1851
Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
1 5 10 15

Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
20 25 30

Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
35 40 45

Lys Lys Lys Leu Ala Lys Met Asn Leu Met Lys Ser Ile Ser Ser Trp
50 55 60

Asp Pro Trp Lys Asn Ser Ser Leu Lys Arg Trp Thr Pro Glu Lys Leu
65 70 75 80

Thr Arg Lys Gly Lys Ser Gln Met Lys Leu Trp Arg Asn
85 90

<210> 1852
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 490; "

<220>
<221> source
<223> /note="Gene Symbol: ACAD9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase
family, member 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478191"

<400> 1852
Met Glu Glu Gln Leu Val Leu Lys Gly Gly Gln His Pro His Gln Pro
1 5 10 15

Val Trp His Asp Gly Arg Ala Val Ala Gly Gln Pro Leu His Pro His
20 25 30

Trp Ala Pro Gln Pro Arg Pro Arg Gly Ser Leu Gly Gln His Leu Leu
35 40 45

Arg Gly Ser Leu Leu Ala Glu Ser Leu Gln Pro Leu Ser Ala Gly Gln
50 55 60

Val Cys Ser Arg Lys Pro Arg Ser Arg Leu Arg Lys Cys Pro Ser Arg
65 70 75 80

Ser Leu Arg Ser Glu Pro Ile Ser Val Pro Thr Leu Trp Thr Gly His
85 90 95

Ala Glu Arg Gly Gln Cys Pro Leu Leu Pro Pro Ala Pro Thr His Gly
100 105 110

Pro Leu Leu Asp Asp Cys Tyr Ser Phe Phe Arg Arg Leu Gly Leu Ser
115 120 125

Gln Val Lys Pro Phe Val Pro Arg Leu His Leu Lys Gly Cys Arg Leu
130 135 140

Ala Trp Glu Ser Leu Phe Gln Val Leu Thr Cys Arg Gln Cys Ser Leu
145 150 155 160

Thr Gly Pro Ser Gln Leu Leu Asn
165

<210> 1853
<211> 412

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 491; "

<220>
<221> source
<223> /note="Gene Symbol: ACADS; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-2 to C-3 short chain; "

<220>
<221> source
<223> /note="Uniprot ID: P16219; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000242592"

<400> 1853
Met Ala Ala Ala Leu Leu Ala Arg Ala Ser Gly Pro Ala Arg Arg Ala
1 5 10 15

Leu Cys Pro Arg Ala Trp Arg Gln Leu His Thr Ile Tyr Gln Ser Val
20 25 30

Glu Leu Pro Glu Thr His Gln Met Leu Leu Gln Thr Cys Arg Asp Phe
35 40 45

Ala Glu Lys Glu Leu Phe Pro Ile Ala Ala Gln Val Asp Lys Glu His
50 55 60

Leu Phe Pro Ala Ala Gln Val Lys Lys Met Gly Gly Leu Gly Leu Leu
65 70 75 80

Ala Met Asp Val Pro Glu Glu Leu Gly Gly Ala Gly Leu Asp Tyr Leu
85 90 95

Ala Tyr Ala Ile Ala Met Glu Glu Ile Ser Arg Gly Cys Ala Ser Thr
100 105 110

Gly Val Ile Met Ser Val Asn Asn Ser Leu Tyr Leu Gly Pro Ile Leu
115 120 125

```
Lys Phe Gly Ser Lys Glu Gln Lys Gln Ala Trp Val Thr Pro Phe Thr
    130                 135                 140

Ser Gly Asp Lys Ile Gly Cys Phe Ala Leu Ser Glu Pro Gly Asn Gly
145                 150                 155                 160

Ser Asp Ala Gly Ala Ala Ser Thr Thr Ala Arg Ala Glu Gly Asp Ser
                165                 170                 175

Trp Val Leu Asn Gly Thr Lys Ala Trp Ile Thr Asn Ala Trp Glu Ala
            180                 185                 190

Ser Ala Ala Val Val Phe Ala Ser Thr Asp Arg Ala Leu Gln Asn Lys
        195                 200                 205

Gly Ile Ser Ala Phe Leu Val Pro Met Pro Thr Pro Gly Leu Thr Leu
    210                 215                 220

Gly Lys Lys Glu Asp Lys Leu Gly Ile Arg Gly Ser Ser Thr Ala Asn
225                 230                 235                 240

Leu Ile Phe Glu Asp Cys Arg Ile Pro Lys Asp Ser Ile Leu Gly Glu
                245                 250                 255

Pro Gly Met Gly Phe Lys Ile Ala Met Gln Thr Leu Asp Met Gly Arg
            260                 265                 270

Ile Gly Ile Ala Ser Gln Ala Leu Gly Ile Ala Gln Thr Ala Leu Asp
        275                 280                 285

Cys Ala Val Asn Tyr Ala Glu Asn Arg Met Ala Phe Gly Ala Pro Leu
    290                 295                 300

Thr Lys Leu Gln Val Ile Gln Phe Lys Leu Ala Asp Met Ala Leu Ala
305                 310                 315                 320

Leu Glu Ser Ala Arg Leu Leu Thr Trp Arg Ala Ala Met Leu Lys Asp
                325                 330                 335

Asn Lys Lys Pro Phe Ile Lys Glu Ala Ala Met Ala Lys Leu Ala Ala
            340                 345                 350

Ser Glu Ala Ala Thr Ala Ile Ser His Gln Ala Ile Gln Ile Leu Gly
```

```
        355                 360                 365

Gly Met Gly Tyr Val Thr Glu Met Pro Ala Glu Arg His Tyr Arg Asp
    370                 375                 380

Ala Arg Ile Thr Glu Ile Tyr Glu Gly Thr Ser Glu Ile Gln Arg Leu
385                 390                 395                 400

Val Ile Ala Gly His Leu Leu Arg Ser Tyr Arg Ser
                405                 410


<210> 1854
<211> 408
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 491; "

<220>
<221> source
<223> /note="Gene Symbol: ACADS; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, C-2 to C-3 short chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401045"

<400> 1854
Met Ala Ala Ala Leu Leu Ala Arg Ala Ser Gly Pro Ala Arg Arg Ala
1               5                   10                  15

Leu Cys Pro Arg Ala Trp Arg Gln Leu His Thr Ile Tyr Gln Ser Val
            20                  25                  30

Glu Leu Pro Glu Thr His Gln Met Leu Leu Gln Thr Cys Arg Asp Phe
        35                  40                  45

Ala Glu Lys Glu Leu Phe Pro Ile Ala Ala Gln Val Asp Lys Glu His
    50                  55                  60

Leu Phe Pro Ala Ala Gln Val Lys Lys Met Gly Gly Leu Gly Leu Leu
65                  70                  75                  80
```

```
Ala Met Asp Val Pro Glu Glu Leu Gly Gly Ala Gly Leu Asp Tyr Leu
                85                  90                  95

Ala Tyr Ala Ile Ala Met Glu Glu Ile Ser Arg Gly Cys Ala Ser Thr
            100                 105                 110

Gly Val Ile Met Ser Val Asn Asn Ser Leu Tyr Leu Gly Pro Ile Leu
        115                 120                 125

Lys Phe Gly Ser Lys Glu Gln Lys Gln Ala Trp Val Thr Pro Phe Thr
    130                 135                 140

Ser Gly Asp Lys Ile Gly Cys Phe Ala Leu Ser Glu Pro Gly Pro Ser
145                 150                 155                 160

Leu Leu Gly Pro Thr Gly Pro Ile Phe Ala Leu Gly Gln Val Gly Cys
                165                 170                 175

Pro Cys Pro Ser Ser Ala Ala Thr Glu Ala Cys Thr Phe Pro Arg Ser
            180                 185                 190

Arg Gln Arg Val Ser Arg Pro Glu Leu Leu Arg Glu Gly Ile Ser Ala
        195                 200                 205

Phe Leu Val Pro Met Pro Thr Pro Gly Leu Thr Leu Gly Lys Lys Glu
    210                 215                 220

Asp Lys Leu Gly Ile Arg Gly Ser Ser Thr Ala Asn Leu Ile Phe Glu
225                 230                 235                 240

Asp Cys Arg Ile Pro Lys Asp Ser Ile Leu Gly Glu Pro Gly Met Gly
                245                 250                 255

Phe Lys Ile Ala Met Gln Thr Leu Asp Met Gly Arg Ile Gly Ile Ala
            260                 265                 270

Ser Gln Ala Leu Gly Ile Ala Gln Thr Ala Leu Asp Cys Ala Val Asn
        275                 280                 285

Tyr Ala Glu Asn Arg Met Ala Phe Gly Ala Pro Leu Thr Lys Leu Gln
    290                 295                 300
```

```
Val Ile Gln Phe Lys Leu Ala Asp Met Ala Leu Ala Leu Glu Ser Ala
305                 310                 315                 320

Arg Leu Leu Thr Trp Arg Ala Ala Met Leu Lys Asp Asn Lys Lys Pro
                325                 330                 335

Phe Ile Lys Glu Ala Ala Met Ala Lys Leu Ala Ala Ser Glu Ala Ala
            340                 345                 350

Thr Ala Ile Ser His Gln Ala Ile Gln Ile Leu Gly Gly Met Gly Tyr
        355                 360                 365

Val Thr Glu Met Pro Ala Glu Arg His Tyr Arg Asp Ala Arg Ile Thr
    370                 375                 380

Glu Ile Tyr Glu Gly Thr Ser Glu Ile Gln Arg Leu Val Ile Ala Gly
385                 390                 395                 400

His Leu Leu Arg Ser Tyr Arg Ser
                405
```

<210> 1855
<211> 454
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359871"

<400> 1855

```
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Val Leu Arg Ser Ile Ser
1               5                   10                  15

Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn Arg Gln Arg Glu
            20                  25                  30
```

```
Pro Gly Leu Gly Phe Ser Phe Glu Phe Thr Glu Gln Gln Lys Glu Phe
        35                  40                  45

Gln Ala Thr Ala Arg Lys Phe Ala Arg Glu Glu Ile Ile Pro Val Ala
    50                  55                  60

Ala Glu Tyr Asp Lys Thr Gly Glu Tyr Pro Val Pro Leu Ile Arg Arg
65                  70                  75                  80

Ala Trp Glu Leu Gly Leu Met Asn Thr His Ile Pro Glu Asn Cys Asp
                85                  90                  95

Tyr Ser Val Cys Pro Leu Leu Glu Ala Cys Thr Leu Tyr Leu Asp Ala
            100                 105                 110

Phe Phe Leu Leu Leu Thr Gly Ser Asn Leu Asn Leu His Leu Asn Leu
        115                 120                 125

Gly Gly Leu Gly Leu Gly Thr Phe Asp Ala Cys Leu Ile Ser Glu Glu
    130                 135                 140

Leu Ala Tyr Gly Cys Thr Gly Val Gln Thr Ala Ile Glu Gly Asn Ser
145                 150                 155                 160

Leu Gly Gln Met Pro Ile Ile Ile Ala Gly Asn Asp Gln Gln Lys Lys
                165                 170                 175

Lys Tyr Leu Gly Arg Met Thr Glu Glu Pro Leu Met Cys Ala Tyr Cys
            180                 185                 190

Val Thr Glu Pro Gly Ala Gly Ser Asp Val Ala Gly Ile Lys Thr Lys
        195                 200                 205

Ala Glu Lys Lys Gly Asp Glu Tyr Ile Ile Asn Gly Gln Lys Met Trp
    210                 215                 220

Ile Thr Asn Gly Gly Lys Ala Asn Trp Tyr Phe Leu Leu Ala Arg Ser
225                 230                 235                 240

Asp Pro Asp Pro Lys Ala Pro Ala Asn Lys Ala Phe Thr Gly Phe Ile
                245                 250                 255
```

```
Val Glu Ala Asp Thr Pro Gly Ile Gln Ile Gly Arg Lys Glu Leu Asn
            260                 265                 270

Met Gly Gln Arg Cys Ser Asp Thr Arg Gly Ile Val Phe Glu Asp Val
        275                 280                 285

Lys Val Pro Lys Glu Asn Val Leu Ile Gly Asp Gly Ala Gly Phe Lys
    290                 295                 300

Val Ala Met Gly Ala Phe Asp Lys Thr Arg Pro Val Val Ala Ala Gly
305                 310                 315                 320

Ala Val Gly Leu Ala Gln Arg Ala Leu Asp Glu Ala Thr Lys Tyr Ala
                325                 330                 335

Leu Glu Arg Lys Thr Phe Gly Lys Leu Leu Val Glu His Gln Ala Ile
            340                 345                 350

Ser Phe Met Leu Ala Glu Met Ala Met Lys Val Glu Leu Ala Arg Met
        355                 360                 365

Ser Tyr Gln Arg Ala Ala Trp Glu Val Asp Ser Gly Arg Arg Asn Thr
    370                 375                 380

Tyr Tyr Ala Ser Ile Ala Lys Ala Phe Ala Gly Asp Ile Ala Asn Gln
385                 390                 395                 400

Leu Ala Thr Asp Ala Val Gln Ile Leu Gly Gly Asn Gly Phe Asn Thr
                405                 410                 415

Glu Tyr Pro Val Glu Lys Leu Met Arg Asp Ala Lys Ile Tyr Gln Ile
            420                 425                 430

Tyr Glu Gly Thr Ser Gln Ile Gln Arg Leu Ile Val Ala Arg Glu His
        435                 440                 445

Ile Asp Lys Tyr Lys Asn
    450
```

<210> 1856
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="Uniprot ID: P11310; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000359878"

<400> 1856
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Val Leu Arg Ser Ile Ser
1   5   10   15

Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn Arg Gln Arg Glu
            20   25   30

Pro Gly Leu Gly Phe Ser Phe Glu Phe Thr Glu Gln Gln Lys Glu Phe
        35   40   45

Gln Ala Thr Ala Arg Lys Phe Ala Arg Glu Glu Ile Ile Pro Val Ala
    50   55   60

Ala Glu Tyr Asp Lys Thr Gly Glu Tyr Pro Val Pro Leu Ile Arg Arg
65   70   75   80

Ala Trp Glu Leu Gly Leu Met Asn Thr His Ile Pro Glu Asn Cys Gly
                85   90   95

Gly Leu Gly Leu Gly Thr Phe Asp Ala Cys Leu Ile Ser Glu Glu Leu
            100   105   110

Ala Tyr Gly Cys Thr Gly Val Gln Thr Ala Ile Glu Gly Asn Ser Leu
        115   120   125

Gly Gln Met Pro Ile Ile Ile Ala Gly Asn Asp Gln Gln Lys Lys Lys
    130   135   140

```
Tyr Leu Gly Arg Met Thr Glu Glu Pro Leu Met Cys Ala Tyr Cys Val
145                 150                 155                 160

Thr Glu Pro Gly Ala Gly Ser Asp Val Ala Gly Ile Lys Thr Lys Ala
                165                 170                 175

Glu Lys Lys Gly Asp Glu Tyr Ile Ile Asn Gly Gln Lys Met Trp Ile
            180                 185                 190

Thr Asn Gly Gly Lys Ala Asn Trp Tyr Phe Leu Leu Ala Arg Ser Asp
        195                 200                 205

Pro Asp Pro Lys Ala Pro Ala Asn Lys Ala Phe Thr Gly Phe Ile Val
    210                 215                 220

Glu Ala Asp Thr Pro Gly Ile Gln Ile Gly Arg Lys Glu Leu Asn Met
225                 230                 235                 240

Gly Gln Arg Cys Ser Asp Thr Arg Gly Ile Val Phe Glu Asp Val Lys
                245                 250                 255

Val Pro Lys Glu Asn Val Leu Ile Gly Asp Gly Ala Gly Phe Lys Val
            260                 265                 270

Ala Met Gly Ala Phe Asp Lys Thr Arg Pro Val Val Ala Ala Gly Ala
        275                 280                 285

Val Gly Leu Ala Gln Arg Ala Leu Asp Glu Ala Thr Lys Tyr Ala Leu
    290                 295                 300

Glu Arg Lys Thr Phe Gly Lys Leu Leu Val Glu His Gln Ala Ile Ser
305                 310                 315                 320

Phe Met Leu Ala Glu Met Ala Met Lys Val Glu Leu Ala Arg Met Ser
                325                 330                 335

Tyr Gln Arg Ala Ala Trp Glu Val Asp Ser Gly Arg Arg Asn Thr Tyr
            340                 345                 350

Tyr Ala Ser Ile Ala Lys Ala Phe Ala Gly Asp Ile Ala Asn Gln Leu
        355                 360                 365
```

```
Ala Thr Asp Ala Val Gln Ile Leu Gly Gly Asn Gly Phe Asn Thr Glu
    370                 375                 380

Tyr Pro Val Glu Lys Leu Met Arg Asp Ala Lys Ile Tyr Gln Ile Tyr
385                 390                 395                 400

Glu Gly Thr Ser Gln Ile Gln Arg Leu Ile Val Ala Arg Glu His Ile
                405                 410                 415

Asp Lys Tyr Lys Asn
            420
```

<210> 1857
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="Uniprot ID: P11310; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000409612"

<400> 1857

```
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Cys Ser Leu Gln Val Leu
1               5                   10                  15

Arg Ser Ile Ser Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn
            20                  25                  30

Arg Gln Arg Glu Pro Gly Leu Gly Phe Ser Phe Glu Phe Thr Glu Gln
        35                  40                  45

Gln Lys Glu Phe Gln Ala Thr Ala Arg Lys Phe Ala Arg Glu Glu Ile
```

```
    50                  55                  60

Ile Pro Val Ala Ala Glu Tyr Asp Lys Thr Gly Glu Tyr Pro Val Pro
65                  70                  75                  80

Leu Ile Arg Arg Ala Trp Glu Leu Gly Leu Met Asn Thr His Ile Pro
                85                  90                  95

Glu Asn Cys Gly Gly Leu Gly Leu Gly Thr Phe Asp Ala Cys Leu Ile
            100                 105                 110

Ser Glu Glu Leu Ala Tyr Gly Cys Thr Gly Val Gln Thr Ala Ile Glu
        115                 120                 125

Gly Asn Ser Leu Gly Gln Met Pro Ile Ile Ile Ala Gly Asn Asp Gln
    130                 135                 140

Gln Lys Lys Lys Tyr Leu Gly Arg Met Thr Glu Glu Pro Leu Met Cys
145                 150                 155                 160

Ala Tyr Cys Val Thr Glu Pro Gly Ala Gly Ser Asp Val Ala Gly Ile
                165                 170                 175

Lys Thr Lys Ala Glu Lys Lys Gly Asp Glu Tyr Ile Ile Asn Gly Gln
            180                 185                 190

Lys Met Trp Ile Thr Asn Gly Gly Lys Ala Asn Trp Tyr Phe Leu Leu
        195                 200                 205

Ala Arg Ser Asp Pro Asp Pro Lys Ala Pro Ala Asn Lys Ala Phe Thr
    210                 215                 220

Gly Phe Ile Val Glu Ala Asp Thr Pro Gly Ile Gln Ile Gly Arg Lys
225                 230                 235                 240

Glu Leu Asn Met Gly Gln Arg Cys Ser Asp Thr Arg Gly Ile Val Phe
                245                 250                 255

Glu Asp Val Lys Val Pro Lys Glu Asn Val Leu Ile Gly Asp Gly Ala
            260                 265                 270

Gly Phe Lys Val Ala Met Gly Ala Phe Asp Lys Thr Arg Pro Val Val
        275                 280                 285
```

```
Ala Ala Gly Ala Val Gly Leu Ala Gln Arg Ala Leu Asp Glu Ala Thr
    290                 295                 300

Lys Tyr Ala Leu Glu Arg Lys Thr Phe Gly Lys Leu Leu Val Glu His
305                 310                 315                 320

Gln Ala Ile Ser Phe Met Leu Ala Glu Met Ala Met Lys Val Glu Leu
                325                 330                 335

Ala Arg Met Ser Tyr Gln Arg Ala Ala Trp Glu Val Asp Ser Gly Arg
            340                 345                 350

Arg Asn Thr Tyr Tyr Ala Ser Ile Ala Lys Ala Phe Ala Gly Asp Ile
        355                 360                 365

Ala Asn Gln Leu Ala Thr Asp Ala Val Gln Ile Leu Gly Gly Asn Gly
    370                 375                 380

Phe Asn Thr Glu Tyr Pro Val Glu Lys Leu Met Arg Asp Ala Lys Ile
385                 390                 395                 400

Tyr Gln Ile Tyr Glu Gly Thr Ser Gln Ile Gln Arg Leu Ile Val Ala
                405                 410                 415

Arg Glu His Ile Asp Lys Tyr Lys Asn
            420                 425


<210> 1858
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
```

<221> source
<223> /note="ENSP ID: ENSP00000431372"

<400> 1858
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Val Leu Arg Ser Ile Ser
1   5   10   15

Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn Arg Gln Arg Glu
            20   25   30

Pro Gly Leu Gly Phe Ser Phe Gly Leu Leu Cys Asn Arg Thr Trp Ser
        35   40   45

Arg Leu
    50

<210> 1859
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431953"

<400> 1859
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Ser Ser Pro Asn Ser Arg
1   5   10   15

Lys Asn Phe Lys Leu Leu Leu Val Asn Leu Pro Glu Arg Lys Ser Ser
            20   25   30

Gln Trp Leu Gln Asn Met Ile Lys Leu Val Asn Ile Gln Ser Pro
        35   40   45

<210> 1860
<211> 45

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000432522"

<400> 1860
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Val Leu Arg Ser Ile Ser
1 5 10 15

Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn Arg Gln Arg Glu
20 25 30

Pro Gly Leu Gly Phe Ser Phe Val Ser Ser Pro Pro Asn
35 40 45

<210> 1861
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434092"

<400> 1861
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Val Leu Arg Ser Ile Ser

```
1               5                   10                  15

Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn Arg Gln Arg Glu
            20                  25                  30

Pro Gly Leu Gly Phe Ser Phe Glu Phe Thr Glu Gln Gln Lys Glu Phe
        35                  40                  45

Gln Ala Thr Ala Arg Lys Phe Ala Arg Glu Glu Ile Ile Pro Val Ala
    50                  55                  60

Ala Glu Tyr Asp Lys Thr Gly Glu Phe Phe Phe Phe
65                  70                  75


<210> 1862
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434284"

<400> 1862
Leu Ile Gly Asp Gly Ala Gly Phe Lys Val Ala Met Gly Ala Phe Asp
1               5                   10                  15

Lys Thr Arg Pro Val Val Ala Ala Gly Ala Val Gly Leu Ala Gln Arg
            20                  25                  30

Ala Leu Asp Glu Ala Thr Lys Tyr Ala Leu Glu Arg Lys Thr Phe Gly
        35                  40                  45

Lys Leu Leu Val Glu Val Leu Phe Pro Leu His Leu Pro Thr Ser Leu
    50                  55                  60
```

Lys Val Ser
65

<210> 1863
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434823"

<400> 1863
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Ser Ser Pro Asn Ser Arg
1 5 10 15

Lys Asn Phe Lys Leu Leu Leu Val Asn Leu Pro Glu Arg Lys Ser Ser
20 25 30

Gln Trp Leu Gln Asn Met Ile Lys Leu Val Asn Ile Gln Ser Pro
35 40 45

<210> 1864
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435584"

<400> 1864
Met Ala Ala Gly Phe Gly Arg Cys Cys Arg Val Leu Arg Ser Ile Ser
1   5   10   15

Arg Phe His Trp Arg Ser Gln His Thr Lys Ala Asn Arg Gln Arg Glu
            20   25   30

Pro Gly Leu Gly Phe Ser Phe Glu Phe Thr Glu Gln Gln Lys Glu Phe
        35   40   45

Gln Ala Thr Ala Arg Lys Phe Ala Arg Glu Glu Ile Ile Pro Val Ala
    50   55   60

Ala Glu Tyr Asp Lys Thr Gly Glu Tyr Pro Val Pro Leu Ile Arg Arg
65   70   75   80

Ala Trp Glu Leu Gly Leu Met Asn Thr His Ile Pro Glu Asn Cys Ala
                85   90   95

Asn Ala Tyr Tyr Tyr Cys Trp Lys
            100

<210> 1865
<211> 385
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 492; "

<220>
<221> source
<223> /note="Gene Symbol: ACADM; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, C-4 to C-12 straight chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442324"

<400> 1865

```
Met Leu Gln Glu Phe Thr Glu Gln Gln Lys Glu Phe Gln Ala Thr Ala
1               5                  10                  15

Arg Lys Phe Ala Arg Glu Glu Ile Ile Pro Val Ala Ala Glu Tyr Asp
            20                  25                  30

Lys Thr Gly Glu Tyr Pro Val Pro Leu Ile Arg Arg Ala Trp Glu Leu
        35                  40                  45

Gly Leu Met Asn Thr His Ile Pro Glu Asn Cys Gly Gly Leu Gly Leu
    50                  55                  60

Gly Thr Phe Asp Ala Cys Leu Ile Ser Glu Glu Leu Ala Tyr Gly Cys
65                  70                  75                  80

Thr Gly Val Gln Thr Ala Ile Glu Gly Asn Ser Leu Gly Gln Met Pro
                85                  90                  95

Ile Ile Ile Ala Gly Asn Asp Gln Gln Lys Lys Lys Tyr Leu Gly Arg
            100                 105                 110

Met Thr Glu Glu Pro Leu Met Cys Ala Tyr Cys Val Thr Glu Pro Gly
        115                 120                 125

Ala Gly Ser Asp Val Ala Gly Ile Lys Thr Lys Ala Glu Lys Lys Gly
    130                 135                 140

Asp Glu Tyr Ile Ile Asn Gly Gln Lys Met Trp Ile Thr Asn Gly Gly
145                 150                 155                 160

Lys Ala Asn Trp Tyr Phe Leu Leu Ala Arg Ser Asp Pro Asp Pro Lys
                165                 170                 175

Ala Pro Ala Asn Lys Ala Phe Thr Gly Phe Ile Val Glu Ala Asp Thr
            180                 185                 190

Pro Gly Ile Gln Ile Gly Arg Lys Glu Leu Asn Met Gly Gln Arg Cys
        195                 200                 205

Ser Asp Thr Arg Gly Ile Val Phe Glu Asp Val Lys Val Pro Lys Glu
    210                 215                 220

Asn Val Leu Ile Gly Asp Gly Ala Gly Phe Lys Val Ala Met Gly Ala
```

```
225                 230                 235                 240

Phe Asp Lys Thr Arg Pro Val Val Ala Ala Gly Ala Val Gly Leu Ala
                245                 250                 255

Gln Arg Ala Leu Asp Glu Ala Thr Lys Tyr Ala Leu Glu Arg Lys Thr
            260                 265                 270

Phe Gly Lys Leu Leu Val Glu His Gln Ala Ile Ser Phe Met Leu Ala
        275                 280                 285

Glu Met Ala Met Lys Val Glu Leu Ala Arg Met Ser Tyr Gln Arg Ala
    290                 295                 300

Ala Trp Glu Val Asp Ser Gly Arg Arg Asn Thr Tyr Tyr Ala Ser Ile
305                 310                 315                 320

Ala Lys Ala Phe Ala Gly Asp Ile Ala Asn Gln Leu Ala Thr Asp Ala
                325                 330                 335

Val Gln Ile Leu Gly Gly Asn Gly Phe Asn Thr Glu Tyr Pro Val Glu
            340                 345                 350

Lys Leu Met Arg Asp Ala Lys Ile Tyr Gln Ile Tyr Glu Gly Thr Ser
        355                 360                 365

Gln Ile Gln Arg Leu Ile Val Ala Arg Glu His Ile Asp Lys Tyr Lys
    370                 375                 380

Asn
385


<210> 1866
<211> 430
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 493; "

<220>
<221> source
<223> /note="Gene Symbol: ACADL; "

<220>
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<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, long chain; "

<220>
<221> source
<223> /note="Uniprot ID: P28330; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000233710"

<400> 1866

```
Met Ala Ala Arg Leu Leu Arg Gly Ser Leu Arg Val Leu Gly Gly His
1               5                  10                  15

Arg Ala Pro Arg Gln Leu Pro Ala Ala Arg Cys Ser His Ser Gly Gly
            20                  25                  30

Glu Glu Arg Leu Glu Thr Pro Ser Ala Lys Lys Leu Thr Asp Ile Gly
        35                  40                  45

Ile Arg Arg Ile Phe Ser Pro Glu His Asp Ile Phe Arg Lys Ser Val
    50                  55                  60

Arg Lys Phe Phe Gln Glu Glu Val Ile Pro His His Ser Glu Trp Glu
65                  70                  75                  80

Lys Ala Gly Glu Val Ser Arg Glu Val Trp Glu Lys Ala Gly Lys Gln
                85                  90                  95

Gly Leu Leu Gly Val Asn Ile Ala Glu His Leu Gly Gly Ile Gly Gly
            100                 105                 110

Asp Leu Tyr Ser Ala Ala Ile Val Trp Glu Glu Gln Ala Tyr Ser Asn
        115                 120                 125

Cys Ser Gly Pro Gly Phe Ser Ile His Ser Gly Ile Val Met Ser Tyr
    130                 135                 140

Ile Thr Asn His Gly Ser Glu Glu Gln Ile Lys His Phe Ile Pro Gln
145                 150                 155                 160

Met Thr Ala Gly Lys Cys Ile Gly Ala Ile Ala Met Thr Glu Pro Gly
                165                 170                 175
```

```
Ala Gly Ser Asp Leu Gln Gly Ile Lys Thr Asn Ala Lys Lys Asp Gly
            180                 185                 190

Ser Asp Trp Ile Leu Asn Gly Ser Lys Val Phe Ile Ser Asn Gly Ser
        195                 200                 205

Leu Ser Asp Val Val Ile Val Val Ala Val Thr Asn His Glu Ala Pro
    210                 215                 220

Ser Pro Ala His Gly Ile Ser Leu Phe Leu Val Glu Asn Gly Met Lys
225                 230                 235                 240

Gly Phe Ile Lys Gly Arg Lys Leu His Lys Met Gly Leu Lys Ala Gln
                245                 250                 255

Asp Thr Ala Glu Leu Phe Phe Glu Asp Ile Arg Leu Pro Ala Ser Ala
            260                 265                 270

Leu Leu Gly Glu Glu Asn Lys Gly Phe Tyr Tyr Ile Met Lys Glu Leu
        275                 280                 285

Pro Gln Glu Arg Leu Leu Ile Ala Asp Val Ala Ile Ser Ala Ser Glu
    290                 295                 300

Phe Met Phe Glu Glu Thr Arg Asn Tyr Val Lys Gln Arg Lys Ala Phe
305                 310                 315                 320

Gly Lys Thr Val Ala His Leu Gln Thr Val Gln His Lys Leu Ala Glu
                325                 330                 335

Leu Lys Thr His Ile Cys Val Thr Arg Ala Phe Val Asp Asn Cys Leu
            340                 345                 350

Gln Leu His Glu Ala Lys Arg Leu Asp Ser Ala Thr Ala Cys Met Ala
        355                 360                 365

Lys Tyr Trp Ala Ser Glu Leu Gln Asn Ser Val Ala Tyr Asp Cys Val
    370                 375                 380

Gln Leu His Gly Gly Trp Gly Tyr Met Trp Glu Tyr Pro Ile Ala Lys
385                 390                 395                 400

Ala Tyr Val Asp Ala Arg Val Gln Pro Ile Tyr Gly Gly Thr Asn Glu
```

405 410 415

Ile Met Lys Glu Leu Ile Ala Arg Glu Ile Val Phe Asp Lys
420 425 430

<210> 1867
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 494; "

<220>
<221> source
<223> /note="Gene Symbol: ACADSB; "

<220>
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<223> /note="Gene Name:
acyl-CoA dehydrogenase, short/branched chain; "

<220>
<221> source
<223> /note="Uniprot ID: P45954; "

<220>
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<223> /note="ENSP ID: ENSP00000357862"

<400> 1867
Met Gly Ile Glu Val Asp Pro Glu Tyr Gly Gly Thr Gly Ala Ser Phe
1 5 10 15

Leu Ser Thr Val Leu Val Ile Glu Glu Leu Ala Lys Val Asp Ala Ser
20 25 30

Val Ala Val Phe Cys Glu Ile Gln Asn Thr Leu Ile Asn Thr Leu Ile
35 40 45

Arg Lys His Gly Thr Glu Glu Gln Lys Ala Thr Tyr Leu Pro Gln Leu
50 55 60

Thr Thr Glu Lys Val Gly Ser Phe Cys Leu Ser Glu Ala Gly Ala Gly
65 70 75 80

Ser Asp Ser Phe Ala Leu Lys Thr Arg Ala Asp Lys Glu Gly Asp Tyr
85 90 95

```
Tyr Val Leu Asn Gly Ser Lys Met Trp Ile Ser Ser Ala Glu His Ala
            100                 105                 110

Gly Leu Phe Leu Val Met Ala Asn Val Asp Pro Thr Ile Gly Tyr Lys
        115                 120                 125

Gly Ile Thr Ser Phe Leu Val Asp Arg Asp Thr Pro Gly Leu His Ile
    130                 135                 140

Gly Lys Pro Glu Asn Lys Leu Gly Leu Arg Ala Ser Ser Thr Cys Pro
145                 150                 155                 160

Leu Thr Phe Glu Asn Val Lys Val Pro Glu Ala Asn Ile Leu Gly Gln
                165                 170                 175

Ile Gly His Gly Tyr Lys Tyr Ala Ile Gly Ser Leu Asn Glu Gly Arg
            180                 185                 190

Ile Gly Ile Ala Ala Gln Met Leu Gly Leu Ala Gln Gly Cys Phe Asp
        195                 200                 205

Tyr Thr Ile Pro Tyr Ile Lys Glu Arg Ile Gln Phe Gly Lys Arg Leu
    210                 215                 220

Phe Asp Phe Gln Gly Leu Gln His Gln Val Ala His Val Ala Thr Gln
225                 230                 235                 240

Leu Glu Ala Ala Arg Leu Leu Thr Tyr Asn Ala Ala Arg Leu Leu Glu
                245                 250                 255

Ala Gly Lys Pro Phe Ile Lys Glu Ala Ser Met Ala Lys Tyr Tyr Ala
            260                 265                 270

Ser Glu Ile Ala Gly Gln Thr Thr Ser Lys Cys Ile Glu Trp Met Gly
        275                 280                 285

Gly Val Gly Tyr Thr Lys Asp Tyr Pro Val Glu Lys Tyr Phe Arg Asp
    290                 295                 300

Ala Lys Ile Gly Thr Ile Tyr Glu Gly Ala Ser Asn Ile Gln Leu Asn
305                 310                 315                 320
```

Thr Ile Ala Lys His Ile Asp Ala Glu Tyr
325 330

<210> 1868
<211> 432
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA dehydrogenase, short/branched chain; "

<220>
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<223> /note="Uniprot ID: P45954; "

<220>
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<223> /note="ENSP ID: ENSP00000357873"

<400> 1868
Met Glu Gly Leu Ala Val Arg Leu Leu Arg Gly Ser Arg Leu Leu Arg
1 5 10 15

Arg Asn Phe Leu Thr Cys Leu Ser Ser Trp Lys Ile Pro Pro His Val
20 25 30

Ser Lys Ser Ser Gln Ser Glu Ala Leu Leu Asn Ile Thr Asn Asn Gly
35 40 45

Ile His Phe Ala Pro Leu Gln Thr Phe Thr Asp Glu Glu Met Met Ile
50 55 60

Lys Ser Ser Val Lys Lys Phe Ala Gln Glu Gln Ile Ala Pro Leu Val
65 70 75 80

Ser Thr Met Asp Glu Asn Ser Lys Met Glu Lys Ser Val Ile Gln Gly
85 90 95

Leu Phe Gln Gln Gly Leu Met Gly Ile Glu Val Asp Pro Glu Tyr Gly
100 105 110

```
Gly Thr Gly Ala Ser Phe Leu Ser Thr Val Leu Val Ile Glu Glu Leu
        115                 120                 125

Ala Lys Val Asp Ala Ser Val Ala Val Phe Cys Glu Ile Gln Asn Thr
    130                 135                 140

Leu Ile Asn Thr Leu Ile Arg Lys His Gly Thr Glu Glu Gln Lys Ala
145                 150                 155                 160

Thr Tyr Leu Pro Gln Leu Thr Thr Glu Lys Val Gly Ser Phe Cys Leu
                165                 170                 175

Ser Glu Ala Gly Ala Gly Ser Asp Ser Phe Ala Leu Lys Thr Arg Ala
            180                 185                 190

Asp Lys Glu Gly Asp Tyr Tyr Val Leu Asn Gly Ser Lys Met Trp Ile
        195                 200                 205

Ser Ser Ala Glu His Ala Gly Leu Phe Leu Val Met Ala Asn Val Asp
    210                 215                 220

Pro Thr Ile Gly Tyr Lys Gly Ile Thr Ser Phe Leu Val Asp Arg Asp
225                 230                 235                 240

Thr Pro Gly Leu His Ile Gly Lys Pro Glu Asn Lys Leu Gly Leu Arg
                245                 250                 255

Ala Ser Ser Thr Cys Pro Leu Thr Phe Glu Asn Val Lys Val Pro Glu
            260                 265                 270

Ala Asn Ile Leu Gly Gln Ile Gly His Gly Tyr Lys Tyr Ala Ile Gly
        275                 280                 285

Ser Leu Asn Glu Gly Arg Ile Gly Ile Ala Ala Gln Met Leu Gly Leu
    290                 295                 300

Ala Gln Gly Cys Phe Asp Tyr Thr Ile Pro Tyr Ile Lys Glu Arg Ile
305                 310                 315                 320

Gln Phe Gly Lys Arg Leu Phe Asp Phe Gln Gly Leu Gln His Gln Val
                325                 330                 335
```

```
Ala His Val Ala Thr Gln Leu Glu Ala Ala Arg Leu Leu Thr Tyr Asn
            340                 345                 350

Ala Ala Arg Leu Leu Glu Ala Gly Lys Pro Phe Ile Lys Glu Ala Ser
        355                 360                 365

Met Ala Lys Tyr Tyr Ala Ser Glu Ile Ala Gly Gln Thr Thr Ser Lys
    370                 375                 380

Cys Ile Glu Trp Met Gly Gly Val Gly Tyr Thr Lys Asp Tyr Pro Val
385                 390                 395                 400

Glu Lys Tyr Phe Arg Asp Ala Lys Ile Gly Thr Ile Tyr Glu Gly Ala
                405                 410                 415

Ser Asn Ile Gln Leu Asn Thr Ile Ala Lys His Ile Asp Ala Glu Tyr
            420                 425                 430
```

<210> 1869
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000325395"

<400> 1869

```
Met Gln Ala Ala Arg Met Ala Ala Ser Leu Gly Arg Gln Leu Leu Arg
1               5                   10                  15

Leu Gly Gly Gly Arg Ser Val Cys Asp Lys Arg Asp Gly Gly Gln Arg
            20                  25                  30

Pro Trp Ala Pro Gly Arg His
```

35

<210> 1870
<211> 633
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="Uniprot ID: P49748; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000344152"

<400> 1870
Met Gln Ala Ala Arg Met Ala Ala Ser Leu Gly Arg Gln Leu Leu Arg
1   5   10   15

Leu Gly Gly Gly Ser Ser Arg Leu Thr Ala Leu Leu Gly Gln Pro Arg
            20   25   30

Pro Gly Pro Ala Arg Arg Pro Tyr Ala Gly Gly Ala Ala Gln Glu Ser
        35   40   45

Lys Ser Phe Ala Val Gly Met Phe Lys Gly Gln Leu Thr Thr Asp Gln
    50   55   60

Val Phe Pro Tyr Pro Ser Val Leu Asn Glu Glu Gln Thr Gln Phe Leu
65   70   75   80

Lys Glu Leu Val Glu Pro Val Ser Arg Phe Phe Glu Glu Val Asn Asp
                85   90   95

Pro Ala Lys Asn Asp Ala Leu Glu Met Val Glu Glu Thr Thr Trp Gln
            100   105   110

```
Gly Leu Lys Glu Leu Gly Ala Phe Gly Leu Gln Val Pro Ser Glu Leu
        115                 120                 125

Gly Gly Val Gly Leu Cys Asn Thr Gln Tyr Ala Arg Leu Val Glu Ile
    130                 135                 140

Val Gly Met His Asp Leu Gly Val Gly Ile Thr Leu Gly Ala His Gln
145                 150                 155                 160

Ser Ile Gly Phe Lys Gly Ile Leu Leu Phe Gly Thr Lys Ala Gln Lys
                165                 170                 175

Glu Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu Thr Val Ala Ala Phe
            180                 185                 190

Cys Leu Thr Glu Pro Ser Ser Gly Ser Asp Ala Ala Ser Ile Arg Thr
        195                 200                 205

Ser Ala Val Pro Ser Pro Cys Gly Lys Tyr Tyr Thr Leu Asn Gly Ser
    210                 215                 220

Lys Leu Trp Ile Ser Asn Gly Gly Leu Ala Asp Ile Phe Thr Val Phe
225                 230                 235                 240

Ala Lys Thr Pro Val Thr Asp Pro Ala Thr Gly Ala Val Lys Glu Lys
                245                 250                 255

Ile Thr Ala Phe Val Val Glu Arg Gly Phe Gly Gly Ile Thr His Gly
            260                 265                 270

Pro Pro Glu Lys Lys Met Gly Ile Lys Ala Ser Asn Thr Ala Glu Val
        275                 280                 285

Phe Phe Asp Gly Val Arg Val Pro Ser Glu Asn Val Leu Gly Glu Val
    290                 295                 300

Gly Ser Gly Phe Lys Val Ala Met His Ile Leu Asn Asn Gly Arg Phe
305                 310                 315                 320

Gly Met Ala Ala Ala Leu Ala Gly Thr Met Arg Gly Ile Ile Ala Lys
                325                 330                 335
```

```
Ala Val Asp His Ala Thr Asn Arg Thr Gln Phe Gly Glu Lys Ile His
            340                 345                 350

Asn Phe Gly Leu Ile Gln Glu Lys Leu Ala Arg Met Val Met Leu Gln
        355                 360                 365

Tyr Val Thr Glu Ser Met Ala Tyr Met Val Ser Ala Asn Met Asp Gln
    370                 375                 380

Gly Ala Thr Asp Phe Gln Ile Glu Ala Ala Ile Ser Lys Ile Phe Gly
385                 390                 395                 400

Ser Glu Ala Ala Trp Lys Val Thr Asp Glu Cys Ile Gln Ile Met Gly
                405                 410                 415

Gly Met Gly Phe Met Lys Glu Pro Gly Val Glu Arg Val Leu Arg Asp
            420                 425                 430

Leu Arg Ile Phe Arg Ile Phe Glu Gly Thr Asn Asp Ile Leu Arg Leu
        435                 440                 445

Phe Val Ala Leu Gln Gly Cys Met Asp Lys Gly Lys Glu Leu Ser Gly
    450                 455                 460

Leu Gly Ser Ala Leu Lys Asn Pro Phe Gly Asn Ala Gly Leu Leu Leu
465                 470                 475                 480

Gly Glu Ala Gly Lys Gln Leu Arg Arg Arg Ala Gly Leu Gly Ser Gly
                485                 490                 495

Leu Ser Leu Ser Gly Leu Val His Pro Glu Leu Ser Arg Ser Gly Glu
            500                 505                 510

Leu Ala Val Arg Ala Leu Glu Gln Phe Ala Thr Val Val Glu Ala Lys
        515                 520                 525

Leu Ile Lys His Lys Lys Gly Ile Val Asn Glu Gln Phe Leu Leu Gln
    530                 535                 540

Arg Leu Ala Asp Gly Ala Ile Asp Leu Tyr Ala Met Val Val Val Leu
545                 550                 555                 560

Ser Arg Ala Ser Arg Ser Leu Ser Glu Gly His Pro Thr Ala Gln His
```

565 570 575

Glu Lys Met Leu Cys Asp Thr Trp Cys Ile Glu Ala Ala Ala Arg Ile
580 585 590

Arg Glu Gly Met Ala Ala Leu Gln Ser Asp Pro Trp Gln Gln Glu Leu
595 600 605

Tyr Arg Asn Phe Lys Ser Ile Ser Lys Ala Leu Val Glu Arg Gly Gly
610 615 620

Val Val Thr Ser Asn Pro Leu Gly Phe
625 630

<210> 1871
<211> 655
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="Uniprot ID: P49748; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000349297"

<400> 1871
Met Gln Ala Ala Arg Met Ala Ala Ser Leu Gly Arg Gln Leu Leu Arg
1 5 10 15

Leu Gly Gly Gly Ser Ser Arg Leu Thr Ala Leu Leu Gly Gln Pro Arg
20 25 30

Pro Gly Pro Ala Arg Arg Pro Tyr Ala Gly Gly Ala Ala Gln Leu Ala
35 40 45

```
Leu Asp Lys Ser Asp Ser His Pro Ser Asp Ala Leu Thr Arg Lys Lys
    50                  55                  60

Pro Ala Lys Ala Glu Ser Lys Ser Phe Ala Val Gly Met Phe Lys Gly
65                  70                  75                  80

Gln Leu Thr Thr Asp Gln Val Phe Pro Tyr Pro Ser Val Leu Asn Glu
                85                  90                  95

Glu Gln Thr Gln Phe Leu Lys Glu Leu Val Glu Pro Val Ser Arg Phe
            100                 105                 110

Phe Glu Glu Val Asn Asp Pro Ala Lys Asn Asp Ala Leu Glu Met Val
        115                 120                 125

Glu Glu Thr Thr Trp Gln Gly Leu Lys Glu Leu Gly Ala Phe Gly Leu
    130                 135                 140

Gln Val Pro Ser Glu Leu Gly Gly Val Gly Leu Cys Asn Thr Gln Tyr
145                 150                 155                 160

Ala Arg Leu Val Glu Ile Val Gly Met His Asp Leu Gly Val Gly Ile
                165                 170                 175

Thr Leu Gly Ala His Gln Ser Ile Gly Phe Lys Gly Ile Leu Leu Phe
            180                 185                 190

Gly Thr Lys Ala Gln Lys Glu Lys Tyr Leu Pro Lys Leu Ala Ser Gly
        195                 200                 205

Glu Thr Val Ala Ala Phe Cys Leu Thr Glu Pro Ser Ser Gly Ser Asp
    210                 215                 220

Ala Ala Ser Ile Arg Thr Ser Ala Val Pro Ser Pro Cys Gly Lys Tyr
225                 230                 235                 240

Tyr Thr Leu Asn Gly Ser Lys Leu Trp Ile Ser Asn Gly Gly Leu Ala
                245                 250                 255

Asp Ile Phe Thr Val Phe Ala Lys Thr Pro Val Thr Asp Pro Ala Thr
            260                 265                 270
```

```
Gly Ala Val Lys Glu Lys Ile Thr Ala Phe Val Val Glu Arg Gly Phe
        275                 280                 285

Gly Gly Ile Thr His Gly Pro Pro Glu Lys Lys Met Gly Ile Lys Ala
    290                 295                 300

Ser Asn Thr Ala Glu Val Phe Phe Asp Gly Val Arg Val Pro Ser Glu
305                 310                 315                 320

Asn Val Leu Gly Glu Val Gly Ser Gly Phe Lys Val Ala Met His Ile
                325                 330                 335

Leu Asn Asn Gly Arg Phe Gly Met Ala Ala Ala Leu Ala Gly Thr Met
            340                 345                 350

Arg Gly Ile Ile Ala Lys Ala Val Asp His Ala Thr Asn Arg Thr Gln
        355                 360                 365

Phe Gly Glu Lys Ile His Asn Phe Gly Leu Ile Gln Glu Lys Leu Ala
    370                 375                 380

Arg Met Val Met Leu Gln Tyr Val Thr Glu Ser Met Ala Tyr Met Val
385                 390                 395                 400

Ser Ala Asn Met Asp Gln Gly Ala Thr Asp Phe Gln Ile Glu Ala Ala
                405                 410                 415

Ile Ser Lys Ile Phe Gly Ser Glu Ala Ala Trp Lys Val Thr Asp Glu
            420                 425                 430

Cys Ile Gln Ile Met Gly Gly Met Gly Phe Met Lys Glu Pro Gly Val
        435                 440                 445

Glu Arg Val Leu Arg Asp Leu Arg Ile Phe Arg Ile Phe Glu Gly Thr
    450                 455                 460

Asn Asp Ile Leu Arg Leu Phe Val Ala Leu Gln Gly Cys Met Asp Lys
465                 470                 475                 480

Gly Lys Glu Leu Ser Gly Leu Gly Ser Ala Leu Lys Asn Pro Phe Gly
                485                 490                 495

Asn Ala Gly Leu Leu Leu Gly Glu Ala Gly Lys Gln Leu Arg Arg Arg
```

```
            500                 505                 510

Ala Gly Leu Gly Ser Gly Leu Ser Leu Ser Gly Leu Val His Pro Glu
        515                 520                 525

Leu Ser Arg Ser Gly Glu Leu Ala Val Arg Ala Leu Glu Gln Phe Ala
    530                 535                 540

Thr Val Val Glu Ala Lys Leu Ile Lys His Lys Lys Gly Ile Val Asn
545                 550                 555                 560

Glu Gln Phe Leu Leu Gln Arg Leu Ala Asp Gly Ala Ile Asp Leu Tyr
                565                 570                 575

Ala Met Val Val Val Leu Ser Arg Ala Ser Arg Ser Leu Ser Glu Gly
            580                 585                 590

His Pro Thr Ala Gln His Glu Lys Met Leu Cys Asp Thr Trp Cys Ile
        595                 600                 605

Glu Ala Ala Ala Arg Ile Arg Glu Gly Met Ala Ala Leu Gln Ser Asp
    610                 615                 620

Pro Trp Gln Gln Glu Leu Tyr Arg Asn Phe Lys Ser Ile Ser Lys Ala
625                 630                 635                 640

Leu Val Glu Arg Gly Gly Val Val Thr Ser Asn Pro Leu Gly Phe
                645                 650                 655


<210> 1872
<211> 678
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, very long chain; "
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<220>
<221> source
<223> /note="Uniprot ID: P49748; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438689"

<400> 1872
Met Leu Gly Gly Leu Ala Ala Ala Ala Gly Thr Arg Ile Met Gly Lys
1   5   10   15

Glu Ile Glu Ala Glu Ala Gln Arg Pro Leu Arg Gln Thr Trp Arg Pro
            20   25   30

Gly Gln Pro Pro Ala Met Thr Ala Lys Thr Met Ser Ser Arg Leu Thr
        35   40   45

Ala Leu Leu Gly Gln Pro Arg Pro Gly Pro Ala Arg Arg Pro Tyr Ala
    50   55   60

Gly Gly Ala Ala Gln Leu Ala Leu Asp Lys Ser Asp Ser His Pro Ser
65   70   75   80

Asp Ala Leu Thr Arg Lys Lys Pro Ala Lys Ala Glu Ser Lys Ser Phe
                85   90   95

Ala Val Gly Met Phe Lys Gly Gln Leu Thr Thr Asp Gln Val Phe Pro
            100   105   110

Tyr Pro Ser Val Leu Asn Glu Glu Gln Thr Gln Phe Leu Lys Glu Leu
        115   120   125

Val Glu Pro Val Ser Arg Phe Phe Glu Glu Val Asn Asp Pro Ala Lys
    130   135   140

Asn Asp Ala Leu Glu Met Val Glu Glu Thr Thr Trp Gln Gly Leu Lys
145   150   155   160

Glu Leu Gly Ala Phe Gly Leu Gln Val Pro Ser Glu Leu Gly Gly Val
                165   170   175

Gly Leu Cys Asn Thr Gln Tyr Ala Arg Leu Val Glu Ile Val Gly Met
            180   185   190

```
His Asp Leu Gly Val Gly Ile Thr Leu Gly Ala His Gln Ser Ile Gly
        195                 200                 205

Phe Lys Gly Ile Leu Leu Phe Gly Thr Lys Ala Gln Lys Glu Lys Tyr
    210                 215                 220

Leu Pro Lys Leu Ala Ser Gly Glu Thr Val Ala Ala Phe Cys Leu Thr
225                 230                 235                 240

Glu Pro Ser Ser Gly Ser Asp Ala Ala Ser Ile Arg Thr Ser Ala Val
                245                 250                 255

Pro Ser Pro Cys Gly Lys Tyr Tyr Thr Leu Asn Gly Ser Lys Leu Trp
            260                 265                 270

Ile Ser Asn Gly Gly Leu Ala Asp Ile Phe Thr Val Phe Ala Lys Thr
        275                 280                 285

Pro Val Thr Asp Pro Ala Thr Gly Ala Val Lys Glu Lys Ile Thr Ala
    290                 295                 300

Phe Val Val Glu Arg Gly Phe Gly Gly Ile Thr His Gly Pro Pro Glu
305                 310                 315                 320

Lys Lys Met Gly Ile Lys Ala Ser Asn Thr Ala Glu Val Phe Phe Asp
                325                 330                 335

Gly Val Arg Val Pro Ser Glu Asn Val Leu Gly Glu Val Gly Ser Gly
            340                 345                 350

Phe Lys Val Ala Met His Ile Leu Asn Asn Gly Arg Phe Gly Met Ala
        355                 360                 365

Ala Ala Leu Ala Gly Thr Met Arg Gly Ile Ile Ala Lys Ala Val Asp
    370                 375                 380

His Ala Thr Asn Arg Thr Gln Phe Gly Glu Lys Ile His Asn Phe Gly
385                 390                 395                 400

Leu Ile Gln Glu Lys Leu Ala Arg Met Val Met Leu Gln Tyr Val Thr
                405                 410                 415

Glu Ser Met Ala Tyr Met Val Ser Ala Asn Met Asp Gln Gly Ala Thr
```

```
            420                 425                 430

Asp Phe Gln Ile Glu Ala Ala Ile Ser Lys Ile Phe Gly Ser Glu Ala
        435                 440                 445

Ala Trp Lys Val Thr Asp Glu Cys Ile Gln Ile Met Gly Gly Met Gly
    450                 455                 460

Phe Met Lys Glu Pro Gly Val Glu Arg Val Leu Arg Asp Leu Arg Ile
465                 470                 475                 480

Phe Arg Ile Phe Glu Gly Thr Asn Asp Ile Leu Arg Leu Phe Val Ala
                485                 490                 495

Leu Gln Gly Cys Met Asp Lys Gly Lys Glu Leu Ser Gly Leu Gly Ser
            500                 505                 510

Ala Leu Lys Asn Pro Phe Gly Asn Ala Gly Leu Leu Leu Gly Glu Ala
        515                 520                 525

Gly Lys Gln Leu Arg Arg Arg Ala Gly Leu Gly Ser Gly Leu Ser Leu
    530                 535                 540

Ser Gly Leu Val His Pro Glu Leu Ser Arg Ser Gly Glu Leu Ala Val
545                 550                 555                 560

Arg Ala Leu Glu Gln Phe Ala Thr Val Val Glu Ala Lys Leu Ile Lys
                565                 570                 575

His Lys Lys Gly Ile Val Asn Glu Gln Phe Leu Leu Gln Arg Leu Ala
            580                 585                 590

Asp Gly Ala Ile Asp Leu Tyr Ala Met Val Val Val Leu Ser Arg Ala
        595                 600                 605

Ser Arg Ser Leu Ser Glu Gly His Pro Thr Ala Gln His Glu Lys Met
    610                 615                 620

Leu Cys Asp Thr Trp Cys Ile Glu Ala Ala Ala Arg Ile Arg Glu Gly
625                 630                 635                 640

Met Ala Ala Leu Gln Ser Asp Pro Trp Gln Gln Glu Leu Tyr Arg Asn
                645                 650                 655
```

```
Phe Lys Ser Ile Ser Lys Ala Leu Val Glu Arg Gly Gly Val Val Thr
            660                 665                 670

Ser Asn Pro Leu Gly Phe
        675


<210> 1873
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442082"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1873
Xaa Lys Leu Ala Arg Met Val Met Leu Gln Tyr Val Thr Glu Ser Met
1               5                   10                  15

Ala Tyr Met Val Ser Ala Asn Met Asp Gln Gly Ala Thr Asp Phe Gln
            20                  25                  30

Ile Glu Ala Ala Ile Ser Lys Ile Phe Gly Ser Glu Ala Ala Trp Lys
        35                  40                  45

Val Thr Asp Glu Cys Ile Gln Ile Met Gly Gly Met Gly Phe Met Lys
    50                  55                  60

Glu Pro Gly Val Glu Arg Val Leu Arg Asp Leu Arg Ile Phe Arg Ile
65                  70                  75                  80
```

```
Phe Glu Gly Thr Asn Asp Ile Leu Arg Leu Phe Val Ala Leu Gln Gly
                85                  90                  95

Cys Met Asp Lys Gly Lys Glu Leu Ser Gly Leu Gly Ser Ala Leu Lys
            100                 105                 110

Asn Pro Phe Gly Asn Ala Gly Leu Leu Leu Gly Glu Ala Gly Lys Gln
        115                 120                 125

Leu Arg Arg Arg Ala Gly Leu Gly Ser Gly Leu Ser Leu Ser Gly Leu
    130                 135                 140

Val His Pro Glu Leu Ser Arg Ser Gly Glu Leu Ala Val Arg Ala Leu
145                 150                 155                 160

Glu Gln Phe Ala Thr Val Val Glu Ala Lys Leu Ile Lys His Lys Lys
                165                 170                 175

Gly Ile Val Ser Glu Glu Ala Gly Arg Glu Cys Leu Ser Arg Arg Gly
            180                 185                 190

Pro Gly Pro Gly Ser Gln Pro Ala Gln Ile Tyr Phe His Leu Leu Leu
        195                 200                 205

Pro Ala Arg Ala Ser Arg Ser Leu Ser Glu Gly His Pro Thr Ala Gln
    210                 215                 220

His Glu Lys Met Leu Cys Asp Thr Trp Cys Ile Glu Ala Ala Ala Arg
225                 230                 235                 240

Ile Arg Glu Gly Met Ala Ala Leu Gln Ser Asp Pro Trp Gln Gln Glu
                245                 250                 255

Leu Tyr Arg Asn Phe Lys Ser Ile Ser Lys Ala Leu Val Glu Arg Gly
            260                 265                 270

Gly Val Val Thr Ser Asn Pro Leu Gly Phe
        275                 280
```

<210> 1874
<211> 76
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462366"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1874
Xaa Leu Lys Glu Leu Val Glu Pro Val Ser Arg Phe Phe Glu Glu Val
1 5 10 15

Asn Asp Pro Ala Lys Asn Asp Ala Leu Glu Met Val Glu Glu Thr Thr
20 25 30

Trp Gln Gly Leu Lys Glu Leu Gly Ala Phe Gly Leu Gln Val Pro Ser
35 40 45

Glu Leu Gly Gly Val Gly Leu Cys Asn Thr Gln Ile Pro Ala Ser Pro
50 55 60

Pro Val Arg Pro Phe Gly Gly Asp Arg Gly His Ala
65 70 75

<210> 1875
<211> 204
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source

<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000462611"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1875

```
Xaa Glu Val Gly Ser Gly Phe Lys Val Ala Met His Ile Leu Asn Asn
1               5                  10                  15

Gly Arg Phe Gly Met Ala Ala Ala Leu Ala Gly Thr Met Arg Gly Ile
            20                  25                  30

Ile Ala Lys Ala Val Asp His Ala Thr Asn Arg Thr Gln Phe Gly Glu
        35                  40                  45

Lys Ile His Asn Phe Gly Leu Ile Gln Glu Lys Leu Ala Arg Met Val
    50                  55                  60

Met Leu Gln Tyr Val Thr Glu Ser Met Ala Tyr Met Val Ser Ala Asn
65                  70                  75                  80

Met Asp Gln Gly Ala Thr Asp Phe Gln Ile Glu Ala Ala Ile Ser Lys
                85                  90                  95

Ile Phe Gly Ser Glu Ala Ala Trp Lys Val Thr Asp Glu Cys Ile Gln
            100                 105                 110

Ile Met Gly Gly Met Gly Phe Met Lys Glu Pro Gly Val Glu Arg Val
        115                 120                 125

Leu Arg Asp Leu Arg Ile Phe Arg Ile Phe Glu Gly Thr Asn Asp Ile
    130                 135                 140

Leu Arg Leu Phe Val Ala Leu Gln Gly Cys Met Ala Gly Arg Ala Gly
145                 150                 155                 160
```

```
Gln Arg Pro Glu Ser Gln Arg Thr Cys Pro Pro Gly Val Glu Ser Glu
                165                 170                 175

Trp Arg Ala Gly Ser Thr Gly Ser Gly Ala Val Cys His Cys Gly Gly
            180                 185                 190

Gly Gln Ala Asp Lys Thr Gln Glu Gly Asp Cys Gln
        195                 200


<210> 1876
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000463246"

<400> 1876
Met Gln Ala Ala Arg Met Ala Ala Ser Leu Gly Arg Gln Leu Leu Arg
1               5                   10                  15

Leu Gly Gly Gly Ser Ser Arg Leu Thr Ala Leu Leu Gly Gln Pro Arg
            20                  25                  30

Pro Gly Pro Ala Arg Arg Pro Tyr Ala Gly Gly Ala Ala Gln Leu Ala
        35                  40                  45

Leu Asp Lys Ser Asp Ser His Pro Ser Asp Ala Leu Thr Arg Lys Lys
    50                  55                  60

Pro Ala Lys Asn Asp Ala Leu Glu Met Val Glu Glu Thr Thr Trp Gln
65                  70                  75                  80

Gly Leu Lys Glu Leu Gly Ala Phe Gly Leu Gln Val Pro Ser Glu Leu
```

```
                85                  90                  95

Gly Gly Val Gly Leu Cys Asn Thr Gln Tyr Ala Arg Leu Val Glu Ile
            100                 105                 110

Val Gly Met His Asp Leu Gly Val Gly Ile Thr Leu Gly Ala His Gln
        115                 120                 125

Ser Ile Gly Phe Lys Gly Ile Leu Leu Phe Gly Thr Lys Ala Gln Lys
    130                 135                 140

Glu Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu
145                 150                 155


<210> 1877
<211> 194
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000464254"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1877
Xaa Leu Gln Tyr Val Thr Glu Ser Met Ala Tyr Met Val Ser Ala Asn
1               5                   10                  15

Met Asp Gln Gly Ala Thr Asp Phe Gln Ile Glu Ala Ala Ile Ser Lys
            20                  25                  30

Ile Phe Gly Ser Glu Ala Ala Trp Lys Val Thr Asp Glu Cys Ile Gln
```

```
        35                  40                  45

Ile Met Gly Gly Met Gly Phe Met Lys Glu Pro Gly Val Glu Arg Val
    50                  55                  60

Leu Arg Asp Leu Arg Ile Phe Arg Ile Phe Glu Gly Thr Asn Asp Ile
65                  70                  75                  80

Leu Arg Leu Phe Val Ala Leu Gln Gly Cys Met Ala Gly Arg Ala Gly
                85                  90                  95

Gln Arg Pro Glu Ser Gln Arg Thr Cys Pro Pro Gly Val Glu Ser Glu
            100                 105                 110

Trp Arg Ala Val Arg Ala Leu Glu Gln Phe Ala Thr Val Val Glu Ala
        115                 120                 125

Lys Leu Ile Lys His Lys Lys Gly Ile Val Asn Glu Gln Phe Leu Leu
    130                 135                 140

Gln Arg Leu Ala Asp Gly Ala Ile Asp Leu Tyr Ala Met Val Val Val
145                 150                 155                 160

Leu Ser Arg Ala Ser Arg Ser Leu Ser Glu Gly His Pro Thr Ala Gln
                165                 170                 175

His Glu Lys Met Leu Cys Asp Thr Trp Cys Ile Glu Ala Ala Ala Arg
            180                 185                 190

Ile Arg


<210> 1878
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
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<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465353"

<400> 1878
Met Gln Ala Ala Arg Met Ala Ala Ser Leu Gly Arg Gln Leu Leu Arg
1 5 10 15

Leu Gly Gly Gly Ser Ser Arg Leu Thr Ala Leu Leu Gly Gln Pro Arg
20 25 30

Pro Gly Pro Ala Arg Arg Pro Tyr Ala Gly Gly Ala Ala Gln Leu Ala
35 40 45

Leu Asp Lys Ser Asp Ser His Pro Ser Asp Ala Leu Thr Arg Lys Lys
50 55 60

Pro Ala Lys Ala Glu Ser Lys Ser Phe Ala Val Gly Met Phe Lys Gly
65 70 75 80

Gln Leu Thr Thr Asp Gln Val Phe Pro Tyr Pro Ser Val Leu Asn Glu
85 90 95

Glu Gln Thr Gln Phe Leu Lys Glu Leu Val Glu Pro Val Ser Arg Phe
100 105 110

Phe Glu Glu Pro Gly Cys Gly Ile Leu Cys Leu Pro Gln Glu Val Asn
115 120 125

Asp Pro Ala Lys Asn Asp Ala Leu Glu Met Val Glu Glu Thr Thr Trp
130 135 140

Gln Gly Leu Lys Glu Leu Gly Ala Phe Gly Leu Gln Val
145 150 155

<210> 1879
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466487"

<400> 1879
Ala Leu Glu Gln Phe Ala Thr Val Val Glu Ala Lys Leu Ile Lys His
1 5 10 15

Lys Lys Gly Ile Val Thr Ala Gly Arg Arg Gly His Arg Pro Leu Cys
20 25 30

His Gly Gly Gly Ser Leu Glu Gly Leu Lys Ile Pro Glu
35 40 45

<210> 1880
<211> 224
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 495; "

<220>
<221> source
<223> /note="Gene Symbol: ACADVL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA dehydrogenase, very long chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467920"

<400> 1880
Met Gln Ala Ala Arg Met Ala Ala Ser Leu Gly Arg Gln Leu Leu Arg
1 5 10 15

Leu Gly Gly Gly Ser Ser Arg Leu Thr Ala Leu Leu Gly Gln Pro Arg
20 25 30

```
Pro Gly Pro Ala Arg Arg Pro Tyr Ala Gly Gly Ala Ala Gln Leu Ala
        35                  40                  45

Leu Asp Lys Ser Asp Ser His Pro Ser Asp Ala Leu Thr Arg Lys Lys
    50                  55                  60

Pro Ala Lys Ala Glu Ser Lys Ser Phe Ala Val Gly Met Phe Lys Gly
65                  70                  75                  80

Gln Leu Thr Thr Asp Gln Val Phe Pro Tyr Pro Ser Val Leu Asn Glu
                85                  90                  95

Glu Gln Thr Gln Phe Leu Lys Glu Leu Val Glu Pro Val Ser Arg Phe
            100                 105                 110

Phe Glu Glu Val Asn Asp Pro Ala Lys Asn Asp Ala Leu Glu Met Val
        115                 120                 125

Glu Glu Thr Thr Trp Gln Gly Leu Lys Glu Leu Gly Ala Phe Gly Leu
    130                 135                 140

Gln Val Pro Ser Glu Leu Gly Gly Val Gly Leu Cys Asn Thr Gln Tyr
145                 150                 155                 160

Ala Arg Leu Val Glu Ile Val Gly Met His Asp Leu Gly Val Gly Ile
                165                 170                 175

Thr Leu Gly Ala His Gln Ser Ile Gly Phe Lys Gly Ile Leu Leu Phe
            180                 185                 190

Gly Thr Lys Ala Gln Lys Glu Lys Tyr Leu Pro Lys Leu Ala Ser Ala
        195                 200                 205

Leu Ser Pro Thr Gly Glu Thr Val Ala Ala Phe Cys Leu Thr Glu Pro
    210                 215                 220


<210> 1881
<211> 660
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "
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<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="Uniprot ID: Q15067; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000293217"

<400> 1881
Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro
1   5   10   15

Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg
            20   25   30

Arg Arg Glu Ile Glu Asn Met Ile Leu Asn Asp Pro Asp Phe Gln His
        35   40   45

Glu Asp Leu Asn Phe Leu Thr Arg Ser Gln Arg Tyr Glu Val Ala Val
    50   55   60

Arg Lys Ser Ala Ile Met Val Lys Lys Met Arg Glu Phe Gly Ile Ala
65   70   75   80

Asp Pro Asp Glu Ile Met Trp Phe Lys Asn Phe Val His Arg Gly Arg
                85   90   95

Pro Glu Pro Leu Asp Leu His Leu Gly Met Phe Leu Pro Thr Leu Leu
            100   105   110

His Gln Ala Thr Ala Glu Gln Gln Glu Arg Phe Phe Met Pro Ala Trp
        115   120   125

Asn Leu Glu Ile Ile Gly Thr Tyr Ala Gln Thr Glu Met Gly His Gly
    130   135   140

Thr His Leu Arg Gly Leu Glu Thr Thr Ala Thr Tyr Asp Pro Glu Thr
145   150   155   160

```
Gln Glu Phe Ile Leu Asn Ser Pro Thr Val Thr Ser Ile Lys Trp Trp
                165                 170                 175

Pro Gly Gly Leu Gly Lys Thr Ser Asn His Ala Ile Val Leu Ala Gln
            180                 185                 190

Leu Ile Thr Lys Gly Lys Cys Tyr Gly Leu His Ala Phe Ile Val Pro
        195                 200                 205

Ile Arg Glu Ile Gly Thr His Lys Pro Leu Pro Gly Ile Thr Val Gly
    210                 215                 220

Asp Ile Gly Pro Lys Phe Gly Tyr Asp Glu Ile Asp Asn Gly Tyr Leu
225                 230                 235                 240

Lys Met Asp Asn His Arg Ile Pro Arg Glu Asn Met Leu Met Lys Tyr
                245                 250                 255

Ala Gln Val Lys Pro Asp Gly Thr Tyr Val Lys Pro Leu Ser Asn Lys
            260                 265                 270

Leu Thr Tyr Gly Thr Met Val Phe Val Arg Ser Phe Leu Val Gly Glu
        275                 280                 285

Ala Ala Arg Ala Leu Ser Lys Ala Cys Thr Ile Ala Ile Arg Tyr Ser
    290                 295                 300

Ala Val Arg His Gln Ser Glu Ile Lys Pro Gly Glu Pro Glu Pro Gln
305                 310                 315                 320

Ile Leu Asp Phe Gln Thr Gln Gln Tyr Lys Leu Phe Pro Leu Leu Ala
                325                 330                 335

Thr Ala Tyr Ala Phe Gln Phe Val Gly Ala Tyr Met Lys Glu Thr Tyr
            340                 345                 350

His Arg Ile Asn Glu Gly Ile Gly Gln Gly Asp Leu Ser Glu Leu Pro
        355                 360                 365

Glu Leu His Ala Leu Thr Ala Gly Leu Lys Ala Phe Thr Ser Trp Thr
    370                 375                 380
```

```
Ala Asn Thr Gly Ile Glu Ala Cys Arg Met Ala Cys Gly Gly His Gly
385                 390                 395                 400

Tyr Ser His Cys Ser Gly Leu Pro Asn Ile Tyr Val Asn Phe Thr Pro
                405                 410                 415

Ser Cys Thr Phe Glu Gly Glu Asn Thr Val Met Met Leu Gln Thr Ala
            420                 425                 430

Arg Phe Leu Met Lys Ser Tyr Asp Gln Val His Ser Gly Lys Leu Val
        435                 440                 445

Cys Gly Met Val Ser Tyr Leu Asn Asp Leu Pro Ser Gln Arg Ile Gln
    450                 455                 460

Pro Gln Gln Val Ala Val Trp Pro Thr Met Val Asp Ile Asn Ser Pro
465                 470                 475                 480

Glu Ser Leu Thr Glu Ala Tyr Lys Leu Arg Ala Ala Arg Leu Val Glu
                485                 490                 495

Ile Ala Ala Lys Asn Leu Gln Lys Glu Val Ile His Arg Lys Ser Lys
            500                 505                 510

Glu Val Ala Trp Asn Leu Thr Ser Val Asp Leu Val Arg Ala Ser Glu
        515                 520                 525

Ala His Cys His Tyr Val Val Val Lys Leu Phe Ser Glu Lys Leu Leu
    530                 535                 540

Lys Ile Gln Asp Lys Ala Ile Gln Ala Val Leu Arg Ser Leu Cys Leu
545                 550                 555                 560

Leu Tyr Ser Leu Tyr Gly Ile Ser Gln Asn Ala Gly Asp Phe Leu Gln
                565                 570                 575

Gly Ser Ile Met Thr Glu Pro Gln Ile Thr Gln Val Asn Gln Arg Val
            580                 585                 590

Lys Glu Leu Leu Thr Leu Ile Arg Ser Asp Ala Val Ala Leu Val Asp
        595                 600                 605
```

```
Ala Phe Asp Phe Gln Asp Val Thr Leu Gly Ser Val Leu Gly Arg Tyr
    610                 615                 620

Asp Gly Asn Val Tyr Glu Asn Leu Phe Glu Trp Ala Lys Asn Ser Pro
625                 630                 635                 640

Leu Asn Lys Ala Glu Val His Glu Ser Tyr Lys His Leu Lys Ser Leu
                645                 650                 655

Gln Ser Lys Leu
            660
```

<210> 1882
<211> 660
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="Uniprot ID: Q15067; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000301608"

<400> 1882

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Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro
1               5                   10                  15

Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg
            20                  25                  30

Arg Arg Glu Ile Glu Asn Met Ile Leu Asn Asp Pro Asp Phe Gln His
        35                  40                  45

Glu Asp Leu Asn Phe Leu Thr Arg Ser Gln Arg Tyr Glu Val Ala Val
    50                  55                  60
```

Arg Lys Ser Ala Ile Met Val Lys Lys Met Arg Glu Phe Gly Ile Ala
65 70 75 80

Asp Pro Asp Glu Ile Met Trp Phe Lys Lys Leu His Leu Val Asn Phe
85 90 95

Val Glu Pro Val Gly Leu Asn Tyr Ser Met Phe Ile Pro Thr Leu Leu
100 105 110

Asn Gln Gly Thr Thr Ala Gln Lys Glu Lys Trp Leu Leu Ser Ser Lys
115 120 125

Gly Leu Gln Ile Ile Gly Thr Tyr Ala Gln Thr Glu Met Gly His Gly
130 135 140

Thr His Leu Arg Gly Leu Glu Thr Thr Ala Thr Tyr Asp Pro Glu Thr
145 150 155 160

Gln Glu Phe Ile Leu Asn Ser Pro Thr Val Thr Ser Ile Lys Trp Trp
165 170 175

Pro Gly Gly Leu Gly Lys Thr Ser Asn His Ala Ile Val Leu Ala Gln
180 185 190

Leu Ile Thr Lys Gly Lys Cys Tyr Gly Leu His Ala Phe Ile Val Pro
195 200 205

Ile Arg Glu Ile Gly Thr His Lys Pro Leu Pro Gly Ile Thr Val Gly
210 215 220

Asp Ile Gly Pro Lys Phe Gly Tyr Asp Glu Ile Asp Asn Gly Tyr Leu
225 230 235 240

Lys Met Asp Asn His Arg Ile Pro Arg Glu Asn Met Leu Met Lys Tyr
245 250 255

Ala Gln Val Lys Pro Asp Gly Thr Tyr Val Lys Pro Leu Ser Asn Lys
260 265 270

Leu Thr Tyr Gly Thr Met Val Phe Val Arg Ser Phe Leu Val Gly Glu
275 280 285

```
Ala Ala Arg Ala Leu Ser Lys Ala Cys Thr Ile Ala Ile Arg Tyr Ser
    290                 295                 300

Ala Val Arg His Gln Ser Glu Ile Lys Pro Gly Glu Pro Glu Pro Gln
305                 310                 315                 320

Ile Leu Asp Phe Gln Thr Gln Gln Tyr Lys Leu Phe Pro Leu Leu Ala
                325                 330                 335

Thr Ala Tyr Ala Phe Gln Phe Val Gly Ala Tyr Met Lys Glu Thr Tyr
            340                 345                 350

His Arg Ile Asn Glu Gly Ile Gly Gln Gly Asp Leu Ser Glu Leu Pro
        355                 360                 365

Glu Leu His Ala Leu Thr Ala Gly Leu Lys Ala Phe Thr Ser Trp Thr
    370                 375                 380

Ala Asn Thr Gly Ile Glu Ala Cys Arg Met Ala Cys Gly Gly His Gly
385                 390                 395                 400

Tyr Ser His Cys Ser Gly Leu Pro Asn Ile Tyr Val Asn Phe Thr Pro
                405                 410                 415

Ser Cys Thr Phe Glu Gly Glu Asn Thr Val Met Met Leu Gln Thr Ala
            420                 425                 430

Arg Phe Leu Met Lys Ser Tyr Asp Gln Val His Ser Gly Lys Leu Val
        435                 440                 445

Cys Gly Met Val Ser Tyr Leu Asn Asp Leu Pro Ser Gln Arg Ile Gln
    450                 455                 460

Pro Gln Gln Val Ala Val Trp Pro Thr Met Val Asp Ile Asn Ser Pro
465                 470                 475                 480

Glu Ser Leu Thr Glu Ala Tyr Lys Leu Arg Ala Ala Arg Leu Val Glu
                485                 490                 495

Ile Ala Ala Lys Asn Leu Gln Lys Glu Val Ile His Arg Lys Ser Lys
            500                 505                 510
```

```
Glu Val Ala Trp Asn Leu Thr Ser Val Asp Leu Val Arg Ala Ser Glu
        515                 520                 525

Ala His Cys His Tyr Val Val Val Lys Leu Phe Ser Glu Lys Leu Leu
    530                 535                 540

Lys Ile Gln Asp Lys Ala Ile Gln Ala Val Leu Arg Ser Leu Cys Leu
545                 550                 555                 560

Leu Tyr Ser Leu Tyr Gly Ile Ser Gln Asn Ala Gly Asp Phe Leu Gln
                565                 570                 575

Gly Ser Ile Met Thr Glu Pro Gln Ile Thr Gln Val Asn Gln Arg Val
            580                 585                 590

Lys Glu Leu Leu Thr Leu Ile Arg Ser Asp Ala Val Ala Leu Val Asp
        595                 600                 605

Ala Phe Asp Phe Gln Asp Val Thr Leu Gly Ser Val Leu Gly Arg Tyr
    610                 615                 620

Asp Gly Asn Val Tyr Glu Asn Leu Phe Glu Trp Ala Lys Asn Ser Pro
625                 630                 635                 640

Leu Asn Lys Ala Glu Val His Glu Ser Tyr Lys His Leu Lys Ser Leu
                645                 650                 655

Gln Ser Lys Leu
            660


<210> 1883
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 1, palmitoyl; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000458325"

<400> 1883
Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro
1   5   10   15

Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg
            20   25   30

Arg Arg Glu Ile Glu Asn Met Ile Leu Asn Asp Pro Asp Phe Gln His
        35   40   45

Glu Asp Leu Asn Phe Leu Thr Arg Ser Gln Arg Tyr Glu Val Ala Val
    50   55   60

Arg Lys Ser Ala Ile Met Val Lys Lys Met Arg Glu Phe Gly Ile Ala
65   70   75   80

Asp Pro Asp Glu Ile Met Trp Phe Lys Lys Leu His Leu Val Asn Phe
                85   90   95

Val Glu Pro Val Gly Leu Asn Tyr Ser Met Phe Ile Pro Thr Leu Leu
            100   105   110

Asn Gln Gly Thr Thr Ala Gln Lys Glu Lys Trp Leu Leu Ser Ser Lys
        115   120   125

Gly Leu Gln Ile Ile Gly Thr Tyr Ala Gln Thr Glu Met Gly His Val
    130   135   140

Leu Cys Thr Glu Gly Gly Leu Ser Leu Trp Ile Phe Thr Trp Ala Cys
145   150   155   160

Ser Cys Pro Pro Cys Phe Thr Arg Gln Leu Arg Ser Ser Arg Ser Ala
                165   170   175

Ser Ser Cys Pro Pro Gly Thr Trp Arg Ser Leu Ala Leu Met Pro Arg
            180   185   190

Gln Arg Trp Val Met Glu Leu Thr Phe Glu Ala Trp Lys Pro Gln Pro
        195   200   205

```
Arg Met Thr Leu Lys Pro Arg Ser Ser Phe Ser Thr Val Leu Leu
    210                 215                 220


<210> 1884
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459936"

<400> 1884
Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro
1               5                   10                  15


Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg
            20                  25                  30


Arg Arg Glu Ile Gly Glu Gly Gly Gly Arg Asp Leu Pro Pro Phe Pro
        35                  40                  45


Arg Lys Ala Gly Asp Ser Leu Asp Ala Glu Ser Gly Ala Leu Trp Gly
    50                  55                  60


Leu Gly Pro Leu Ala Gln Arg
65                  70


<210> 1885
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "
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<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461486"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1885
Xaa Asn Met Ile Leu Asn Asp Pro Asp Phe Gln His Glu Asp Leu Asn
1 5 10 15

Phe Leu Thr Arg Ser Gln Arg Tyr Glu Val Ala Val Arg Lys Ser Ala
20 25 30

Ile Met Val Lys Lys Met Arg Glu Phe Gly Ile Ala Asp Pro Asp Glu
35 40 45

Ile Met Trp Phe Lys Lys Leu His Leu Val Asn Phe Val Glu Pro Val
50 55 60

Gly Leu Asn Tyr Ser Met Phe Ile Pro Thr Leu Leu Asn Gln Gly Thr
65 70 75 80

Thr Ala Gln Lys Glu Lys Trp Leu Leu Ser Ser Lys Gly Leu Gln Ile
85 90 95

Ile Gly Thr Tyr Ala Gln Thr Glu Met Gly His Gly
100 105

<210> 1886
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466210"

<400> 1886
Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro
1 5 10 15

Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg
20 25 30

Arg Arg Glu Ile Glu Asn Met Ile Leu Asn Asp Pro Asp Phe Gln His
35 40 45

Glu Asp Leu Asn Phe Leu Thr Arg Ser Gln Arg Tyr Glu Val Ala Val
50 55 60

Arg Lys Ser Ala Ile Met Val Lys Lys Met Arg Glu Phe Gly Ile Ala
65 70 75 80

Asp Pro Asp Glu Ile Met Trp Phe Lys Lys Leu His Leu Val Asn Phe
85 90 95

Val Glu Pro Val Gly Leu Asn Tyr Ser Met Phe Ile Pro Thr Leu Leu
100 105 110

Asn Gln Gly Thr Thr Ala Gln Lys Glu Lys Trp Leu Leu Ser Ser Lys
115 120 125

Gly Leu Gln Ile Ile Gly Thr Tyr Ala Gln Thr Glu Met Gly His Val
130 135 140

Gly Lys Thr Ser Asn His Ala Ile Val Leu Ala Gln
145 150 155

<210> 1887
<211> 132
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466921"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1887

Xaa	His	Cys	His	Tyr	Val	Val	Val	Lys	Leu	Phe	Ser	Glu	Lys	Leu	Leu
1				5				10					15		

Lys	Ile	Gln	Asp	Lys	Ala	Ile	Gln	Ala	Val	Leu	Arg	Ser	Leu	Cys	Leu
			20					25					30		

Leu	Tyr	Ser	Leu	Tyr	Gly	Ile	Ser	Gln	Asn	Ala	Gly	Asp	Phe	Leu	Gln
		35					40					45			

Gly	Ser	Ile	Met	Thr	Glu	Pro	Gln	Ile	Thr	Gln	Val	Asn	Gln	Arg	Val
	50					55					60				

Lys	Glu	Leu	Leu	Thr	Leu	Ile	Arg	Ser	Asp	Ala	Val	Ala	Leu	Val	Asp
65					70					75					80

Ala	Phe	Asp	Phe	Gln	Asp	Val	Thr	Leu	Gly	Ser	Val	Leu	Gly	Arg	Tyr
				85					90					95	

Asp	Gly	Asn	Val	Tyr	Glu	Asn	Leu	Phe	Glu	Trp	Ala	Lys	Asn	Ser	Pro
			100					105					110		

Leu	Asn	Lys	Ala	Glu	Val	His	Glu	Ser	Tyr	Lys	His	Leu	Lys	Ser	Leu
			115					120					125		

Gln Ser Lys Leu
130

<210> 1888
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468435"

<400> 1888
Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro
1 5 10 15

Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg
20 25 30

Arg Arg Glu Ile Gly Glu Gly Gly Gly Arg Asp Leu Pro Pro Phe Pro
35 40 45

Arg Lys Ala Gly Asp Ser Leu Asp Ala Glu Ser Gly Ala Leu Trp Gly
50 55 60

Leu Gly Pro Leu Ala Gln Arg
65 70

<210> 1889
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 496; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 1, palmitoyl; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468651"

<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 1889
Xaa Asn Leu Thr Ser Val Asp Leu Val Arg Ala Ser Glu Ala His Cys
1 5 10 15

His Tyr Val Val Val Lys Leu Phe Ser Glu Lys Leu Leu Lys Ile Gln
20 25 30

Asp Lys Ala Ile Gln Ala Val Leu Arg Ser Leu Cys Leu Leu Tyr Ser
35 40 45

Leu Tyr Gly Ile Ser Gln Asn Ala Gly Asp Phe Leu Gln Gly Ser Ile
50 55 60

Met Thr Glu Pro Gln Ile Thr Gln Val Asn Gln Arg Val Lys Glu Leu
65 70 75 80

Leu Thr Leu Ile Arg Ser Asp Ala Val Ala Leu Val Asp Ala Phe Asp
85 90 95

Phe Gln Asp Val Thr Leu Gly Ser Val Leu Gly Arg Tyr Asp Gly Asn
100 105 110

Val Tyr Glu Asn Leu Phe Glu Trp Ala Lys Asn Ser Pro Leu Asn Lys
115 120 125

Ala Glu Gly Phe Gly Trp Arg Asn Lys Thr Leu Gln Met His Asp Leu
130 135 140

Gly Asp Pro Cys Glu Ser Ile Ile Leu

145 150

<210> 1890
<211> 681
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 497; "

<220>
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<223> /note="Gene Symbol: ACOX2; "

<220>
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<223> /note="Gene Name:
acyl-CoA oxidase 2, branched chain; "

<220>
<221> source
<223> /note="Uniprot ID: Q99424; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000307697"

<400> 1890
Met Gly Ser Pro Val His Arg Val Ser Leu Gly Asp Thr Trp Ser Arg
1 5 10 15

Gln Met His Pro Asp Ile Glu Ser Glu Arg Tyr Met Gln Ser Phe Asp
20 25 30

Val Glu Arg Leu Thr Asn Ile Leu Asp Gly Gly Ala Gln Asn Thr Ala
35 40 45

Leu Arg Arg Lys Val Glu Ser Ile Ile His Ser Tyr Pro Glu Phe Ser
50 55 60

Cys Lys Asp Asn Tyr Phe Met Thr Gln Asn Glu Arg Tyr Lys Ala Ala
65 70 75 80

Met Arg Arg Ala Phe His Ile Arg Leu Ile Ala Arg Arg Leu Gly Trp
85 90 95

Leu Glu Asp Gly Arg Glu Leu Gly Tyr Ala Tyr Arg Ala Leu Ser Gly
100 105 110

```
Asp Val Ala Leu Asn Ile His Arg Val Phe Val Arg Ala Leu Arg Ser
        115                 120                 125

Leu Gly Ser Glu Glu Gln Ile Ala Lys Trp Asp Pro Leu Cys Lys Asn
    130                 135                 140

Ile Gln Ile Ile Ala Thr Tyr Ala Gln Thr Glu Leu Gly His Gly Thr
145                 150                 155                 160

Tyr Leu Gln Gly Leu Glu Thr Glu Ala Thr Tyr Asp Ala Ala Thr Gln
                165                 170                 175

Glu Phe Val Ile His Ser Pro Thr Leu Thr Ala Thr Lys Trp Trp Pro
            180                 185                 190

Gly Asp Leu Gly Arg Ser Ala Thr His Ala Leu Val Gln Ala Gln Leu
        195                 200                 205

Ile Cys Ser Gly Ala Arg Arg Gly Met His Ala Phe Ile Val Pro Ile
    210                 215                 220

Arg Ser Leu Gln Asp His Thr Pro Leu Pro Gly Ile Ile Ile Gly Asp
225                 230                 235                 240

Ile Gly Pro Lys Met Asp Phe Asp Gln Thr Asp Asn Gly Phe Leu Gln
                245                 250                 255

Leu Asn His Val Arg Val Pro Arg Glu Asn Met Leu Ser Arg Phe Ala
            260                 265                 270

Gln Val Leu Pro Asp Gly Thr Tyr Val Lys Leu Gly Thr Ala Gln Ser
        275                 280                 285

Asn Tyr Leu Pro Met Val Val Val Arg Val Glu Leu Leu Ser Gly Glu
    290                 295                 300

Ile Leu Pro Ile Leu Gln Lys Ala Cys Val Ile Ala Met Arg Tyr Ser
305                 310                 315                 320

Val Ile Arg Arg Gln Ser Arg Leu Arg Pro Ser Asp Pro Glu Ala Lys
                325                 330                 335
```

```
Val Leu Asp Tyr Gln Thr Gln Gln Gln Lys Leu Phe Pro Gln Leu Ala
            340                 345                 350

Ile Ser Tyr Ala Phe His Phe Leu Ala Val Ser Leu Leu Glu Phe Phe
        355                 360                 365

Gln His Ser Tyr Thr Ala Ile Leu Asn Gln Asp Phe Ser Phe Leu Pro
    370                 375                 380

Glu Leu His Ala Leu Ser Thr Gly Met Lys Ala Met Met Ser Glu Phe
385                 390                 395                 400

Cys Thr Gln Gly Ala Glu Met Cys Arg Arg Ala Cys Gly Gly His Gly
                405                 410                 415

Tyr Ser Lys Leu Ser Gly Leu Pro Ser Leu Val Thr Lys Leu Ser Ala
            420                 425                 430

Ser Cys Thr Tyr Glu Gly Glu Asn Thr Val Leu Tyr Leu Gln Val Ala
        435                 440                 445

Arg Phe Leu Val Lys Ser Tyr Leu Gln Thr Gln Met Ser Pro Gly Ser
    450                 455                 460

Thr Pro Gln Arg Ser Leu Ser Pro Ser Val Ala Tyr Leu Thr Ala Pro
465                 470                 475                 480

Asp Leu Ala Arg Cys Pro Ala Gln Arg Ala Ala Asp Phe Leu Cys Pro
                485                 490                 495

Glu Leu Tyr Thr Thr Ala Trp Ala His Val Ala Val Arg Leu Ile Lys
            500                 505                 510

Asp Ser Val Gln His Leu Gln Thr Leu Thr Gln Ser Gly Ala Asp Gln
        515                 520                 525

His Glu Ala Trp Asn Gln Thr Thr Val Ile His Leu Gln Ala Ala Lys
    530                 535                 540

Val His Cys Tyr Tyr Val Thr Val Lys Gly Phe Thr Glu Ala Leu Glu
545                 550                 555                 560

Lys Leu Glu Asn Glu Pro Ala Ile Gln Gln Val Leu Lys Arg Leu Cys
```

```
                565                 570                 575

Asp Leu His Ala Ile His Gly Ile Leu Thr Asn Ser Gly Asp Phe Leu
            580                 585                 590

His Asp Ala Phe Leu Ser Gly Ala Gln Val Asp Met Ala Arg Thr Ala
        595                 600                 605

Tyr Leu Asp Leu Leu Arg Leu Ile Arg Lys Asp Ala Ile Leu Leu Thr
    610                 615                 620

Asp Ala Phe Asp Phe Thr Asp Gln Cys Leu Asn Ser Ala Leu Gly Cys
625                 630                 635                 640

Tyr Asp Gly Asn Val Tyr Glu Arg Leu Phe Gln Trp Ala Gln Lys Ser
                645                 650                 655

Pro Thr Asn Thr Gln Glu Asn Pro Ala Tyr Glu Glu Tyr Ile Arg Pro
            660                 665                 670

Leu Leu Gln Ser Trp Arg Ser Lys Leu
        675                 680


<210> 1891
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 497; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 2, branched chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417877"

<400> 1891
Glu Ala Leu Glu Lys Leu Glu Asn Glu Pro Ala Ile Gln Gln Val Leu
1               5                   10                  15
```

```
Lys Arg Leu Cys Asp Leu His Ala Ile His Gly Ile Leu Thr Asn Ser
            20                  25                  30

Gly Asp Phe Leu His Asp Ala Phe Leu Ser Gly Ala Gln Val Asp Met
        35                  40                  45

Ala Arg Thr Ala Tyr Leu Asp Leu Leu Arg Leu Ile Arg Glu Ile Arg
    50                  55                  60

Cys Lys Ala Ile Gln Ala Lys Glu Met Gly Lys Val Asp Ser Val Asn
65                  70                  75                  80

Leu Arg Ile Lys Glu Met Glu Gly Cys His Pro Val Asn
                85                  90


<210> 1892
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 497; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 2, branched chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418515"

<400> 1892
Gly Thr Tyr Leu Gln Gly Leu Glu Thr Glu Ala Thr Tyr Asp Ala Ala
1               5                   10                  15

Thr Gln Glu Phe Val Ile His Ser Pro Thr Leu Thr Ala Thr Lys Trp
            20                  25                  30

Trp Pro Gly Asp Leu Gly Arg Ser Ala Thr His Ala Leu Val Gln Ala
        35                  40                  45

Gln Leu Ile Cys Ser Gly Ala Arg Arg Gly Met His Ala Phe Ile Val
```

```
    50                  55                  60

Pro Ile Arg Ser Leu Gln Asp His Thr Pro Leu Pro Gly Val Leu Ile
65                  70                  75                  80

Ser Ile Ser Phe Lys Glu Ser Ser Leu Gly Thr Ser Asp Pro Arg Trp
                85                  90                  95

Thr Leu Ile Lys Gln Thr Met Ala Ser Cys Ser
            100                 105


<210> 1893
<211> 667
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 497; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 2, branched chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418562"

<400> 1893
Met Gly Ser Pro Val His Arg Val Ser Leu Gly Asp Thr Trp Ser Arg
1               5                   10                  15

Gln Met His Pro Asp Ile Glu Ser Glu Arg Tyr Met Gln Ser Phe Asp
            20                  25                  30

Val Glu Arg Leu Thr Asn Ile Leu Asp Gly Gly Ala Gln Asn Thr Ala
        35                  40                  45

Leu Arg Arg Lys Val Glu Ser Ile Ile His Ser Tyr Pro Glu Phe Ser
    50                  55                  60

Cys Lys Asp Asn Tyr Phe Met Thr Gln Asn Glu Arg Tyr Lys Ala Ala
65                  70                  75                  80
```

```
Met Arg Arg Ala Phe His Ile Arg Leu Ile Ala Arg Arg Leu Gly Trp
                85                  90                  95

Leu Glu Asp Gly Arg Glu Leu Gly Tyr Ala Tyr Arg Ala Leu Ser Gly
            100                 105                 110

Asp Val Ala Leu Asn Ile His Arg Val Phe Val Arg Ala Leu Arg Ser
        115                 120                 125

Leu Gly Ser Glu Glu Gln Ile Ala Lys Trp Asp Pro Leu Cys Lys Asn
    130                 135                 140

Ile Gln Ile Ile Ala Thr Tyr Ala Gln Thr Glu Leu Gly His Gly Thr
145                 150                 155                 160

Tyr Leu Gln Gly Leu Glu Thr Glu Ala Thr Tyr Asp Ala Ala Thr Gln
                165                 170                 175

Glu Phe Val Ile His Ser Pro Thr Leu Thr Ala Thr Lys Trp Trp Pro
            180                 185                 190

Gly Asp Leu Gly Arg Ser Ala Thr His Ala Leu Val Gln Ala Gln Leu
        195                 200                 205

Ile Cys Ser Gly Ala Arg Arg Gly Met His Ala Phe Ile Val Pro Ile
    210                 215                 220

Arg Ser Leu Gln Asp His Thr Pro Leu Pro Gly Ile Ile Ile Gly Asp
225                 230                 235                 240

Ile Gly Pro Lys Met Asp Phe Asp Gln Thr Asp Asn Gly Phe Leu Gln
                245                 250                 255

Leu Asn His Val Leu Pro Asp Gly Thr Tyr Val Lys Leu Gly Thr Ala
            260                 265                 270

Gln Ser Asn Tyr Leu Pro Met Val Val Val Arg Val Glu Leu Leu Ser
        275                 280                 285

Gly Glu Ile Leu Pro Ile Leu Gln Lys Ala Cys Val Ile Ala Met Arg
    290                 295                 300
```

```
Tyr Ser Val Ile Arg Arg Gln Ser Arg Leu Arg Pro Ser Asp Pro Glu
305                 310                 315                 320

Ala Lys Val Leu Asp Tyr Gln Thr Gln Gln Gln Lys Leu Phe Pro Gln
                325                 330                 335

Leu Ala Ile Ser Tyr Ala Phe His Phe Leu Ala Val Ser Leu Leu Glu
            340                 345                 350

Phe Phe Gln His Ser Tyr Thr Ala Ile Leu Asn Gln Asp Phe Ser Phe
        355                 360                 365

Leu Pro Glu Leu His Ala Leu Ser Thr Gly Met Lys Ala Met Met Ser
    370                 375                 380

Glu Phe Cys Thr Gln Gly Ala Glu Met Cys Arg Arg Ala Cys Gly Gly
385                 390                 395                 400

His Gly Tyr Ser Lys Leu Ser Gly Leu Pro Ser Leu Val Thr Lys Leu
                405                 410                 415

Ser Ala Ser Cys Thr Tyr Glu Gly Glu Asn Thr Val Leu Tyr Leu Gln
            420                 425                 430

Val Ala Arg Phe Leu Val Lys Ser Tyr Leu Gln Thr Gln Met Ser Pro
        435                 440                 445

Gly Ser Thr Pro Gln Arg Ser Leu Ser Pro Ser Val Ala Tyr Leu Thr
    450                 455                 460

Ala Pro Asp Leu Ala Arg Cys Pro Ala Gln Arg Ala Ala Asp Phe Leu
465                 470                 475                 480

Cys Pro Glu Leu Tyr Thr Thr Ala Trp Ala His Val Ala Val Arg Leu
                485                 490                 495

Ile Lys Asp Ser Val Gln His Leu Gln Thr Leu Thr Gln Ser Gly Ala
            500                 505                 510

Asp Gln His Glu Ala Trp Asn Gln Thr Thr Val Ile His Leu Gln Ala
        515                 520                 525

Ala Lys Val His Cys Tyr Tyr Val Thr Val Lys Gly Phe Thr Glu Ala
```

```
    530                 535                 540

Leu Glu Lys Leu Glu Asn Glu Pro Ala Ile Gln Gln Val Leu Lys Arg
545                 550                 555                 560

Leu Cys Asp Leu His Ala Ile His Gly Ile Leu Thr Asn Ser Gly Asp
                565                 570                 575

Phe Leu His Asp Ala Phe Leu Ser Gly Ala Gln Val Asp Met Ala Arg
            580                 585                 590

Thr Ala Tyr Leu Asp Leu Leu Arg Leu Ile Arg Lys Asp Ala Ile Leu
        595                 600                 605

Leu Thr Asp Ala Phe Asp Phe Thr Asp Gln Cys Leu Asn Ser Ala Leu
    610                 615                 620

Gly Cys Tyr Asp Gly Asn Val Tyr Glu Arg Leu Phe Gln Trp Ala Gln
625                 630                 635                 640

Lys Ser Pro Thr Asn Thr Gln Glu Asn Pro Ala Tyr Glu Glu Tyr Ile
                645                 650                 655

Arg Pro Leu Leu Gln Ser Trp Arg Ser Lys Leu
            660                 665


<210> 1894
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 497; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 2, branched chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419133"
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1894
Xaa Ala Gln Asn Thr Ala Leu Arg Arg Lys Val Asp Pro
1   5   10

<210> 1895
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 497; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 2, branched chain; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419927"

<400> 1895
Met Gly Ser Pro Val His Arg Val Ser Leu Gly Asp Thr Trp Ser Arg
1   5   10   15

Gln Met His Pro Asp Ile Glu Ser Glu Arg Tyr Met Gln Ser Phe Asp
            20   25   30

Val Glu Arg Leu Thr Asn Ile Leu Asp Gly Gly Ala Gln Asn Thr Ala
        35   40   45

Leu Arg Arg Lys Val Glu Ser Ile Ile His Ser Tyr Pro Glu Phe Ser
    50   55   60

Cys Lys Asp Asn Tyr Phe Met Thr Gln Asn Glu Arg Tyr Lys Ala Ala
65   70   75   80

Met Arg Arg Ala Phe His Ile Arg Leu Ile Ala Arg Arg Leu Gly Trp
                85   90   95

```
Leu Glu Asp Gly Arg Glu Leu Gly Tyr Ala Tyr Arg Ala Leu Ser Gly
            100                 105                 110

Asp Val Ala Leu Asn Ile His Arg Val Phe Val Arg Ala Leu Arg Ser
        115                 120                 125

Leu Gly Ser Glu Glu Gln Ile Ala Lys Trp Asp Pro Leu Cys Lys Asn
    130                 135                 140

Ile Gln Ile Ile Ala Thr Tyr Ala Gln Thr Glu Leu Gly His Gly Thr
145                 150                 155                 160

Tyr Leu Gln Gly Leu Glu Thr Glu Ala Thr Tyr
                165                 170


<210> 1896
<211> 700
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 498; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 3, pristanoyl; "

<220>
<221> source
<223> /note="Uniprot ID:  O15254; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000348775"

<400> 1896
Met Ala Ser Thr Val Glu Gly Gly Asp Thr Ala Leu Leu Pro Glu Phe
1               5                   10                  15

Pro Arg Gly Pro Leu Asp Ala Tyr Arg Ala Arg Ala Ser Phe Ser Trp
            20                  25                  30

Lys Glu Leu Ala Leu Phe Thr Glu Gly Glu Gly Met Leu Arg Phe Lys
```

```
        35                  40                  45

Lys Thr Ile Phe Ser Ala Leu Glu Asn Asp Pro Leu Phe Ala Arg Ser
    50                  55                  60

Pro Gly Ala Asp Leu Ser Leu Glu Lys Tyr Arg Glu Leu Asn Phe Leu
65                  70                  75                  80

Arg Cys Lys Arg Ile Phe Glu Tyr Asp Phe Leu Ser Val Glu Asp Met
                85                  90                  95

Phe Lys Ser Pro Leu Lys Val Pro Ala Leu Ile Gln Cys Leu Gly Met
            100                 105                 110

Tyr Asp Ser Ser Leu Ala Ala Lys Tyr Leu Leu His Ser Leu Val Phe
        115                 120                 125

Gly Ser Ala Val Tyr Ser Ser Gly Ser Glu Arg His Leu Thr Tyr Ile
    130                 135                 140

Gln Lys Ile Phe Arg Met Glu Ile Phe Gly Cys Phe Ala Leu Thr Glu
145                 150                 155                 160

Leu Ser His Gly Ser Asn Thr Lys Ala Ile Arg Thr Thr Ala His Tyr
                165                 170                 175

Asp Pro Ala Thr Glu Glu Phe Ile Ile His Ser Pro Asp Phe Glu Ala
            180                 185                 190

Ala Lys Phe Trp Val Gly Asn Met Gly Lys Thr Ala Thr His Ala Val
        195                 200                 205

Val Phe Ala Lys Leu Cys Val Pro Gly Asp Gln Cys His Gly Leu His
    210                 215                 220

Pro Phe Ile Val Gln Ile Arg Asp Pro Lys Thr Leu Leu Pro Met Pro
225                 230                 235                 240

Gly Val Met Val Gly Asp Ile Gly Lys Lys Leu Gly Gln Asn Gly Leu
                245                 250                 255

Asp Asn Gly Phe Ala Met Phe His Lys Val Arg Val Pro Arg Gln Ser
            260                 265                 270
```

```
Leu Leu Asn Arg Met Gly Asp Val Thr Pro Glu Gly Thr Tyr Val Ser
        275                 280                 285

Pro Phe Lys Asp Val Arg Gln Arg Phe Gly Ala Ser Leu Gly Ser Leu
    290                 295                 300

Ser Ser Gly Arg Val Ser Ile Val Ser Leu Ala Ile Leu Asn Leu Lys
305                 310                 315                 320

Leu Ala Val Ala Ile Ala Leu Arg Phe Ser Ala Thr Arg Arg Gln Phe
                325                 330                 335

Gly Pro Thr Glu Glu Glu Glu Ile Pro Val Leu Glu Tyr Pro Met Gln
            340                 345                 350

Gln Trp Arg Leu Leu Pro Tyr Leu Ala Ala Val Tyr Ala Leu Asp His
        355                 360                 365

Phe Ser Lys Ser Leu Phe Leu Asp Leu Val Glu Leu Gln Arg Gly Leu
    370                 375                 380

Ala Ser Gly Asp Arg Ser Ala Arg Gln Ala Glu Leu Gly Arg Glu Ile
385                 390                 395                 400

His Ala Leu Ala Ser Ala Ser Lys Pro Leu Ala Ser Trp Thr Thr Gln
                405                 410                 415

Gln Gly Ile Gln Glu Cys Arg Glu Ala Cys Gly Gly His Gly Tyr Leu
            420                 425                 430

Ala Met Asn Arg Leu Gly Val Leu Arg Asp Asp Asn Asp Pro Asn Cys
        435                 440                 445

Thr Tyr Glu Gly Asp Asn Asn Ile Leu Leu Gln Gln Thr Ser Asn Tyr
    450                 455                 460

Leu Leu Gly Leu Leu Ala His Gln Val His Asp Gly Ala Cys Phe Arg
465                 470                 475                 480

Ser Pro Leu Lys Ser Val Asp Phe Leu Asp Ala Tyr Pro Gly Ile Leu
                485                 490                 495
```

```
Asp Gln Lys Phe Glu Val Ser Ser Val Ala Asp Cys Leu Asp Ser Ala
            500                 505                 510

Val Ala Leu Ala Ala Tyr Lys Trp Leu Val Cys Tyr Leu Leu Arg Glu
        515                 520                 525

Thr Tyr Gln Lys Leu Asn Gln Glu Lys Arg Ser Gly Ser Ser Asp Phe
    530                 535                 540

Glu Ala Arg Asn Lys Cys Gln Val Ser His Gly Arg Pro Leu Ala Leu
545                 550                 555                 560

Ala Phe Val Glu Leu Thr Val Val Gln Arg Phe His Glu His Val His
                565                 570                 575

Gln Pro Ser Val Pro Pro Ser Leu Arg Ala Val Leu Gly Arg Leu Ser
            580                 585                 590

Ala Leu Tyr Ala Leu Trp Ser Leu Ser Arg His Ala Ala Leu Leu Tyr
        595                 600                 605

Arg Gly Gly Tyr Phe Ser Gly Glu Gln Ala Gly Glu Val Leu Glu Ser
    610                 615                 620

Ala Val Leu Ala Leu Cys Ser Gln Leu Lys Asp Asp Ala Val Ala Leu
625                 630                 635                 640

Val Asp Val Ile Ala Pro Pro Asp Phe Val Leu Asp Ser Pro Ile Gly
                645                 650                 655

Arg Ala Asp Gly Glu Leu Tyr Lys Asn Leu Trp Gly Ala Val Leu Gln
            660                 665                 670

Glu Ser Lys Val Leu Glu Arg Ala Ser Trp Trp Pro Glu Phe Ser Val
        675                 680                 685

Asn Lys Pro Val Ile Gly Ser Leu Lys Ser Lys Leu
    690                 695                 700
```

<210> 1897
<211> 624
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 498; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase 3, pristanoyl; "

<220>
<221> source
<223> /note="Uniprot ID: O15254; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413994"

<400> 1897
Met Ala Ser Thr Val Glu Gly Gly Asp Thr Ala Leu Leu Pro Glu Phe
1   5   10   15

Pro Arg Gly Pro Leu Asp Ala Tyr Arg Ala Arg Ala Ser Phe Ser Trp
            20   25   30

Lys Glu Leu Ala Leu Phe Thr Glu Gly Glu Gly Met Leu Arg Phe Lys
        35   40   45

Lys Thr Ile Phe Ser Ala Leu Glu Asn Asp Pro Leu Phe Ala Arg Ser
    50   55   60

Pro Gly Ala Asp Leu Ser Leu Glu Lys Tyr Arg Glu Leu Asn Phe Leu
65   70   75   80

Arg Cys Lys Arg Ile Phe Glu Tyr Asp Phe Leu Ser Val Glu Asp Met
                85   90   95

Phe Lys Ser Pro Leu Lys Val Pro Ala Leu Ile Gln Cys Leu Gly Met
            100   105   110

Tyr Asp Ser Ser Leu Ala Ala Lys Tyr Leu Leu His Ser Leu Val Phe
        115   120   125

Gly Ser Ala Val Tyr Ser Ser Gly Ser Glu Arg His Leu Thr Tyr Ile
    130   135   140

```
Gln Lys Ile Phe Arg Met Glu Ile Phe Gly Cys Phe Ala Leu Thr Glu
145                 150                 155                 160

Leu Ser His Gly Ser Asn Thr Lys Ala Ile Arg Thr Thr Ala His Tyr
                165                 170                 175

Asp Pro Ala Thr Glu Glu Phe Ile Ile His Ser Pro Asp Phe Glu Ala
            180                 185                 190

Ala Lys Phe Trp Val Gly Asn Met Gly Lys Thr Ala Thr His Ala Val
        195                 200                 205

Val Phe Ala Lys Leu Cys Val Pro Gly Asp Gln Cys His Gly Leu His
    210                 215                 220

Pro Phe Ile Val Gln Ile Arg Asp Pro Lys Thr Leu Leu Pro Met Pro
225                 230                 235                 240

Gly Val Met Val Gly Asp Ile Gly Lys Lys Leu Gly Gln Asn Gly Leu
                245                 250                 255

Asp Asn Gly Phe Ala Met Phe His Lys Val Arg Val Pro Arg Gln Ser
            260                 265                 270

Leu Leu Asn Arg Met Gly Asp Val Thr Pro Glu Gly Thr Tyr Val Ser
        275                 280                 285

Pro Phe Lys Asp Val Arg Gln Arg Phe Gly Ala Ser Leu Gly Ser Leu
    290                 295                 300

Ser Ser Gly Arg Val Ser Ile Val Ser Leu Ala Ile Leu Asn Leu Lys
305                 310                 315                 320

Leu Ala Val Ala Ile Ala Leu Arg Phe Ser Ala Thr Arg Arg Gln Phe
                325                 330                 335

Gly Pro Thr Glu Glu Glu Glu Ile Pro Val Leu Glu Tyr Pro Met Gln
            340                 345                 350

Gln Trp Arg Leu Leu Pro Tyr Leu Ala Ala Val Tyr Ala Leu Asp His
        355                 360                 365
```

```
Phe Ser Lys Ser Leu Phe Leu Asp Leu Val Glu Leu Gln Arg Gly Leu
    370                 375                 380

Ala Ser Gly Asp Arg Ser Ala Arg Gln Ala Glu Leu Gly Arg Glu Ile
385                 390                 395                 400

His Ala Leu Ala Ser Ala Ser Lys Pro Leu Ala Ser Trp Thr Thr Gln
                405                 410                 415

Gln Gly Ile Gln Glu Cys Arg Glu Ala Cys Gly Gly His Gly Tyr Leu
            420                 425                 430

Ala Met Asn Arg Leu Gly Val Leu Arg Asp Asp Asn Asp Pro Asn Cys
        435                 440                 445

Thr Tyr Glu Gly Asp Asn Asn Ile Leu Leu Gln Gln Thr Ser Asn Tyr
    450                 455                 460

Leu Leu Gly Leu Leu Ala His Gln Val His Asp Gly Ala Cys Phe Arg
465                 470                 475                 480

Ser Pro Leu Lys Ser Val Asp Phe Leu Asp Ala Tyr Pro Gly Ile Leu
                485                 490                 495

Asp Gln Lys Phe Glu Val Ser Ser Val Ala Asp Cys Leu Asp Ser Ala
            500                 505                 510

Val Ala Leu Ala Ala Tyr Lys Trp Leu Val Cys Tyr Leu Leu Arg Glu
        515                 520                 525

Thr Tyr Gln Lys Leu Asn Gln Glu Lys Arg Ser Gly Ser Ser Asp Phe
    530                 535                 540

Glu Ala Arg Asn Lys Cys Gln Val Ser His Gly Arg Pro Leu Ala Leu
545                 550                 555                 560

Ala Phe Val Glu Leu Thr Val Val Gln Arg Phe His Glu His Val His
                565                 570                 575

Gln Pro Ser Val Pro Pro Ser Leu Arg Ala Val Leu Gly Arg Leu Ser
            580                 585                 590
```

```
Ala Leu Tyr Ala Leu Trp Ser Leu Ser Arg His Ala Ala Leu Leu Tyr
        595                 600                 605


Arg Ala Glu Arg Arg Cys Ser Cys Pro Gly Arg Arg Asp Arg Ser Ser
    610                 615                 620


<210> 1898
<211> 700
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 498; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 3, pristanoyl; "

<220>
<221> source
<223> /note="Uniprot ID:  O15254; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421625"

<400> 1898
Met Ala Ser Thr Val Glu Gly Gly Asp Thr Ala Leu Leu Pro Glu Phe
1               5                   10                  15


Pro Arg Gly Pro Leu Asp Ala Tyr Arg Ala Arg Ala Ser Phe Ser Trp
            20                  25                  30


Lys Glu Leu Ala Leu Phe Thr Glu Gly Glu Gly Met Leu Arg Phe Lys
        35                  40                  45


Lys Thr Ile Phe Ser Ala Leu Glu Asn Asp Pro Leu Phe Ala Arg Ser
    50                  55                  60


Pro Gly Ala Asp Leu Ser Leu Glu Lys Tyr Arg Glu Leu Asn Phe Leu
65                  70                  75                  80


Arg Cys Lys Arg Ile Phe Glu Tyr Asp Phe Leu Ser Val Glu Asp Met
                85                  90                  95
```

```
Phe Lys Ser Pro Leu Lys Val Pro Ala Leu Ile Gln Cys Leu Gly Met
            100                 105                 110

Tyr Asp Ser Ser Leu Ala Ala Lys Tyr Leu Leu His Ser Leu Val Phe
        115                 120                 125

Gly Ser Ala Val Tyr Ser Ser Gly Ser Glu Arg His Leu Thr Tyr Ile
    130                 135                 140

Gln Lys Ile Phe Arg Met Glu Ile Phe Gly Cys Phe Ala Leu Thr Glu
145                 150                 155                 160

Leu Ser His Gly Ser Asn Thr Lys Ala Ile Arg Thr Thr Ala His Tyr
                165                 170                 175

Asp Pro Ala Thr Glu Glu Phe Ile Ile His Ser Pro Asp Phe Glu Ala
            180                 185                 190

Ala Lys Phe Trp Val Gly Asn Met Gly Lys Thr Ala Thr His Ala Val
        195                 200                 205

Val Phe Ala Lys Leu Cys Val Pro Gly Asp Gln Cys His Gly Leu His
    210                 215                 220

Pro Phe Ile Val Gln Ile Arg Asp Pro Lys Thr Leu Leu Pro Met Pro
225                 230                 235                 240

Gly Val Met Val Gly Asp Ile Gly Lys Lys Leu Gly Gln Asn Gly Leu
                245                 250                 255

Asp Asn Gly Phe Ala Met Phe His Lys Val Arg Val Pro Arg Gln Ser
            260                 265                 270

Leu Leu Asn Arg Met Gly Asp Val Thr Pro Glu Gly Thr Tyr Val Ser
        275                 280                 285

Pro Phe Lys Asp Val Arg Gln Arg Phe Gly Ala Ser Leu Gly Ser Leu
    290                 295                 300

Ser Ser Gly Arg Val Ser Ile Val Ser Leu Ala Ile Leu Asn Leu Lys
305                 310                 315                 320
```

```
Leu Ala Val Ala Ile Ala Leu Arg Phe Ser Ala Thr Arg Arg Gln Phe
                325                 330                 335

Gly Pro Thr Glu Glu Glu Glu Ile Pro Val Leu Glu Tyr Pro Met Gln
            340                 345                 350

Gln Trp Arg Leu Leu Pro Tyr Leu Ala Ala Val Tyr Ala Leu Asp His
        355                 360                 365

Phe Ser Lys Ser Leu Phe Leu Asp Leu Val Glu Leu Gln Arg Gly Leu
    370                 375                 380

Ala Ser Gly Asp Arg Ser Ala Arg Gln Ala Glu Leu Gly Arg Glu Ile
385                 390                 395                 400

His Ala Leu Ala Ser Ala Ser Lys Pro Leu Ala Ser Trp Thr Thr Gln
                405                 410                 415

Gln Gly Ile Gln Glu Cys Arg Glu Ala Cys Gly Gly His Gly Tyr Leu
            420                 425                 430

Ala Met Asn Arg Leu Gly Val Leu Arg Asp Asp Asn Asp Pro Asn Cys
        435                 440                 445

Thr Tyr Glu Gly Asp Asn Asn Ile Leu Leu Gln Gln Thr Ser Asn Tyr
    450                 455                 460

Leu Leu Gly Leu Leu Ala His Gln Val His Asp Gly Ala Cys Phe Arg
465                 470                 475                 480

Ser Pro Leu Lys Ser Val Asp Phe Leu Asp Ala Tyr Pro Gly Ile Leu
                485                 490                 495

Asp Gln Lys Phe Glu Val Ser Ser Val Ala Asp Cys Leu Asp Ser Ala
            500                 505                 510

Val Ala Leu Ala Ala Tyr Lys Trp Leu Val Cys Tyr Leu Leu Arg Glu
        515                 520                 525

Thr Tyr Gln Lys Leu Asn Gln Glu Lys Arg Ser Gly Ser Ser Asp Phe
    530                 535                 540
```

```
Glu Ala Arg Asn Lys Cys Gln Val Ser His Gly Arg Pro Leu Ala Leu
545                 550                 555                 560

Ala Phe Val Glu Leu Thr Val Val Gln Arg Phe His Glu His Val His
                565                 570                 575

Gln Pro Ser Val Pro Pro Ser Leu Arg Ala Val Leu Gly Arg Leu Ser
            580                 585                 590

Ala Leu Tyr Ala Leu Trp Ser Leu Ser Arg His Ala Ala Leu Leu Tyr
        595                 600                 605

Arg Gly Gly Tyr Phe Ser Gly Glu Gln Ala Gly Glu Val Leu Glu Ser
    610                 615                 620

Ala Val Leu Ala Leu Cys Ser Gln Leu Lys Asp Asp Ala Val Ala Leu
625                 630                 635                 640

Val Asp Val Ile Ala Pro Pro Asp Phe Val Leu Asp Ser Pro Ile Gly
                645                 650                 655

Arg Ala Asp Gly Glu Leu Tyr Lys Asn Leu Trp Gly Ala Val Leu Gln
            660                 665                 670

Glu Ser Lys Val Leu Glu Arg Ala Ser Trp Trp Pro Glu Phe Ser Val
        675                 680                 685

Asn Lys Pro Val Ile Gly Ser Leu Lys Ser Lys Leu
    690                 695                 700


<210> 1899
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 498; "

<220>
<221> source
<223> /note="Gene Symbol: ACOX3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase 3, pristanoyl; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000427321"

<400> 1899
Met Phe Lys Ser Pro Leu Lys Val Pro Ala Leu Ile Gln Cys Leu Gly
1   5   10   15

Met Tyr Asp Ser Ser Leu Ala Ala Lys Tyr Leu Leu His Ser Leu Val
            20   25   30

Phe Gly Ser Ala Val Tyr Ser Ser Gly Ser Glu Arg His Leu Thr Tyr
        35   40   45

Ile Gln Lys Ile Phe Arg Met Glu Ile Phe Gly Cys Phe Ala Leu Thr
    50   55   60

Glu Leu Ser His Gly Ser Asn Thr Lys Ala Ile Arg Thr Thr Ala His
65   70   75   80

Tyr Asp Pro Ala Thr Glu Glu Phe Ile Ile His Ser Pro Asp Phe Glu
                85   90   95

Ala Ala Lys Phe Trp Val Gly Asn Met Gly Lys Thr Ala Thr
            100   105   110

<210> 1900
<211> 279
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
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<223> /note="Gene Name:
      acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUZ1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000343717"

<400> 1900
Met Arg Ala Leu Thr Val Gln Arg Val Lys Phe Ala Met Asp Leu Pro
1 5 10 15

Leu Leu Lys Arg Ala Gly Gln Asp Leu Ala Glu Lys Thr Lys Asn Phe
20 25 30

Val Ser Arg Ser Leu Val Ile Gly Glu Val Leu Ser Met Ala Asp Met
35 40 45

Ala Thr Gly Val Lys Cys Gly Ile Ile Tyr Trp Leu Phe Gly Gly Ala
50 55 60

Ile Arg Asn Leu Gly Ser Pro Glu His Val Thr Lys Trp Phe Gln Pro
65 70 75 80

Leu Gln Glu Gln Lys Tyr Thr Gly Met Phe Ala Met Thr Glu Arg Gly
85 90 95

His Gly Ser Asn Ala Arg Gly Ile Gln Thr Glu Ala Thr Phe Asp Leu
100 105 110

Ser Ala Gln Glu Phe Val Ile Asp Thr Pro Cys Glu Asn Ala Glu Lys
115 120 125

Met Tyr Ile Gly Asn Ala Met Tyr Gly Asn Tyr Ala Ala Val Phe Ala
130 135 140

Gln Leu Ile Ile Asp Gly Arg Ser Gln Gly Pro His Cys Phe Ile Val
145 150 155 160

Pro Val Arg Asp Glu Asn Gly Ser Leu Tyr Pro Gly Val Thr Ala Ile
165 170 175

Asp Met Met Tyr Lys Glu Gly Leu His Gly Val Asp Asn Gly Ile Leu
180 185 190

Ile Phe Asp Lys Val Arg Ile Pro Arg Glu Asn Leu Leu Asp Lys Phe
195 200 205

Gly Ser Val Ala Pro Asp Gly Gln Tyr His Ser Pro Ile Arg Asn Lys

```
    210                 215                 220

Ser Ala Arg Phe Asn Ala Met Leu Ala Ala Leu Thr Pro Ser Arg Leu
225                 230                 235                 240

Ala Val Ala Phe Gln Ala Met Gly Ala Met Lys Leu Gly Leu Thr Ile
                245                 250                 255

Ala Ile Arg Tyr Ser His Arg Ser Arg Ile Ile Ser Gln Asn Cys Cys
            260                 265                 270

Ser Ala Pro Ala Gly Leu Tyr
        275


<210> 1901
<211> 547
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NUZ1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000374461"

<400> 1901
Met Arg Ala Leu Thr Val Gln Arg Val Lys Phe Ala Met Asp Leu Pro
1               5                   10                  15

Leu Leu Lys Arg Ala Gly Gln Asp Leu Ala Glu Lys Thr Lys Asn Phe
            20                  25                  30

Val Ser Arg Ser Leu Val Ile Gly Glu Val Leu Ser Met Ala Asp Met
        35                  40                  45
```

```
Ala Thr Gly Val Lys Cys Gly Ile Ile Tyr Trp Leu Phe Gly Gly Ala
    50                  55                  60

Ile Arg Asn Leu Gly Ser Pro Glu His Val Thr Lys Trp Phe Gln Pro
65                  70                  75                  80

Leu Gln Glu Gln Lys Tyr Thr Gly Met Phe Ala Met Thr Glu Arg Gly
                85                  90                  95

His Gly Ser Asn Ala Arg Gly Ile Gln Thr Glu Ala Thr Phe Asp Leu
            100                 105                 110

Ser Ala Gln Glu Phe Val Ile Asp Thr Pro Cys Glu Asn Ala Glu Lys
        115                 120                 125

Met Tyr Ile Gly Asn Ala Met Tyr Gly Asn Tyr Ala Ala Val Phe Ala
    130                 135                 140

Gln Leu Ile Ile Asp Gly Arg Ser Gln Gly Pro His Cys Phe Ile Val
145                 150                 155                 160

Pro Val Arg Asp Glu Asn Gly Ser Leu Tyr Pro Gly Val Thr Ala Ile
                165                 170                 175

Asp Met Met Tyr Lys Glu Gly Leu His Gly Val Asp Asn Gly Ile Leu
            180                 185                 190

Ile Phe Asp Lys Val Arg Ile Pro Arg Glu Asn Leu Leu Asp Lys Phe
        195                 200                 205

Gly Ser Val Ala Pro Asp Gly Gln Tyr His Ser Pro Ile Arg Asn Lys
    210                 215                 220

Ser Ala Arg Phe Asn Ala Met Leu Ala Ala Leu Thr Pro Ser Arg Leu
225                 230                 235                 240

Ala Val Ala Phe Gln Ala Met Gly Ala Met Lys Leu Gly Leu Thr Ile
                245                 250                 255

Ala Ile Arg Tyr Ser His Ser Arg Arg Gln Phe Gly Pro Lys Thr Lys
            260                 265                 270
```

```
Glu Glu Val Lys Ile Ile Glu His Gln Thr Gln Thr Leu Arg Leu Met
        275                 280                 285

Pro His Leu Ala Thr Ala Leu Ala Leu Thr Phe Val Ser Arg Tyr Ala
    290                 295                 300

Gly Ala Leu Leu Asp Glu Asp Val Phe Gln Gly Lys Glu Leu Val Asn
305                 310                 315                 320

Ser Arg Ser Leu Gln Ala Leu Val Ala Gly Leu Lys Ala Tyr Ser Thr
                325                 330                 335

Trp Glu Asn Ile Arg Cys Leu Gln Asp Cys Arg Glu Cys Thr Gly Gly
            340                 345                 350

Met Gly Tyr Met Met Glu Asn Arg Ile Ser Gly Leu Lys Cys Asp Thr
        355                 360                 365

Asp Val Phe Ala Thr Phe Glu Gly Asp Asp Val Val Met Leu Gln Val
    370                 375                 380

Val Gly Arg Glu Leu Leu Ala Gln Tyr Thr Lys Gln Tyr Glu Glu Lys
385                 390                 395                 400

Pro Leu Phe Gly Leu Leu Gln Asn Trp Ala Glu Ser Val Gly Asp Lys
                405                 410                 415

Leu Arg Thr Ser Phe Leu Ala Phe Asn Met Asp Thr Val Asp Asp Leu
            420                 425                 430

Ala Phe Leu Leu Lys Ala Val Lys Phe Arg Glu Arg Val Leu Gln Arg
        435                 440                 445

Gly Leu Val Ala Arg Ile Tyr Tyr Lys Val Lys Thr Lys Lys Glu Asp
    450                 455                 460

Phe Phe His Ala Trp Asn Ser Cys Leu His His Val Ala Ser Leu Ser
465                 470                 475                 480

Leu Ala His Thr His Arg Val Thr Leu Glu Gln Phe Ser Leu Ala Val
                485                 490                 495

Lys Ser Cys Pro Asp Gln Glu Asp Gln Thr Leu Leu Met Lys Phe Cys
```

```
            500                 505                 510

Leu Leu Tyr Gly Thr Lys Leu Val Phe Gln Glu Arg Ala Trp Tyr Leu
        515                 520                 525

Glu His Lys Tyr Leu Thr Pro Met Ala Ser Thr Arg Ile Arg Asn Gln
    530                 535                 540

Glu Arg Cys
545


<210> 1902
<211> 355
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000387832"

<400> 1902
Arg Asp Glu Asn Gly Ser Leu Tyr Pro Gly Val Thr Ala Ile Asp Met
1               5                   10                  15

Met Tyr Lys Glu Gly Leu His Gly Val Asp Asn Gly Ile Leu Ile Phe
            20                  25                  30

Asp Lys Val Arg Ile Pro Arg Glu Asn Leu Leu Asp Lys Phe Gly Ser
        35                  40                  45

Val Ala Pro Asp Gly Gln Tyr His Ser Pro Ile Arg Asn Lys Ser Ala
    50                  55                  60

Arg Phe Asn Ala Met Leu Ala Ala Leu Thr Pro Ser Arg Leu Ala Val
65                  70                  75                  80
```

```
Ala Phe Gln Ala Met Gly Ala Met Lys Leu Gly Leu Thr Ile Ala Ile
                85                  90                  95

Arg Tyr Ser His Ser Arg Arg Gln Phe Gly Pro Lys Thr Lys Glu Glu
            100                 105                 110

Val Lys Ile Ile Glu His Gln Thr Gln Thr Leu Arg Leu Met Pro His
        115                 120                 125

Leu Ala Thr Ala Leu Ala Leu Thr Phe Val Ser Arg Tyr Ala Gly Ala
    130                 135                 140

Leu Leu Asp Glu Asp Val Phe Gln Gly Lys Glu Leu Val Asn Ser Arg
145                 150                 155                 160

Ser Leu Gln Ala Leu Val Ala Gly Leu Lys Ala Tyr Ser Thr Trp Glu
                165                 170                 175

Asn Ile Arg Cys Leu Gln Asp Cys Arg Glu Cys Thr Gly Gly Met Val
            180                 185                 190

Val Gly Arg Glu Leu Leu Ala Gln Tyr Thr Lys Gln Tyr Glu Glu Lys
        195                 200                 205

Pro Leu Phe Gly Leu Leu Gln Asn Trp Ala Glu Ser Val Gly Asp Lys
    210                 215                 220

Leu Arg Thr Ser Phe Leu Ala Phe Asn Met Asp Thr Val Asp Asp Leu
225                 230                 235                 240

Ala Phe Leu Leu Lys Ala Val Lys Phe Arg Glu Arg Val Leu Gln Arg
                245                 250                 255

Gly Leu Val Ala Arg Ile Tyr Tyr Lys Val Lys Thr Lys Lys Glu Asp
            260                 265                 270

Phe Phe His Ala Trp Asn Ser Cys Leu His His Val Ala Ser Leu Ser
        275                 280                 285

Leu Ala His Thr His Arg Val Thr Leu Glu Gln Phe Ser Leu Ala Val
    290                 295                 300
```

```
Lys Ser Cys Pro Asp Gln Glu Asp Gln Thr Leu Leu Met Lys Phe Cys
305                 310                 315                 320


Leu Leu Tyr Gly Thr Lys Leu Val Phe Gln Glu Arg Ala Trp Tyr Leu
                325                 330                 335


Glu His Lys Tyr Leu Thr Pro Met Ala Ser Thr Arg Ile Arg Asn Gln
            340                 345                 350


Glu Arg Cys
        355


<210> 1903
<211> 93
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393823"

<400> 1903
Gly Asp Lys Leu Arg Thr Ser Phe Leu Ala Phe Asn Met Asp Thr Val
1               5                   10                  15


Asp Asp Leu Ala Phe Leu Leu Lys Ala Val Lys Phe Arg Glu Arg Val
            20                  25                  30


Leu Gln Arg Gly Leu Val Ala Arg Ile Tyr Tyr Lys Val Lys Thr Lys
        35                  40                  45


Lys Glu Asp Phe Phe His Ala Trp Asn Ser Cys Leu His His Val Ala
    50                  55                  60


Ser Leu Ser Leu Ala His Thr His Arg Val Leu Ser Val Val Trp Asn
65                  70                  75                  80
```

Gln Ala Gly Val Ser Gly Ala Gly Leu Val Phe Arg Thr
85 90

<210> 1904
<211> 70
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394701"

<400> 1904
Met Arg Ala Leu Thr Val Gln Arg Val Lys Phe Ala Met Asp Leu Pro
1 5 10 15

Leu Leu Lys Arg Ala Gly Gln Asp Leu Ala Glu Lys Thr Lys Asn Phe
20 25 30

Val Ser Arg Ser Leu Val Ile Gly Glu Val Leu Ser Met Ala Asp Met
35 40 45

Ala Thr Gly Val Lys Cys Gly Ile Ile Tyr Trp Leu Phe Gly Gly Ala
50 55 60

Ile Arg Asn Leu Gly Ser
65 70

<210> 1905
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000406774"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1905
Xaa Arg Phe Asn Ala Met Leu Ala Ala Leu Thr Pro Ser Arg Leu Ala
1 5 10 15

Val Ala Phe Gln Ala Met Gly Ala Met Lys Leu Gly Leu Thr Ile Ala
20 25 30

Ile Arg Tyr Ser His Arg Tyr Ala Gly Ala Leu Leu Asp Glu Asp Val
35 40 45

Phe Gln Gly Lys Glu Leu Val Asn Ser Arg Ser Leu Gln Ala Leu Val
50 55 60

Ala Gly Leu Lys Ala Tyr Ser Thr Trp Glu Asn Ile Arg Cys Leu Gln
65 70 75 80

Asp Cys Arg Glu Cys Thr Gly Gly Met Gly Tyr Met Met Glu Asn Arg
85 90 95

Ile Ser Gly Leu Lys Cys Asp Thr Asp Val Phe Ala Thr Phe Glu Gly
100 105 110

Asp Asp Val Val Met Leu Gln Val Val Gly Arg Glu Leu Leu Ala Gln
115 120 125

Tyr Thr Lys Gln Tyr Glu Glu Lys Pro Leu Phe Gly Leu Leu Gln Asn
130 135 140

```
Trp Ala Glu Ser Val Gly Asp Lys Leu Arg Thr Ser Phe Leu Ala Phe
145                 150                 155                 160


Asn



<210> 1906
<211> 580
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
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<223> /note="Gene Name:
      acyl-CoA oxidase-like; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NUZ1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000407761"

<400> 1906
Met Arg Ala Leu Thr Val Gln Arg Val Lys Phe Ala Met Asp Leu Pro
1               5                   10                  15


Leu Leu Lys Arg Ala Gly Gln Asp Leu Ala Glu Lys Thr Lys Asn Phe
            20                  25                  30


Val Ser Arg Ser Leu Val Ile Gly Glu Val Leu Ser Met Ala Asp Met
        35                  40                  45


Ala Thr Gly Val Lys Cys Gly Ile Ile Tyr Trp Leu Phe Gly Gly Ala
    50                  55                  60


Ile Arg Asn Leu Gly Ser Pro Glu His Val Thr Lys Trp Phe Gln Pro
65                  70                  75                  80


Leu Gln Glu Gln Lys Tyr Thr Gly Met Phe Ala Met Thr Glu Arg Gly
                85                  90                  95
```

```
His Gly Ser Asn Ala Arg Gly Ile Gln Thr Glu Ala Thr Phe Asp Leu
            100                 105                 110

Ser Ala Gln Glu Phe Val Ile Asp Thr Pro Cys Glu Asn Ala Glu Lys
        115                 120                 125

Met Tyr Ile Gly Asn Ala Met Tyr Gly Asn Tyr Ala Ala Val Phe Ala
    130                 135                 140

Gln Leu Ile Ile Asp Gly Arg Ser Gln Gly Pro His Cys Phe Ile Val
145                 150                 155                 160

Pro Val Arg Asp Glu Asn Gly Ser Leu Tyr Pro Gly Val Thr Ala Ile
                165                 170                 175

Asp Met Met Tyr Lys Glu Gly Leu His Gly Val Asp Asn Gly Ile Leu
            180                 185                 190

Ile Phe Asp Lys Val Arg Ile Pro Arg Glu Asn Leu Leu Asp Lys Phe
        195                 200                 205

Gly Ser Val Ala Pro Asp Gly Gln Tyr His Ser Pro Ile Arg Asn Lys
    210                 215                 220

Ser Ala Arg Phe Asn Ala Met Leu Ala Ala Leu Thr Pro Ser Arg Leu
225                 230                 235                 240

Ala Val Ala Phe Gln Ala Met Gly Ala Met Lys Leu Gly Leu Thr Ile
                245                 250                 255

Ala Ile Arg Tyr Ser His Ser Arg Arg Gln Phe Gly Pro Lys Thr Lys
            260                 265                 270

Glu Glu Val Lys Ile Ile Glu His Gln Thr Gln Thr Leu Arg Leu Met
        275                 280                 285

Pro His Leu Ala Thr Ala Leu Ala Leu Thr Phe Val Ser Arg Tyr Ala
    290                 295                 300

Gly Ala Leu Leu Asp Glu Asp Val Phe Gln Gly Lys Glu Leu Val Asn
305                 310                 315                 320
```

Ser Arg Ser Leu Gln Ala Leu Val Ala Gly Leu Lys Ala Tyr Ser Thr
325 330 335

Trp Glu Asn Ile Arg Cys Leu Gln Asp Cys Arg Glu Cys Thr Gly Gly
340 345 350

Met Val Val Gly Arg Glu Leu Leu Ala Gln Tyr Thr Lys Gln Tyr Glu
355 360 365

Glu Lys Pro Leu Phe Gly Leu Leu Gln Asn Trp Ala Glu Ser Val Gly
370 375 380

Asp Lys Leu Arg Thr Ser Phe Leu Ala Phe Asn Met Asp Thr Val Asp
385 390 395 400

Asp Leu Ala Phe Leu Leu Lys Ala Val Lys Phe Arg Glu Arg Val Leu
405 410 415

Gln Arg Gly Leu Val Ala Arg Ile Tyr Tyr Lys Val Lys Thr Lys Lys
420 425 430

Glu Asp Phe Phe His Ala Trp Asn Ser Cys Leu His His Val Ala Ser
435 440 445

Leu Ser Leu Ala His Thr His Arg Val Thr Leu Glu Gln Phe Ser Leu
450 455 460

Ala Val Lys Ser Cys Pro Asp Gln Glu Asp Gln Thr Leu Leu Met Lys
465 470 475 480

Phe Cys Leu Leu Tyr Gly Thr Lys Leu Val Phe Gln Glu Arg Ala Trp
485 490 495

Tyr Leu Glu His Lys Tyr Leu Thr Pro Met Ala Ser Thr Arg Ile Arg
500 505 510

Asn Gln Leu Leu Asp Leu Cys Asp Ser Val Lys Asp Asp Ala Arg Arg
515 520 525

Val Ile Ser Thr Phe Asn Ile Pro His Thr Tyr Leu His Ala Pro Ile
530 535 540

```
Ala Gly Ile Ser Asn Pro Arg Ala Ala Trp Ala Phe Tyr Pro Ala Pro
545                 550                 555                 560


Leu Gln Pro Arg Pro Arg Glu Glu Ala Arg Ser Arg Arg Pro Lys Leu
                565                 570                 575


Gly Ala Lys Leu
            580


<210> 1907
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 499; "

<220>
<221> source
<223> /note="Gene Symbol: ACOXL; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000409500"

<400> 1907
Gly Tyr Met Met Glu Asn Arg Ile Ser Gly Leu Lys Cys Asp Thr Asp
1               5                   10                  15


Val Phe Ala Thr Phe Glu Gly Asp Asp Val Val Met Leu Gln Val Val
            20                  25                  30


Gly Arg Glu Leu Leu Ala Gln Tyr Thr Lys Gln Tyr Glu Glu Lys Pro
        35                  40                  45


Leu Phe Gly Leu Leu Gln Asn Trp Ala Glu Ser Val Gly Asp Lys Leu
    50                  55                  60


Arg Thr Ser Phe Leu Ala Phe Asn Met Asp Thr Val Asp Asp Leu Ala
65                  70                  75                  80


Phe Leu Leu Lys Ala Val Lys Phe Arg Glu Arg Val Leu Gln Arg Gly
                85                  90                  95
```

```
Leu Val Ala Arg Ile Tyr Tyr Lys Leu Pro
            100                 105


<210> 1908
<211> 724
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 500; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase bubblegum family
      member 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96GR2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000258873"

<400> 1908
Met Pro Arg Asn Ser Gly Ala Gly Tyr Gly Cys Pro His Gly Asp Pro
1               5                  10                  15


Ser Met Leu Asp Ser Arg Glu Thr Pro Gln Glu Ser Arg Gln Asp Met
            20                  25                  30


Ile Val Arg Thr Thr Gln Glu Lys Leu Lys Thr Ser Ser Leu Thr Asp
        35                  40                  45


Arg Gln Pro Leu Ser Lys Glu Ser Leu Asn His Ala Leu Glu Leu Ser
    50                  55                  60


Val Pro Glu Lys Val Asn Asn Ala Gln Trp Asp Ala Pro Glu Glu Ala
65                  70                  75                  80


Leu Trp Thr Thr Arg Ala Asp Gly Arg Val Arg Leu Arg Ile Asp Pro
                85                  90                  95
```

```
Ser Cys Pro Gln Leu Pro Tyr Thr Val His Arg Met Phe Tyr Glu Ala
            100                 105                 110

Leu Asp Lys Tyr Gly Asp Leu Ile Ala Leu Gly Phe Lys Arg Gln Asp
        115                 120                 125

Lys Trp Glu His Ile Ser Tyr Ser Gln Tyr Tyr Leu Leu Ala Arg Arg
    130                 135                 140

Ala Ala Lys Gly Phe Leu Lys Leu Gly Leu Lys Gln Ala His Ser Val
145                 150                 155                 160

Ala Ile Leu Gly Phe Asn Ser Pro Glu Trp Phe Phe Ser Ala Val Gly
                165                 170                 175

Thr Val Phe Ala Gly Gly Ile Val Thr Gly Ile Tyr Thr Thr Ser Ser
            180                 185                 190

Pro Glu Ala Cys Gln Tyr Ile Ala Tyr Asp Cys Cys Ala Asn Val Ile
        195                 200                 205

Met Val Asp Thr Gln Lys Gln Leu Glu Lys Ile Leu Lys Ile Trp Lys
    210                 215                 220

Gln Leu Pro His Leu Lys Ala Val Val Ile Tyr Lys Glu Pro Pro Pro
225                 230                 235                 240

Asn Lys Met Ala Asn Val Tyr Thr Met Glu Glu Phe Met Glu Leu Gly
                245                 250                 255

Asn Glu Val Pro Glu Glu Ala Leu Asp Ala Ile Ile Asp Thr Gln Gln
            260                 265                 270

Pro Asn Gln Cys Cys Val Leu Val Tyr Thr Ser Gly Thr Thr Gly Asn
        275                 280                 285

Pro Lys Gly Val Met Leu Ser Gln Asp Asn Ile Thr Trp Thr Ala Arg
    290                 295                 300

Tyr Gly Ser Gln Ala Gly Asp Ile Arg Pro Ala Glu Val Gln Gln Glu
305                 310                 315                 320
```

```
Val Val Val Ser Tyr Leu Pro Leu Ser His Ile Ala Ala Gln Ile Tyr
                325                 330                 335

Asp Leu Trp Thr Gly Ile Gln Trp Gly Ala Gln Val Cys Phe Ala Glu
            340                 345                 350

Pro Asp Ala Leu Lys Gly Ser Leu Val Asn Thr Leu Arg Glu Val Glu
        355                 360                 365

Pro Thr Ser His Met Gly Val Pro Arg Val Trp Glu Lys Ile Met Glu
    370                 375                 380

Arg Ile Gln Glu Val Ala Ala Gln Ser Gly Phe Ile Arg Arg Lys Met
385                 390                 395                 400

Leu Leu Trp Ala Met Ser Val Thr Leu Glu Gln Asn Leu Thr Cys Pro
                405                 410                 415

Gly Ser Asp Leu Lys Pro Phe Thr Thr Arg Leu Ala Asp Tyr Leu Val
            420                 425                 430

Leu Ala Lys Val Arg Gln Ala Leu Gly Phe Ala Lys Cys Gln Lys Asn
        435                 440                 445

Phe Tyr Gly Ala Ala Pro Met Met Ala Glu Thr Gln His Phe Phe Leu
    450                 455                 460

Gly Leu Asn Ile Arg Leu Tyr Ala Gly Tyr Gly Leu Ser Glu Thr Ser
465                 470                 475                 480

Gly Pro His Phe Met Ser Ser Pro Tyr Asn Tyr Arg Leu Tyr Ser Ser
                485                 490                 495

Gly Lys Leu Val Pro Gly Cys Arg Val Lys Leu Val Asn Gln Asp Ala
            500                 505                 510

Glu Gly Ile Gly Glu Ile Cys Leu Trp Gly Arg Thr Ile Phe Met Gly
        515                 520                 525

Tyr Leu Asn Met Glu Asp Lys Thr Cys Glu Ala Ile Asp Glu Glu Gly
    530                 535                 540

Trp Leu His Thr Gly Asp Ala Gly Arg Leu Asp Ala Asp Gly Phe Leu
```

545 550 555 560

Tyr Ile Thr Gly Arg Leu Lys Glu Leu Ile Ile Thr Ala Gly Gly Glu
565 570 575

Asn Val Pro Pro Val Pro Ile Glu Glu Ala Val Lys Met Glu Leu Pro
580 585 590

Ile Ile Ser Asn Ala Met Leu Ile Gly Asp Gln Arg Lys Phe Leu Ser
595 600 605

Met Leu Leu Thr Leu Lys Cys Thr Leu Asp Pro Asp Thr Ser Asp Gln
610 615 620

Thr Asp Asn Leu Thr Glu Gln Ala Met Glu Phe Cys Gln Arg Val Gly
625 630 635 640

Ser Arg Ala Thr Thr Val Ser Glu Ile Ile Glu Lys Lys Asp Glu Ala
645 650 655

Val Tyr Gln Ala Ile Glu Glu Gly Ile Arg Arg Val Asn Met Asn Ala
660 665 670

Ala Ala Arg Pro Tyr His Ile Gln Lys Trp Ala Ile Leu Glu Arg Asp
675 680 685

Phe Ser Ile Ser Gly Gly Glu Leu Gly Pro Thr Met Lys Leu Lys Arg
690 695 700

Leu Thr Val Leu Glu Lys Tyr Lys Gly Ile Ile Asp Ser Phe Tyr Gln
705 710 715 720

Glu Gln Lys Met

<210> 1909
<211> 80
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 500; "

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<221> source
<223> /note="Gene Symbol: ACSBG1; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453447"

<400> 1909
Met Pro Arg Asn Ser Gly Ala Gly Tyr Gly Cys Pro His Gly Asp Pro
1 5 10 15

Ser Met Leu Asp Ser Arg Glu Thr Pro Gln Glu Ser Arg Gln Asp Met
20 25 30

Ile Val Arg Thr Thr Gln Glu Lys Leu Lys Thr Arg Gly Gly Ala Val
35 40 45

Asp Asp Ser Gly Arg Trp Ala Gly Ala Pro Ala His Arg Pro Gln Leu
50 55 60

Pro Thr Ala Ser Leu His Cys Ala Ser Asp Val Leu Arg Gly Pro Gly
65 70 75 80

<210> 1910
<211> 482
<212> PRT
<213> Homo sapiens

<220>
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<220>
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member 1; "

<220>
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<223> /note="ENSP ID: ENSP00000453451"

<400> 1910
Met Ala Asn Val Tyr Thr Met Glu Glu Phe Met Glu Leu Gly Asn Glu
1 5 10 15

Val Pro Glu Glu Ala Leu Asp Ala Ile Ile Asp Thr Gln Gln Pro Asn
20 25 30

Gln Cys Cys Val Leu Val Tyr Thr Ser Gly Thr Thr Gly Asn Pro Lys
35 40 45

Gly Val Met Leu Ser Gln Asp Asn Ile Thr Trp Thr Ala Arg Tyr Gly
50 55 60

Ser Gln Ala Gly Asp Ile Arg Pro Ala Glu Val Gln Gln Glu Val Val
65 70 75 80

Val Ser Tyr Leu Pro Leu Ser His Ile Ala Ala Gln Ile Tyr Asp Leu
85 90 95

Trp Thr Gly Ile Gln Trp Gly Ala Gln Val Cys Phe Ala Glu Pro Asp
100 105 110

Ala Leu Lys Gly Ser Leu Val Asn Thr Leu Arg Glu Val Glu Pro Thr
115 120 125

Ser His Met Gly Val Pro Arg Val Trp Glu Lys Ile Met Glu Arg Ile
130 135 140

Gln Glu Val Ala Ala Gln Ser Gly Phe Ile Arg Arg Lys Met Leu Leu
145 150 155 160

Trp Ala Met Ser Val Thr Leu Glu Gln Asn Leu Thr Cys Pro Gly Ser
165 170 175

Asp Leu Lys Pro Phe Thr Thr Arg Leu Ala Asp Tyr Leu Val Leu Ala
180 185 190

Lys Val Arg Gln Ala Leu Gly Phe Ala Lys Cys Gln Lys Asn Phe Tyr
195 200 205

Gly Ala Ala Pro Met Met Ala Glu Thr Gln His Phe Phe Leu Gly Leu
210 215 220

```
Asn Ile Arg Leu Tyr Ala Gly Tyr Gly Leu Ser Glu Thr Ser Gly Pro
225                 230                 235                 240

His Phe Met Ser Ser Pro Tyr Asn Tyr Arg Leu Tyr Ser Ser Gly Lys
                245                 250                 255

Leu Val Pro Gly Cys Arg Val Lys Leu Val Asn Gln Asp Ala Glu Gly
            260                 265                 270

Ile Gly Glu Ile Cys Leu Trp Gly Arg Thr Ile Phe Met Gly Tyr Leu
        275                 280                 285

Asn Met Glu Asp Lys Thr Cys Glu Ala Ile Asp Glu Glu Gly Trp Leu
    290                 295                 300

His Thr Gly Asp Ala Gly Arg Leu Asp Ala Asp Gly Phe Leu Tyr Ile
305                 310                 315                 320

Thr Gly Arg Leu Lys Glu Leu Ile Ile Thr Ala Gly Gly Glu Asn Val
                325                 330                 335

Pro Pro Val Pro Ile Glu Glu Ala Val Lys Met Glu Leu Pro Ile Ile
            340                 345                 350

Ser Asn Ala Met Leu Ile Gly Asp Gln Arg Lys Phe Leu Ser Met Leu
        355                 360                 365

Leu Thr Leu Lys Cys Thr Leu Asp Pro Asp Thr Ser Asp Gln Thr Asp
    370                 375                 380

Asn Leu Thr Glu Gln Ala Met Glu Phe Cys Gln Arg Val Gly Ser Arg
385                 390                 395                 400

Ala Thr Thr Val Ser Glu Ile Ile Glu Lys Lys Asp Glu Ala Val Tyr
                405                 410                 415

Gln Ala Ile Glu Glu Gly Ile Arg Arg Val Asn Met Asn Ala Ala Ala
            420                 425                 430

Arg Pro Tyr His Ile Gln Lys Trp Ala Ile Leu Glu Arg Asp Phe Ser
        435                 440                 445

Ile Ser Gly Gly Glu Leu Gly Pro Thr Met Lys Leu Lys Arg Leu Thr
```

```
    450                 455                 460

Val Leu Glu Lys Tyr Lys Gly Ile Ile Asp Ser Phe Tyr Gln Glu Gln
465                 470                 475                 480

Lys Met


<210> 1911
<211> 243
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACSBG1; "

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      acyl-CoA synthetase bubblegum family
      member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453547"

<400> 1911
Met Pro Glu Val Leu Leu Leu Arg Ser Ala Ser Ser Ile Leu Arg Thr
1               5                   10                  15

Ala Phe Leu Ser Arg Trp Leu Pro Gly Gly Pro Arg Cys Val His Lys
            20                  25                  30

Leu Ser Phe Val Arg Asn Leu Gln Cys Arg Gln Gly Val Arg Leu Asn
        35                  40                  45

Val Arg Ser Ser Ser Leu Thr Asp Arg Gln Pro Leu Ser Lys Glu Ser
    50                  55                  60

Leu Asn His Ala Leu Glu Leu Ser Val Pro Glu Lys Val Asn Asn Ala
65                  70                  75                  80

Gln Trp Asp Ala Pro Glu Glu Ala Leu Trp Thr Thr Arg Ala Asp Gly
                85                  90                  95
```

```
Arg Val Arg Leu Arg Ile Asp Pro Ser Cys Pro Gln Leu Pro Tyr Thr
            100                 105                 110

Val His Arg Met Phe Tyr Glu Ala Leu Asp Lys Tyr Gly Asp Leu Ile
        115                 120                 125

Ala Leu Gly Phe Lys Arg Gln Asp Lys Trp Glu His Ile Ser Tyr Ser
    130                 135                 140

Gln Tyr Tyr Leu Leu Ala Arg Arg Ala Ala Lys Gly Phe Leu Lys Leu
145                 150                 155                 160

Gly Leu Lys Gln Ala His Ser Val Ala Ile Leu Gly Phe Asn Ser Pro
                165                 170                 175

Glu Trp Phe Phe Ser Ala Val Gly Thr Val Phe Ala Gly Gly Ile Val
            180                 185                 190

Thr Gly Ile Tyr Thr Thr Ser Ser Pro Glu Ala Cys Gln Tyr Ile Ala
        195                 200                 205

Tyr Asp Cys Cys Ala Asn Val Ile Met Val Asp Thr Gln Lys Gln Leu
    210                 215                 220

Glu Lys Ile Leu Lys Ile Trp Lys Gln Leu Pro His Leu Lys Ala Val
225                 230                 235                 240

Val Ile Tyr
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<210> 1912
<211> 55
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 500; "

<220>
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<223> /note="Gene Symbol: ACSBG1; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453585"

<400> 1912
Met Pro Arg Asn Ser Gly Ala Gly Tyr Gly Cys Pro His Gly Asp Pro
1 5 10 15

Ser Met Leu Asp Ser Arg Glu Thr Pro Gln Glu Ser Arg Gln Asp Met
20 25 30

Ile Val Arg Thr Thr Gln Glu Lys Leu Lys Thr Arg Asp Gly Val Leu
35 40 45

Leu His Cys Pro Gly Trp Pro
50 55

<210> 1913
<211> 51
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 500; "

<220>
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<223> /note="Gene Symbol: ACSBG1; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453605"

<400> 1913
Met Pro Arg Asn Ser Gly Ala Gly Tyr Gly Cys Pro His Gly Asp Pro
1 5 10 15

Ser Met Leu Asp Ser Arg Glu Thr Pro Gln Glu Ser Arg Gln Asp Met
20 25 30

Ile Val Arg Thr Thr Gln Glu Lys Leu Lys Thr Arg Ser Gly Asn Ser
35 40 45

Cys His Ile
50

<210> 1914
<211> 181
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453800"

<400> 1914
Met Pro Arg Asn Ser Gly Ala Gly Tyr Gly Cys Pro His Gly Asp Pro
1 5 10 15

Ser Met Leu Asp Ser Arg Glu Thr Pro Gln Glu Ser Arg Gln Asp Met
20 25 30

Ile Val Arg Thr Thr Gln Glu Lys Leu Lys Thr Ser Ser Leu Thr Asp
35 40 45

Arg Gln Pro Leu Ser Lys Glu Ser Leu Asn His Ala Leu Glu Leu Ser
50 55 60

Val Pro Glu Lys Val Asn Asn Ala Gln Trp Asp Ala Pro Glu Glu Ala
65 70 75 80

Leu Trp Thr Thr Arg Ala Asp Gly Arg Val Arg Leu Arg Ile Asp Pro
85 90 95

Ser Cys Pro Gln Leu Pro Tyr Thr Val His Arg Met Phe Tyr Glu Ala

```
            100                 105                 110

Leu Asp Lys Tyr Gly Asp Leu Ile Ala Leu Gly Phe Lys Arg Gln Asp
        115                 120                 125

Lys Trp Glu His Ile Ser Tyr Ser Gln Tyr Tyr Leu Leu Ala Arg Arg
    130                 135                 140

Ala Ala Lys Gly Phe Leu Lys Gln Ala His Ser Val Ala Ile Leu Gly
145                 150                 155                 160

Phe Asn Ser Pro Glu Trp Phe Phe Ser Ala Val Gly Thr Val Phe Ala
                165                 170                 175

Gly Gly Ile Val Thr
            180


<210> 1915
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 500; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase bubblegum family
      member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454188"

<400> 1915
Met Phe Tyr Glu Ala Leu Asp Lys Tyr Gly Asp Leu Ile Ala Leu Gly
1               5                   10                  15

Phe Lys Arg Gln Asp Lys Trp Glu His Ile Ser Tyr Ser Gln Tyr Tyr
            20                  25                  30

Leu Leu Ala Arg Arg Ala Ala Lys Gly Phe Leu Lys Leu Gly Leu Lys
        35                  40                  45
```

```
Gln Ala His Ser Val Ala Ile Leu Gly Phe Asn Ser Pro Glu Trp Phe
    50                  55                  60

Phe Ser Ala Val Gly Thr Val Phe Ala Gly Gly Ile Val Thr Gly Ile
65                  70                  75                  80

Tyr Thr Thr Ser Ser Pro Glu Ala Cys Gln Tyr Ile Ala Tyr Asp Cys
                85                  90                  95

Cys Ala Asn Val Ile Met Val Asp Thr Gln Lys Gln Leu Glu Lys Ile
            100                 105                 110

Leu Lys Ile Trp Lys Gln Leu Pro His Leu Lys Ala Val Val Ile Tyr
        115                 120                 125

Lys Glu Pro Pro Pro Asn Lys Met Ala Asn
    130                 135


<210> 1916
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
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<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
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      member 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q5FVE4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000464938"

<400> 1916
Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe Gly Thr
1               5                   10                  15
```

```
Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile Leu Asn
            20                  25                  30

Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser Leu Ile
        35                  40                  45

Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly Phe Asn
    50                  55                  60

Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala Gly Gly
65                  70                  75                  80

Leu Cys Val Gly Ile Tyr Ala Thr Asn Ser Ala Glu Val Cys Gln Tyr
                85                  90                  95

Val Ile Thr His Ala Lys Val Asn Ile Leu Leu Val Glu Asn Asp Gln
            100                 105                 110

Gln Leu Gln Lys Ile Leu Ser Ile Pro Gln Ser Ser Leu Glu Pro Leu
        115                 120                 125

Lys Ala Ile Ile Gln Tyr Arg Leu Pro Met Lys Lys Asn Asn Asn Leu
    130                 135                 140

Tyr Ser Trp Asp Asp Phe Met Glu Leu Gly Arg Ser Ile Pro Asp Thr
145                 150                 155                 160

Gln Leu Glu Gln Val Ile Glu Ser Gln Lys Ala Asn Gln Cys Ala Val
                165                 170                 175

Leu Ile Tyr Thr Ser Gly Thr Thr Gly Ile Pro Lys Gly Val Met Leu
            180                 185                 190

Ser His Asp Asn Ile Thr Trp Ile Ala Gly Ala Val Thr Lys Asp Phe
        195                 200                 205

Lys Leu Thr Asp Lys His Glu Thr Val Val Ser Tyr Leu Pro Leu Ser
    210                 215                 220

His Ile Ala Ala Gln Met Met Asp Ile Trp Val Pro Ile Lys Ile Gly
225                 230                 235                 240
```

```
Ala Leu Thr Tyr Phe Ala Gln Ala Asp Ala Leu Lys Gly Thr Leu Val
                245                 250                 255

Ser Thr Leu Lys Glu Val Lys Pro Thr Val Phe Ile Gly Val Pro Gln
            260                 265                 270

Ile Trp Glu Lys Ile His Glu Met Val Lys Lys Asn Ser Ala Lys Ser
        275                 280                 285

Met Gly Leu Lys Lys Lys Ala Phe Val Trp Ala Arg Asn Ile Gly Phe
    290                 295                 300

Lys Val Asn Ser Lys Lys Met Leu Gly Lys Tyr Asn Thr Pro Val Ser
305                 310                 315                 320

Tyr Arg Met Ala Lys Thr Leu Val Phe Ser Lys Val Lys Thr Ser Leu
                325                 330                 335

Gly Leu Asp His Cys His Ser Phe Ile Ser Gly Thr Ala Pro Leu Asn
            340                 345                 350

Gln Glu Thr Ala Glu Phe Phe Leu Ser Leu Asp Ile Pro Ile Gly Glu
        355                 360                 365

Leu Tyr Gly Leu Ser Glu Ser Ser Gly Pro His Thr Ile Ser Asn Gln
    370                 375                 380

Asn Asn Tyr Arg Leu Leu Ser Cys Gly Lys Ile Leu Thr Gly Cys Lys
385                 390                 395                 400

Asn Met Leu Phe Gln Gln Asn Lys Asp Gly Ile Gly Glu Ile Cys Leu
                405                 410                 415

Trp Gly Arg His Ile Phe Met Gly Tyr Leu Glu Ser Glu Thr Glu Thr
            420                 425                 430

Thr Glu Ala Ile Asp Asp Glu Gly Trp Leu His Ser Gly Asp Leu Gly
        435                 440                 445

Gln Leu Asp Gly Leu Gly Phe Leu Tyr Val Thr Gly His Ile Lys Glu
    450                 455                 460

Ile Leu Ile Thr Ala Gly Gly Glu Asn Val Pro Pro Ile Pro Val Glu
```

```
465                 470                 475                 480

Thr Leu Val Lys Lys Lys Ile Pro Ile Ile Ser Asn Ala Met Leu Val
                485                 490                 495

Gly Asp Lys Leu Lys Phe Leu Ser Met Leu Leu Thr Leu Lys Cys Glu
            500                 505                 510

Met Asn Gln Met Ser Gly Glu Pro Leu Asp Lys Leu Asn Phe Glu Ala
        515                 520                 525

Ile Asn Phe Cys Arg Gly Leu Gly Ser Gln Ala Ser Thr Val Thr Glu
    530                 535                 540

Ile Val Lys Gln Gln Asp Pro Leu Val Tyr Lys Ala Ile Gln Gln Gly
545                 550                 555                 560

Ile Asn Ala Val Asn Gln Glu Ala Met Asn Asn Ala Gln Arg Ile Glu
                565                 570                 575

Lys Trp Val Ile Leu Glu Lys Asp Phe Ser Ile Tyr Gly Gly Glu Leu
            580                 585                 590

Gly Pro Met Met Lys Leu Lys Arg His Phe Val Ala Gln Lys Tyr Lys
        595                 600                 605

Lys Gln Ile Asp His Met Tyr His
    610                 615
```

<210> 1917
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465088"

<400> 1917
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1   5   10   15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
            20   25   30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
        35   40   45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
    50   55   60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile
65   70   75   80

Leu Asn Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser
                85   90   95

Leu Ile Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly
            100   105   110

Phe Asn Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala
        115   120   125

Gly Phe His Arg Ala Ala
    130

<210> 1918
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465581"

<400> 1918
Tyr Ala Thr Asn Ser Ala Glu Val Cys Gln Tyr Val Ile Thr His Ala
1 5 10 15

Lys Val Asn Ile Leu Leu Val Glu Asn Asp Gln Gln Leu Gln Lys Ile
20 25 30

Leu Ser Ile Pro Gln Ser Ser Leu Glu Pro Leu Lys Ala Ile Ile Gln
35 40 45

Tyr Arg Leu Pro Met Lys Lys Asn Asn Asn Leu Tyr Ser Trp Asp Asp
50 55 60

Phe Met Glu Leu Gly Arg Ser Ile Pro Asp Thr Gln Leu Glu Gln Val
65 70 75 80

Ile Glu Ser Gln Lys Ala Asn Gln Cys Ala Val Leu Ile Tyr Thr Ser
85 90 95

Gly Thr Thr Gly Ile Pro Lys Gly Val Met Leu Ser His Asp Asn Lys
100 105 110

Asn Ser Leu Ser Thr
115

<210> 1919
<211> 666
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
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<223> /note="Gene Symbol: ACSBG2; "

<220>
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<223> /note="Gene Name:

acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q5FVE4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465589"

<400> 1919
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1   5   10   15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
            20   25   30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
        35   40   45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
    50   55   60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile
65   70   75   80

Leu Asn Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser
                85   90   95

Leu Ile Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly
            100   105   110

Phe Asn Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala
        115   120   125

Gly Gly Leu Cys Val Gly Ile Tyr Ala Thr Asn Ser Ala Glu Val Cys
    130   135   140

Gln Tyr Val Ile Thr His Ala Lys Val Asn Ile Leu Leu Val Glu Asn
145   150   155   160

Asp Gln Gln Leu Gln Lys Ile Leu Ser Ile Pro Gln Ser Ser Leu Glu
                165   170   175

Pro Leu Lys Ala Ile Ile Gln Tyr Arg Leu Pro Met Lys Lys Asn Asn

```
            180                 185                 190

Asn Leu Tyr Ser Trp Asp Asp Phe Met Glu Leu Gly Arg Ser Ile Pro
        195                 200                 205

Asp Thr Gln Leu Glu Gln Val Ile Glu Ser Gln Lys Ala Asn Gln Cys
    210                 215                 220

Ala Val Leu Ile Tyr Thr Ser Gly Thr Thr Gly Ile Pro Lys Gly Val
225                 230                 235                 240

Met Leu Ser His Asp Asn Ile Thr Trp Ile Ala Gly Ala Val Thr Lys
                245                 250                 255

Asp Phe Lys Leu Thr Asp Lys His Glu Thr Val Val Ser Tyr Leu Pro
            260                 265                 270

Leu Ser His Ile Ala Ala Gln Met Met Asp Ile Trp Val Pro Ile Lys
        275                 280                 285

Ile Gly Ala Leu Thr Tyr Phe Ala Gln Ala Asp Ala Leu Lys Gly Thr
    290                 295                 300

Leu Val Ser Thr Leu Lys Glu Val Lys Pro Thr Val Phe Ile Gly Val
305                 310                 315                 320

Pro Gln Ile Trp Glu Lys Ile His Glu Met Val Lys Lys Asn Ser Ala
                325                 330                 335

Lys Ser Met Gly Leu Lys Lys Lys Ala Phe Val Trp Ala Arg Asn Ile
            340                 345                 350

Gly Phe Lys Val Asn Ser Lys Lys Met Leu Gly Lys Tyr Asn Thr Pro
        355                 360                 365

Val Ser Tyr Arg Met Ala Lys Thr Leu Val Phe Ser Lys Val Lys Thr
    370                 375                 380

Ser Leu Gly Leu Asp His Cys His Ser Phe Ile Ser Gly Thr Ala Pro
385                 390                 395                 400

Leu Asn Gln Glu Thr Ala Glu Phe Phe Leu Ser Leu Asp Ile Pro Ile
                405                 410                 415
```

```
Gly Glu Leu Tyr Gly Leu Ser Glu Ser Ser Gly Pro His Thr Ile Ser
            420                 425                 430

Asn Gln Asn Asn Tyr Arg Leu Leu Ser Cys Gly Lys Ile Leu Thr Gly
        435                 440                 445

Cys Lys Asn Met Leu Phe Gln Gln Asn Lys Asp Gly Ile Gly Glu Ile
    450                 455                 460

Cys Leu Trp Gly Arg His Ile Phe Met Gly Tyr Leu Glu Ser Glu Thr
465                 470                 475                 480

Glu Thr Thr Glu Ala Ile Asp Asp Glu Gly Trp Leu His Ser Gly Asp
                485                 490                 495

Leu Gly Gln Leu Asp Gly Leu Gly Phe Leu Tyr Val Thr Gly His Ile
            500                 505                 510

Lys Glu Ile Leu Ile Thr Ala Gly Gly Glu Asn Val Pro Pro Ile Pro
        515                 520                 525

Val Glu Thr Leu Val Lys Lys Lys Ile Pro Ile Ile Ser Asn Ala Met
    530                 535                 540

Leu Val Gly Asp Lys Leu Lys Phe Leu Ser Met Leu Leu Thr Leu Lys
545                 550                 555                 560

Cys Glu Met Asn Gln Met Ser Gly Glu Pro Leu Asp Lys Leu Asn Phe
                565                 570                 575

Glu Ala Ile Asn Phe Cys Arg Gly Leu Gly Ser Gln Ala Ser Thr Val
            580                 585                 590

Thr Glu Ile Val Lys Gln Gln Asp Pro Leu Val Tyr Lys Ala Ile Gln
        595                 600                 605

Gln Gly Ile Asn Ala Val Asn Gln Glu Ala Met Asn Asn Ala Gln Arg
    610                 615                 620

Ile Glu Lys Trp Val Ile Leu Glu Lys Asp Phe Ser Ile Tyr Gly Gly
625                 630                 635                 640
```

Glu Leu Gly Pro Met Met Lys Leu Lys Arg His Phe Val Ala Gln Lys
645 650 655

Tyr Lys Lys Gln Ile Asp His Met Tyr His
660 665

<210> 1920
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465870"

<400> 1920
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1 5 10 15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
20 25 30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
35 40 45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
50 55 60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile
65 70 75 80

Leu Asn Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser
85 90 95

```
Leu Ile Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly
            100                 105                 110

Phe Asn Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala
        115                 120                 125

Gly Gly Leu Cys Val Gly Ile Tyr Ala Thr Asn Ser Ala Glu
    130                 135                 140


<210> 1921
<211> 479
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase bubblegum family
      member 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q5FVE4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466336"

<400> 1921
Met Lys Lys Asn Asn Asn Leu Tyr Ser Trp Asp Asp Phe Met Glu Leu
1               5                   10                  15

Gly Arg Ser Ile Pro Asp Thr Gln Leu Glu Gln Val Ile Glu Ser Gln
            20                  25                  30

Lys Ala Asn Gln Cys Ala Val Leu Ile Tyr Thr Ser Gly Thr Thr Gly
        35                  40                  45

Ile Pro Lys Gly Val Met Leu Ser His Asp Asn Ile Thr Trp Ile Ala
    50                  55                  60

Gly Ala Val Thr Lys Asp Phe Lys Leu Thr Asp Lys His Glu Thr Val
```

65 70 75 80

Val Ser Tyr Leu Pro Leu Ser His Ile Ala Ala Gln Met Met Asp Ile
85 90 95

Trp Val Pro Ile Lys Ile Gly Ala Leu Thr Tyr Phe Ala Gln Ala Asp
100 105 110

Ala Leu Lys Gly Thr Leu Val Ser Thr Leu Lys Glu Val Lys Pro Thr
115 120 125

Val Phe Ile Gly Val Pro Gln Ile Trp Glu Lys Ile His Glu Met Val
130 135 140

Lys Lys Asn Ser Ala Lys Ser Met Gly Leu Lys Lys Lys Ala Phe Val
145 150 155 160

Trp Ala Arg Asn Ile Gly Phe Lys Val Asn Ser Lys Lys Met Leu Gly
165 170 175

Lys Tyr Asn Thr Pro Val Ser Tyr Arg Met Ala Lys Thr Leu Val Phe
180 185 190

Ser Lys Val Lys Thr Ser Leu Gly Leu Asp His Cys His Ser Phe Ile
195 200 205

Ser Gly Thr Ala Pro Leu Asn Gln Glu Thr Ala Glu Phe Phe Leu Ser
210 215 220

Leu Asp Ile Pro Ile Gly Glu Leu Tyr Gly Leu Ser Glu Ser Ser Gly
225 230 235 240

Pro His Thr Ile Ser Asn Gln Asn Asn Tyr Arg Leu Leu Ser Cys Gly
245 250 255

Lys Ile Leu Thr Gly Cys Lys Asn Met Leu Phe Gln Gln Asn Lys Asp
260 265 270

Gly Ile Gly Glu Ile Cys Leu Trp Gly Arg His Ile Phe Met Gly Tyr
275 280 285

Leu Glu Ser Glu Thr Glu Thr Thr Glu Ala Ile Asp Asp Glu Gly Trp
290 295 300

```
Leu His Ser Gly Asp Leu Gly Gln Leu Asp Gly Leu Gly Phe Leu Tyr
305                 310                 315                 320

Val Thr Gly His Ile Lys Glu Ile Leu Ile Thr Ala Gly Gly Glu Asn
                325                 330                 335

Val Pro Pro Ile Pro Val Glu Thr Leu Val Lys Lys Lys Ile Pro Ile
            340                 345                 350

Ile Ser Asn Ala Met Leu Val Gly Asp Lys Leu Lys Phe Leu Ser Met
        355                 360                 365

Leu Leu Thr Leu Lys Cys Glu Met Asn Gln Met Ser Gly Glu Pro Leu
    370                 375                 380

Asp Lys Leu Asn Phe Glu Ala Ile Asn Phe Cys Arg Gly Leu Gly Ser
385                 390                 395                 400

Gln Ala Ser Thr Val Thr Glu Ile Val Lys Gln Gln Asp Pro Leu Val
                405                 410                 415

Tyr Lys Ala Ile Gln Gln Gly Ile Asn Ala Val Asn Gln Glu Ala Met
            420                 425                 430

Asn Asn Ala Gln Arg Ile Glu Lys Trp Val Ile Leu Glu Lys Asp Phe
        435                 440                 445

Ser Ile Tyr Gly Gly Glu Leu Gly Pro Met Met Lys Leu Lys Arg His
    450                 455                 460

Phe Val Ala Gln Lys Tyr Lys Lys Gln Ile Asp His Met Tyr His
465                 470                 475


<210> 1922
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
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<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466434"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1922
Xaa Thr Leu Val Lys Lys Lys Ile Pro Ile Ile Ser Asn Ala Met Leu
1 5 10 15

Val Gly Asp Lys Leu Lys Phe Leu Ser Met Leu Leu Thr Leu Lys Pro
20 25 30

Gly Ile His Arg Asp
35

<210> 1923
<211> 666
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q5FVE4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467755"

<400> 1923
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1 5 10 15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
20 25 30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
35 40 45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
50 55 60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile
65 70 75 80

Leu Asn Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser
85 90 95

Leu Ile Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly
100 105 110

Phe Asn Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala
115 120 125

Gly Gly Leu Cys Val Gly Ile Tyr Ala Thr Asn Ser Ala Glu Val Cys
130 135 140

Gln Tyr Val Ile Thr His Ala Lys Val Asn Ile Leu Leu Val Glu Asn
145 150 155 160

Asp Gln Gln Leu Gln Lys Ile Leu Ser Ile Pro Gln Ser Ser Leu Glu
165 170 175

Pro Leu Lys Ala Ile Ile Gln Tyr Arg Leu Pro Met Lys Lys Asn Asn
180 185 190

Asn Leu Tyr Ser Trp Asp Asp Phe Met Glu Leu Gly Arg Ser Ile Pro
195 200 205

Asp Thr Gln Leu Glu Gln Val Ile Glu Ser Gln Lys Ala Asn Gln Cys
210 215 220

```
Ala Val Leu Ile Tyr Thr Ser Gly Thr Thr Gly Ile Pro Lys Gly Val
225                 230                 235                 240

Met Leu Ser His Asp Asn Ile Thr Trp Ile Ala Gly Ala Val Thr Lys
                245                 250                 255

Asp Phe Lys Leu Thr Asp Lys His Glu Thr Val Val Ser Tyr Leu Pro
            260                 265                 270

Leu Ser His Ile Ala Ala Gln Met Met Asp Ile Trp Val Pro Ile Lys
        275                 280                 285

Ile Gly Ala Leu Thr Tyr Phe Ala Gln Ala Asp Ala Leu Lys Gly Thr
    290                 295                 300

Leu Val Ser Thr Leu Lys Glu Val Lys Pro Thr Val Phe Ile Gly Val
305                 310                 315                 320

Pro Gln Ile Trp Glu Lys Ile His Glu Met Val Lys Lys Asn Ser Ala
                325                 330                 335

Lys Ser Met Gly Leu Lys Lys Lys Ala Phe Val Trp Ala Arg Asn Ile
            340                 345                 350

Gly Phe Lys Val Asn Ser Lys Lys Met Leu Gly Lys Tyr Asn Thr Pro
        355                 360                 365

Val Ser Tyr Arg Met Ala Lys Thr Leu Val Phe Ser Lys Val Lys Thr
    370                 375                 380

Ser Leu Gly Leu Asp His Cys His Ser Phe Ile Ser Gly Thr Ala Pro
385                 390                 395                 400

Leu Asn Gln Glu Thr Ala Glu Phe Phe Leu Ser Leu Asp Ile Pro Ile
                405                 410                 415

Gly Glu Leu Tyr Gly Leu Ser Glu Ser Ser Gly Pro His Thr Ile Ser
            420                 425                 430

Asn Gln Asn Asn Tyr Arg Leu Leu Ser Cys Gly Lys Ile Leu Thr Gly
        435                 440                 445
```

```
Cys Lys Asn Met Leu Phe Gln Gln Asn Lys Asp Gly Ile Gly Glu Ile
    450                 455                 460

Cys Leu Trp Gly Arg His Ile Phe Met Gly Tyr Leu Glu Ser Glu Thr
465                 470                 475                 480

Glu Thr Thr Glu Ala Ile Asp Asp Glu Gly Trp Leu His Ser Gly Asp
                485                 490                 495

Leu Gly Gln Leu Asp Gly Leu Gly Phe Leu Tyr Val Thr Gly His Ile
            500                 505                 510

Lys Glu Ile Leu Ile Thr Ala Gly Gly Glu Asn Val Pro Pro Ile Pro
        515                 520                 525

Val Glu Thr Leu Val Lys Lys Lys Ile Pro Ile Ile Ser Asn Ala Met
    530                 535                 540

Leu Val Gly Asp Lys Leu Lys Phe Leu Ser Met Leu Leu Thr Leu Lys
545                 550                 555                 560

Cys Glu Met Asn Gln Met Ser Gly Glu Pro Leu Asp Lys Leu Asn Phe
                565                 570                 575

Glu Ala Ile Asn Phe Cys Arg Gly Leu Gly Ser Gln Ala Ser Thr Val
            580                 585                 590

Thr Glu Ile Val Lys Gln Gln Asp Pro Leu Val Tyr Lys Ala Ile Gln
        595                 600                 605

Gln Gly Ile Asn Ala Val Asn Gln Glu Ala Met Asn Asn Ala Gln Arg
    610                 615                 620

Ile Glu Lys Trp Val Ile Leu Glu Lys Asp Phe Ser Ile Tyr Gly Gly
625                 630                 635                 640

Glu Leu Gly Pro Met Met Lys Leu Lys Arg His Phe Val Ala Gln Lys
                645                 650                 655

Tyr Lys Lys Gln Ile Asp His Met Tyr His
            660                 665
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<210> 1924

<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468394"

<400> 1924
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1 5 10 15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
20 25 30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
35 40 45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
50 55 60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile
65 70 75 80

Leu Asn Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser
85 90 95

Leu Ile Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly
100 105 110

Phe Asn Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala
115 120 125

Gly

<210> 1925
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source
<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468652"

<400> 1925
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1 5 10 15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
20 25 30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
35 40 45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
50 55 60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys
65 70 75

<210> 1926
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 501; "

<220>
<221> source

<223> /note="Gene Symbol: ACSBG2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase bubblegum family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468684"

<400> 1926
Met Thr Gly Thr Pro Lys Thr Gln Glu Gly Ala Lys Asp Leu Glu Val
1 5 10 15

Asp Met Asn Lys Thr Glu Val Thr Pro Arg Leu Trp Thr Thr Cys Arg
20 25 30

Asp Gly Glu Val Leu Leu Arg Leu Ser Lys His Gly Pro Gly His Glu
35 40 45

Thr Pro Met Thr Ile Pro Glu Phe Phe Arg Glu Ser Val Asn Arg Phe
50 55 60

Gly Thr Tyr Pro Ala Leu Ala Ser Lys Asn Gly Lys Lys Trp Glu Ile
65 70 75 80

Leu Asn Phe Asn Gln Tyr Tyr Glu Ala Cys Arg Lys Ala Ala Lys Ser
85 90 95

Leu Ile Lys Leu Gly Leu Glu Arg Phe His Gly Val Gly Ile Leu Gly
100 105 110

Phe Asn Ser Ala Glu Trp Phe Ile Thr Ala Val Gly Ala Ile Leu Ala
115 120 125

Gly Phe His Arg Ala Ala
130

<210> 1927
<211> 615
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 502; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q96CM8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000300441"

<400> 1927
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1   5   10   15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
            20   25   30

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
        35   40   45

Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
    50   55   60

Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
65   70   75   80

Thr Ala Gln Arg Val Pro Glu Arg Glu Ala Leu Val Val Leu His Glu
                85   90   95

Asp Val Arg Leu Thr Phe Ala Gln Leu Lys Glu Glu Val Asp Lys Ala
            100   105   110

Ala Ser Gly Leu Leu Ser Ile Gly Leu Cys Lys Gly Asp Arg Leu Gly
        115   120   125

Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
    130   135   140

Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala

145 150 155 160

Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
165 170 175

Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
180 185 190

Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
195 200 205

Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
210 215 220

Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
225 230 235 240

His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp
245 250 255

Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly
260 265 270

Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly
275 280 285

Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile
290 295 300

Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met
305 310 315 320

Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe
325 330 335

Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe
340 345 350

Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp
355 360 365

Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly
370 375 380

```
Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn
385                 390                 395                 400

Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val
                405                 410                 415

Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser
            420                 425                 430

Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu
        435                 440                 445

Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg
    450                 455                 460

Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
465                 470                 475                 480

Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr
                485                 490                 495

Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met
            500                 505                 510

Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe
        515                 520                 525

Phe His Thr His Pro Lys Val Gln Glu Val Gln Val Val Gly Val Lys
    530                 535                 540

Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp
545                 550                 555                 560

Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys
                565                 570                 575

Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr
            580                 585                 590

Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
        595                 600                 605
```

Met Glu Arg His Leu Asn Leu
610 615

<210> 1928
<211> 640
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 502; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q96CM8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000401831"

<400> 1928
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1 5 10 15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
20 25 30

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ala Arg Gly Gly Met
35 40 45

Glu Ala Gly Arg Gln Arg Ile Ser Val Pro Ser Ser Phe Thr Ala Ser
50 55 60

Ala Ala Ala His Ser Arg Glu Val Asp Arg Met Val Ser Thr Pro Ile
65 70 75 80

Gly Gly Leu Ser Tyr Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser
85 90 95

```
Lys Thr Val Gly Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu
            100                 105                 110

Arg Glu Ala Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala
        115                 120                 125

Gln Leu Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile
    130                 135                 140

Gly Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Tyr
145                 150                 155                 160

Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile Leu
                165                 170                 175

Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr Val Leu
            180                 185                 190

Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln Phe Lys Thr
        195                 200                 205

Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro Glu Val Glu Asn
    210                 215                 220

Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu Pro Asp Leu Thr Thr
225                 230                 235                 240

Val Ile Ser Val Asp Ala Pro Leu Pro Gly Thr Leu Leu Leu Asp Glu
                245                 250                 255

Val Val Ala Ala Gly Ser Thr Arg Gln His Leu Asp Gln Leu Gln Tyr
            260                 265                 270

Asn Gln Gln Phe Leu Ser Cys His Asp Pro Ile Asn Ile Gln Phe Thr
        275                 280                 285

Ser Gly Thr Thr Gly Ser Pro Lys Gly Ala Thr Leu Ser His Tyr Asn
    290                 295                 300

Ile Val Asn Asn Ser Asn Ile Leu Gly Glu Arg Leu Lys Leu His Glu
305                 310                 315                 320

Lys Thr Pro Glu Gln Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His
```

```
                325                 330                 335

Cys Leu Gly Ser Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala
            340                 345                 350

Thr Leu Ile Leu Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu
        355                 360                 365

Ala Ile Ser Arg Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met
    370                 375                 380

Phe Val Asp Ile Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser
385                 390                 395                 400

Thr Met Cys Gly Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu Leu
                405                 410                 415

Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp Leu Val Val Ala
            420                 425                 430

Tyr Gly Thr Thr Glu Asn Ser Pro Val Thr Phe Ala His Phe Pro Glu
        435                 440                 445

Asp Thr Val Glu Gln Lys Ala Glu Ser Val Gly Arg Ile Met Pro His
    450                 455                 460

Thr Glu Ala Arg Ile Met Asn Met Glu Ala Gly Thr Leu Ala Lys Leu
465                 470                 475                 480

Asn Thr Pro Gly Glu Leu Cys Ile Arg Gly Tyr Cys Val Met Leu Gly
                485                 490                 495

Tyr Trp Gly Glu Pro Gln Lys Thr Glu Glu Ala Val Asp Gln Asp Lys
            500                 505                 510

Trp Tyr Trp Thr Gly Asp Val Ala Thr Met Asn Glu Gln Gly Phe Cys
        515                 520                 525

Lys Ile Val Gly Arg Ser Lys Asp Met Ile Ile Arg Gly Gly Glu Asn
    530                 535                 540

Ile Tyr Pro Ala Glu Leu Glu Asp Phe Phe His Thr His Pro Lys Val
545                 550                 555                 560
```

```
Gln Glu Val Gln Val Val Gly Val Lys Asp Asp Arg Met Gly Glu Glu
                565                 570                 575

Ile Cys Ala Cys Ile Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu
            580                 585                 590

Glu Ile Lys Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro
        595                 600                 605

Lys Tyr Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys
    610                 615                 620

Ile Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu
625                 630                 635                 640
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<210> 1929
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 502; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421558"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1929

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Xaa Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe
1               5                   10                  15

Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp
```

```
            20                  25                  30

Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly
        35                  40                  45

Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn
    50                  55                  60

Met Lys Asp Leu Val Lys Ser Gln Glu Glu Ile Ala Ala Trp Glu Asp
65                  70                  75                  80

Gly Gln Gln Ser Thr Asp Val Leu Leu Glu Arg Pro Gly Arg Leu Leu
                85                  90                  95

Met Glu Pro Gln Arg Thr Val Pro
            100


<210> 1930
<211> 602
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 502; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96CM8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421884"

<400> 1930
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1               5                   10                  15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
            20                  25                  30
```

```
Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
        35                  40                  45

Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
    50                  55                  60

Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
65                  70                  75                  80

Thr Ala Gln Arg Val Pro Glu Arg Glu Ala Leu Val Val Leu His Glu
                85                  90                  95

Asp Val Arg Leu Thr Phe Ala Gln Leu Lys Glu Glu Val Asp Lys Ala
            100                 105                 110

Ala Ser Gly Leu Leu Ser Ile Gly Leu Cys Lys Gly Asp Arg Leu Gly
        115                 120                 125

Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
    130                 135                 140

Ala Gln Ala Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys
145                 150                 155                 160

Ala Leu Val Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val
                165                 170                 175

Leu Lys Gln Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu
            180                 185                 190

Lys Ser Gln Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala
        195                 200                 205

Pro Leu Pro Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser
    210                 215                 220

Thr Arg Gln His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser
225                 230                 235                 240

Cys His Asp Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser
                245                 250                 255
```

```
Pro Lys Gly Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn
            260                 265                 270

Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu
        275                 280                 285

Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala
    290                 295                 300

Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser
305                 310                 315                 320

Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg
                325                 330                 335

Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn
            340                 345                 350

Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val
        355                 360                 365

Ile Ala Gly Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn
    370                 375                 380

Lys Ile Asn Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn
385                 390                 395                 400

Ser Pro Val Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys
                405                 410                 415

Ala Glu Ser Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met
            420                 425                 430

Asn Met Glu Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu
        435                 440                 445

Cys Ile Arg Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln
    450                 455                 460

Lys Thr Glu Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp
465                 470                 475                 480
```

```
Val Ala Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser
                485                 490                 495

Lys Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu
            500                 505                 510

Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln Val Val
        515                 520                 525

Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg
    530                 535                 540

Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys
545                 550                 555                 560

Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val
                565                 570                 575

Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu
            580                 585                 590

Arg Glu Gln Met Glu Arg His Leu Asn Leu
        595                 600


<210> 1931
<211> 85
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 502; "

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<223> /note="Gene Symbol: ACSF2; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422546"

<400> 1931
Thr Val Pro Pro Ser Ser Trp Pro Leu Pro Ser Ser Met Ala Arg Arg
```

```
1               5                   10                  15

His Trp Arg Pro Ser Ala Glu Arg Gly Val Ile Ala Gly Ser Pro Ala
            20                  25                  30

Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp
        35                  40                  45

Leu Val Lys Ser Gln Glu Glu Ile Ala Ala Trp Glu Asp Gly Gln Gln
    50                  55                  60

Ser Thr Asp Val Leu Leu Glu Arg Pro Gly Arg Leu Leu Met Glu Pro
65                  70                  75                  80

Gln Arg Thr Val Pro
                85


<210> 1932
<211> 183
<212> PRT
<213> Homo sapiens

<220>
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      member 2; "

<220>
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<223> /note="ENSP ID: ENSP00000424842"

<400> 1932
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1               5                   10                  15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
            20                  25                  30

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
        35                  40                  45
```

```
Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
    50                  55                  60

Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
65                  70                  75                  80

Thr Ala Gln Arg Val Pro Glu Arg Glu Ala Leu Val Val Leu His Glu
                85                  90                  95

Asp Val Arg Leu Thr Phe Ala Gln Leu Lys Glu Glu Val Asp Lys Ala
            100                 105                 110

Ala Ser Gly Leu Leu Ser Ile Gly Leu Cys Lys Gly Val Cys Glu Pro
        115                 120                 125

Ser Leu Pro Gly Tyr Gly Thr Gly Val Cys Pro Gln Glu Gly Gly Leu
    130                 135                 140

Gln Gly Pro Cys Val Pro Gln Ala Ile Gln Asp Pro Ala Ile Leu Gln
145                 150                 155                 160

Arg Pro Glu Ala Asp Leu Ser Arg Ser Gly Glu Cys Pro Ala Arg Gly
                165                 170                 175

Leu Glu Glu Ser Glu Ala Pro
            180


<210> 1933
<211> 45
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACSF2; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 2; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000425332"

<400> 1933
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1   5   10   15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
            20   25   30

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Arg Cys Leu
        35   40   45

<210> 1934
<211> 572
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425964"

<400> 1934
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1   5   10   15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
            20   25   30

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
        35   40   45

Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
    50   55   60

```
Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
65                  70                  75                  80

Thr Ala Gln Arg Val Pro Glu Arg Glu Ala Leu Val Val Leu His Glu
                85                  90                  95

Asp Val Arg Leu Thr Phe Ala Gln Leu Lys Glu Glu Val Ser Val Asn
            100                 105                 110

Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly
        115                 120                 125

Cys Lys Ala Leu Val Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr
    130                 135                 140

Asn Val Leu Lys Gln Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly
145                 150                 155                 160

Ala Leu Lys Ser Gln Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val
                165                 170                 175

Asp Ala Pro Leu Pro Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala
            180                 185                 190

Gly Ser Thr Arg Gln His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe
        195                 200                 205

Leu Ser Cys His Asp Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr
    210                 215                 220

Gly Ser Pro Lys Gly Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn
225                 230                 235                 240

Ser Asn Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu
                245                 250                 255

Gln Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser
            260                 265                 270

Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu
        275                 280                 285

Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg
```

290 295 300

Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile
305 310 315 320

Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly
325 330 335

Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile
340 345 350

Ile Asn Lys Ile Asn Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr
355 360 365

Glu Asn Ser Pro Val Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu
370 375 380

Gln Lys Ala Glu Ser Val Gly Arg Ile Met Pro His Thr Glu Ala Arg
385 390 395 400

Ile Met Asn Met Glu Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly
405 410 415

Glu Leu Cys Ile Arg Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu
420 425 430

Pro Gln Lys Thr Glu Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr
435 440 445

Gly Asp Val Ala Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly
450 455 460

Arg Ser Lys Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala
465 470 475 480

Glu Leu Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln
485 490 495

Val Val Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys
500 505 510

Ile Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala
515 520 525

```
Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val
    530                 535                 540

Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe
545                 550                 555                 560

Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu
                565                 570

<210> 1935
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 502; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426730"

<400> 1935
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
1               5                   10                  15

Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser Trp Gln
            20                  25                  30

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Arg Pro Ser Gly Glu Lys
        35                  40                  45

Leu Ala His Gln Gly Val
    50

<210> 1936
<211> 576
<212> PRT
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<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q4G176; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000320646"

<400> 1936
Met Leu Pro His Val Val Leu Thr Phe Arg Arg Leu Gly Cys Ala Leu
1   5   10   15

Ala Ser Cys Arg Leu Ala Pro Ala Arg His Arg Gly Ser Gly Leu Leu
            20   25   30

His Thr Ala Pro Val Ala Arg Ser Asp Arg Ser Ala Pro Val Phe Thr
        35   40   45

Arg Ala Leu Ala Phe Gly Asp Arg Ile Ala Leu Val Asp Gln His Gly
    50   55   60

Arg His Thr Tyr Arg Glu Leu Tyr Ser Arg Ser Leu Arg Leu Ser Gln
65   70   75   80

Glu Ile Cys Arg Leu Cys Gly Cys Val Gly Gly Asp Leu Arg Glu Glu
                85   90   95

Arg Val Ser Phe Leu Cys Ala Asn Asp Ala Ser Tyr Val Val Ala Gln
            100   105   110

Trp Ala Ser Trp Met Ser Gly Gly Val Ala Val Pro Leu Tyr Arg Lys
        115   120   125

```
His Pro Ala Ala Gln Leu Glu Tyr Val Ile Cys Asp Ser Gln Ser Ser
    130                 135                 140

Val Val Leu Ala Ser Gln Glu Tyr Leu Glu Leu Leu Ser Pro Val Val
145                 150                 155                 160

Arg Lys Leu Gly Val Pro Leu Leu Pro Leu Thr Pro Ala Ile Tyr Thr
                165                 170                 175

Gly Ala Val Glu Glu Pro Ala Glu Val Pro Val Pro Glu Gln Gly Trp
            180                 185                 190

Arg Asn Lys Gly Ala Met Ile Ile Tyr Thr Ser Gly Thr Thr Gly Arg
        195                 200                 205

Pro Lys Gly Val Leu Ser Thr His Gln Asn Ile Arg Ala Val Val Thr
    210                 215                 220

Gly Leu Val His Lys Trp Ala Trp Thr Lys Asp Asp Val Ile Leu His
225                 230                 235                 240

Val Leu Pro Leu His His Val His Gly Val Val Asn Ala Leu Leu Cys
                245                 250                 255

Pro Leu Trp Val Gly Ala Thr Cys Val Met Met Pro Glu Phe Ser Pro
            260                 265                 270

Gln Gln Val Trp Glu Lys Phe Leu Ser Ser Glu Thr Pro Arg Ile Asn
        275                 280                 285

Val Phe Met Ala Val Pro Thr Ile Tyr Thr Lys Leu Met Glu Tyr Tyr
    290                 295                 300

Asp Arg His Phe Thr Gln Pro His Ala Gln Asp Phe Leu Arg Ala Val
305                 310                 315                 320

Cys Glu Glu Lys Ile Arg Leu Met Val Ser Gly Ser Ala Ala Leu Pro
                325                 330                 335

Leu Pro Val Leu Glu Lys Trp Lys Asn Ile Thr Gly His Thr Leu Leu
            340                 345                 350

Glu Arg Tyr Gly Met Thr Glu Ile Gly Met Ala Leu Ser Gly Pro Leu
```

355 360 365

Thr Thr Ala Val Arg Leu Pro Gly Ser Val Gly Thr Pro Leu Pro Gly
370 375 380

Val Gln Val Arg Ile Val Ser Glu Asn Pro Gln Arg Glu Ala Cys Ser
385 390 395 400

Tyr Thr Ile His Ala Glu Gly Asp Glu Arg Gly Thr Lys Val Thr Pro
405 410 415

Gly Phe Glu Glu Lys Glu Gly Glu Leu Leu Val Arg Gly Pro Ser Val
420 425 430

Phe Arg Glu Tyr Trp Asn Lys Pro Glu Glu Thr Lys Ser Ala Phe Thr
435 440 445

Leu Asp Gly Trp Phe Lys Thr Gly Asp Thr Val Val Phe Lys Asp Gly
450 455 460

Gln Tyr Trp Ile Arg Gly Arg Thr Ser Val Asp Ile Ile Lys Thr Gly
465 470 475 480

Gly Tyr Lys Val Ser Ala Leu Glu Val Glu Trp His Leu Leu Ala His
485 490 495

Pro Ser Ile Thr Asp Val Ala Val Ile Gly Val Pro Asp Met Thr Trp
500 505 510

Gly Gln Arg Val Thr Ala Val Val Thr Leu Arg Glu Gly His Ser Leu
515 520 525

Ser His Arg Glu Leu Lys Glu Trp Ala Arg Asn Val Leu Ala Pro Tyr
530 535 540

Ala Val Pro Ser Glu Leu Val Leu Val Glu Glu Ile Pro Arg Asn Gln
545 550 555 560

Met Gly Lys Ile Asp Lys Lys Ala Leu Ile Arg His Phe His Pro Ser
565 570 575

<210> 1937
<211> 311

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000367596"

<400> 1937
Met Met Pro Glu Phe Ser Pro Gln Gln Val Trp Glu Lys Phe Leu Ser
1 5 10 15

Ser Glu Thr Pro Arg Ile Asn Val Phe Met Ala Val Pro Thr Ile Tyr
20 25 30

Thr Lys Leu Met Glu Tyr Tyr Asp Arg His Phe Thr Gln Pro His Ala
35 40 45

Gln Asp Phe Leu Arg Ala Val Cys Glu Glu Lys Ile Arg Leu Met Val
50 55 60

Ser Gly Ser Ala Ala Leu Pro Leu Pro Val Leu Glu Lys Trp Lys Asn
65 70 75 80

Ile Thr Gly His Thr Leu Leu Glu Arg Tyr Gly Met Thr Glu Ile Gly
85 90 95

Met Ala Leu Ser Gly Pro Leu Thr Thr Ala Val Arg Leu Pro Gly Ser
100 105 110

Val Gly Thr Pro Leu Pro Gly Val Gln Val Arg Ile Val Ser Glu Asn
115 120 125

Pro Gln Arg Glu Ala Cys Ser Tyr Thr Ile His Ala Glu Gly Asp Glu
130 135 140

```
Arg Gly Thr Lys Val Thr Pro Gly Phe Glu Glu Lys Glu Gly Glu Leu
145                 150                 155                 160

Leu Val Arg Gly Pro Ser Val Phe Arg Glu Tyr Trp Asn Lys Pro Glu
                165                 170                 175

Glu Thr Lys Ser Ala Phe Thr Leu Asp Gly Trp Phe Lys Thr Gly Asp
            180                 185                 190

Thr Val Val Phe Lys Asp Gly Gln Tyr Trp Ile Arg Gly Arg Thr Ser
        195                 200                 205

Val Asp Ile Ile Lys Thr Gly Gly Tyr Lys Val Ser Ala Leu Glu Val
    210                 215                 220

Glu Trp His Leu Leu Ala His Pro Ser Ile Thr Asp Val Ala Val Ile
225                 230                 235                 240

Gly Val Pro Asp Met Thr Trp Gly Gln Arg Val Thr Ala Val Val Thr
                245                 250                 255

Leu Arg Glu Gly His Ser Leu Ser His Arg Glu Leu Lys Glu Trp Ala
            260                 265                 270

Arg Asn Val Leu Ala Pro Tyr Ala Val Pro Ser Glu Leu Val Leu Val
        275                 280                 285

Glu Glu Ile Pro Arg Asn Gln Met Gly Lys Ile Asp Lys Lys Ala Leu
    290                 295                 300

Ile Arg His Phe His Pro Ser
305                 310


<210> 1938
<211> 576
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "
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<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q4G176; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384627"

<400> 1938
Met Leu Pro His Val Val Leu Thr Phe Arg Arg Leu Gly Cys Ala Leu
1   5   10   15

Ala Ser Cys Arg Leu Ala Pro Ala Arg His Arg Gly Ser Gly Leu Leu
            20   25   30

His Thr Ala Pro Val Ala Arg Ser Asp Arg Ser Ala Pro Val Phe Thr
        35   40   45

Arg Ala Leu Ala Phe Gly Asp Arg Ile Ala Leu Val Asp Gln His Gly
    50   55   60

Arg His Thr Tyr Arg Glu Leu Tyr Ser Arg Ser Leu Arg Leu Ser Gln
65   70   75   80

Glu Ile Cys Arg Leu Cys Gly Cys Val Gly Gly Asp Leu Arg Glu Glu
                85   90   95

Arg Val Ser Phe Leu Cys Ala Asn Asp Ala Ser Tyr Val Val Ala Gln
            100   105   110

Trp Ala Ser Trp Met Ser Gly Gly Val Ala Val Pro Leu Tyr Arg Lys
        115   120   125

His Pro Ala Ala Gln Leu Glu Tyr Val Ile Cys Asp Ser Gln Ser Ser
    130   135   140

Val Val Leu Ala Ser Gln Glu Tyr Leu Glu Leu Leu Ser Pro Val Val
145   150   155   160

Arg Lys Leu Gly Val Pro Leu Leu Pro Leu Thr Pro Ala Ile Tyr Thr

```
                165                 170                 175

Gly Ala Val Glu Glu Pro Ala Glu Val Pro Val Pro Glu Gln Gly Trp
            180                 185                 190

Arg Asn Lys Gly Ala Met Ile Ile Tyr Thr Ser Gly Thr Thr Gly Arg
        195                 200                 205

Pro Lys Gly Val Leu Ser Thr His Gln Asn Ile Arg Ala Val Val Thr
    210                 215                 220

Gly Leu Val His Lys Trp Ala Trp Thr Lys Asp Asp Val Ile Leu His
225                 230                 235                 240

Val Leu Pro Leu His His Val His Gly Val Val Asn Ala Leu Leu Cys
                245                 250                 255

Pro Leu Trp Val Gly Ala Thr Cys Val Met Met Pro Glu Phe Ser Pro
            260                 265                 270

Gln Gln Val Trp Glu Lys Phe Leu Ser Ser Glu Thr Pro Arg Ile Asn
        275                 280                 285

Val Phe Met Ala Val Pro Thr Ile Tyr Thr Lys Leu Met Glu Tyr Tyr
    290                 295                 300

Asp Arg His Phe Thr Gln Pro His Ala Gln Asp Phe Leu Arg Ala Val
305                 310                 315                 320

Cys Glu Glu Lys Ile Arg Leu Met Val Ser Gly Ser Ala Ala Leu Pro
                325                 330                 335

Leu Pro Val Leu Glu Lys Trp Lys Asn Ile Thr Gly His Thr Leu Leu
            340                 345                 350

Glu Arg Tyr Gly Met Thr Glu Ile Gly Met Ala Leu Ser Gly Pro Leu
        355                 360                 365

Thr Thr Ala Val Arg Leu Pro Gly Ser Val Gly Thr Pro Leu Pro Gly
    370                 375                 380

Val Gln Val Arg Ile Val Ser Glu Asn Pro Gln Arg Glu Ala Cys Ser
385                 390                 395                 400
```

```
Tyr Thr Ile His Ala Glu Gly Asp Glu Arg Gly Thr Lys Val Thr Pro
                405                 410                 415

Gly Phe Glu Glu Lys Glu Gly Glu Leu Leu Val Arg Gly Pro Ser Val
            420                 425                 430

Phe Arg Glu Tyr Trp Asn Lys Pro Glu Glu Thr Lys Ser Ala Phe Thr
        435                 440                 445

Leu Asp Gly Trp Phe Lys Thr Gly Asp Thr Val Val Phe Lys Asp Gly
    450                 455                 460

Gln Tyr Trp Ile Arg Gly Arg Thr Ser Val Asp Ile Ile Lys Thr Gly
465                 470                 475                 480

Gly Tyr Lys Val Ser Ala Leu Glu Val Glu Trp His Leu Leu Ala His
                485                 490                 495

Pro Ser Ile Thr Asp Val Ala Val Ile Gly Val Pro Asp Met Thr Trp
            500                 505                 510

Gly Gln Arg Val Thr Ala Val Val Thr Leu Arg Glu Gly His Ser Leu
        515                 520                 525

Ser His Arg Glu Leu Lys Glu Trp Ala Arg Asn Val Leu Ala Pro Tyr
    530                 535                 540

Ala Val Pro Ser Glu Leu Val Leu Val Glu Glu Ile Pro Arg Asn Gln
545                 550                 555                 560

Met Gly Lys Ile Asp Lys Lys Ala Leu Ile Arg His Phe His Pro Ser
                565                 570                 575


<210> 1939
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
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<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000439201"

<400> 1939
Met Met Pro Glu Phe Ser Pro Gln Gln Val Trp Glu Lys Phe Leu Ser
1 5 10 15

Ser Glu Thr Pro Arg Ile Asn Val Phe Met Ala Val Pro Thr Ile Tyr
20 25 30

Thr Lys Leu Met Glu Tyr Tyr Asp Arg His Phe Thr Gln Pro His Ala
35 40 45

Gln Asp Phe Leu Arg Ala Val Cys Glu Glu Lys Ile Arg Leu Met Val
50 55 60

Ser Gly Ser Ala Ala Leu Pro Leu Pro Val Leu Glu Lys Trp Lys Asn
65 70 75 80

Ile Thr Gly His Thr Leu Leu Glu Arg Tyr Gly Met Thr Glu Ile Gly
85 90 95

Met Ala Leu Ser Gly Pro Leu Thr Thr
100 105

<210> 1940
<211> 237
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:

acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000440734"

<400> 1940

```
Met Leu Pro His Val Val Leu Thr Phe Arg Arg Leu Gly Cys Ala Leu
1               5                  10                  15

Ala Ser Cys Arg Leu Ala Pro Ala Arg His Arg Gly Ser Gly Leu Leu
            20                  25                  30

His Thr Ala Pro Val Ala Arg Ser Asp Arg Ser Ala Pro Val Phe Thr
        35                  40                  45

Arg Ala Leu Ala Phe Gly Asp Arg Ile Ala Leu Val Asp Gln His Gly
    50                  55                  60

Arg His Thr Tyr Arg Glu Leu Tyr Ser Arg Ser Leu Arg Leu Ser Gln
65                  70                  75                  80

Glu Ile Cys Arg Leu Cys Gly Cys Val Gly Gly Asp Leu Arg Glu Glu
                85                  90                  95

Arg Val Ser Phe Leu Cys Ala Asn Asp Ala Ser Tyr Val Val Ala Gln
            100                 105                 110

Trp Ala Ser Trp Met Ser Gly Gly Val Ala Val Pro Leu Tyr Arg Lys
        115                 120                 125

His Pro Ala Ala Gln Leu Glu Tyr Val Ile Cys Asp Ser Gln Ser Ser
    130                 135                 140

Val Val Leu Ala Ser Gln Glu Tyr Leu Glu Leu Leu Ser Pro Val Val
145                 150                 155                 160

Arg Lys Leu Gly Val Pro Leu Leu Pro Leu Thr Pro Ala Ile Tyr Thr
                165                 170                 175

Gly Ala Val Glu Glu Pro Ala Glu Val Pro Val Pro Glu Gln Gly Trp
            180                 185                 190

Arg Asn Lys Gly Ala Met Ile Ile Tyr Thr Ser Gly Thr Thr Gly Arg
```

```
        195                 200                 205

Pro Lys Gly Val Leu Ser Thr His Gln Asn Ile Arg Ala Val Val Thr
    210                 215                 220

Gly Leu Val His Lys Trp Ala Trp Thr Lys Asp Asp Val
225                 230                 235


<210> 1941
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442683"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1941
Xaa Leu Leu Cys Pro Leu Trp Val Gly Ala Thr Cys Val Met Met Pro
1               5                   10                  15

Glu Phe Ser Pro Gln Gln Val Trp Glu Lys Phe Leu Ser Ser Glu Thr
            20                  25                  30

Pro Arg Ile Asn Val Phe Met Ala Val Pro Thr Ile Tyr Thr Lys Leu
        35                  40                  45

Met Glu Tyr Tyr Asp Arg His Phe Thr Gln Pro His Ala Gln Asp Phe
    50                  55                  60
```

```
Leu Arg Ala Val Cys Glu Glu Lys Ile Arg Leu Met Val Ser Gly Ser
65                  70                  75                  80

Ala Ala Leu Pro Leu Pro Val Leu Glu Lys Trp Lys Asn Ile Thr Gly
                85                  90                  95

His Thr Leu Leu Glu Arg Tyr Gly Met Thr Glu Ile Gly Met Ala Leu
            100                 105                 110

Ser Gly Pro Leu Thr Thr Ala Val Arg Leu Pro Gly Ser Val Gly Thr
        115                 120                 125

Pro Leu Pro Gly Val Gln Val Arg Ile Val Ser Glu Asn Pro Gln Arg
    130                 135                 140

Glu Ala Cys Ser Tyr Thr Ile His Ala Glu Gly Asp Glu Arg Gly Thr
145                 150                 155                 160

Lys Gly Pro Ser Pro Cys Cys Cys Pro Asp Met Pro Leu Leu Gly Phe
                165                 170                 175

Leu Pro Leu Pro Cys Trp Tyr
            180


<210> 1942
<211> 235
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442781"

<400> 1942
Met Met Pro Glu Phe Ser Pro Gln Gln Val Trp Glu Lys Phe Leu Ser
```

```
1               5                   10                  15

Ser Glu Thr Pro Arg Ile Asn Val Phe Met Ala Val Pro Thr Ile Tyr
            20                  25                  30

Thr Lys Leu Met Glu Tyr Tyr Asp Arg His Phe Thr Gln Pro His Ala
        35                  40                  45

Gln Asp Phe Leu Arg Ala Val Cys Glu Glu Lys Ile Arg Leu Met Val
    50                  55                  60

Ser Gly Ser Ala Ala Leu Pro Leu Pro Val Leu Glu Lys Trp Lys Asn
65                  70                  75                  80

Ile Thr Gly His Thr Leu Leu Glu Arg Tyr Gly Met Thr Glu Ile Gly
                85                  90                  95

Met Ala Leu Ser Gly Pro Leu Thr Thr Ala Val Arg Leu Pro Gly Ser
            100                 105                 110

Val Gly Thr Pro Leu Pro Gly Val Gln Val Arg Ile Val Ser Glu Asn
        115                 120                 125

Pro Gln Arg Glu Ala Cys Ser Tyr Thr Ile His Ala Glu Gly Asp Glu
    130                 135                 140

Arg Gly Thr Lys Val Thr Pro Gly Phe Glu Glu Lys Glu Gly Glu Leu
145                 150                 155                 160

Leu Val Arg Gly Pro Ser Val Phe Arg Glu Tyr Trp Asn Lys Pro Glu
                165                 170                 175

Glu Thr Lys Ser Ala Phe Thr Leu Asp Gly Trp Phe Lys Thr Gly Asp
            180                 185                 190

Thr Val Val Phe Lys Asp Gly Gln Tyr Trp Ile Arg Gly Arg Thr Ser
        195                 200                 205

Val Asp Ile Ile Lys Thr Gly Gly Tyr Lys Val Ser Ala Leu Glu Val
    210                 215                 220

Glu Trp His Leu Leu Ala His Pro Ser Ile Thr
225                 230                 235
```

<210> 1943
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443428"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1943

```
Xaa Gly Val Pro Asp Met Thr Trp Gly Gln Arg Val Thr Ala Val Val
1               5                  10                  15

Thr Leu Arg Glu Gly His Ser Leu Ser His Arg Glu Leu Lys Glu Trp
            20                  25                  30

Ala Arg Leu Lys Glu His Pro Thr Lys Arg Arg Glu Asn Ser Ile Leu
        35                  40                  45

Asn Ile Gly Arg Lys Arg Asn Leu Ala Ser Gly Met Arg Ala Leu Thr
    50                  55                  60

Gly Arg Met Ala Ala Arg Arg Ala Ala Val Ser Ser Glu Val Ser Ser
65                  70                  75                  80

Ser Asp Glu Thr Asp Asn Ser Leu Lys Arg His Lys Leu Pro Arg Leu
                85                  90                  95

Thr Gln Thr Leu Lys Gln Thr Glu Gln Phe
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100 105

<210> 1944
<211> 190
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445397"

<400> 1944
Met Met Pro Glu Phe Ser Pro Gln Gln Val Trp Glu Lys Phe Leu Ser
1 5 10 15

Ser Glu Thr Pro Arg Ile Asn Val Phe Met Ala Val Pro Thr Ile Tyr
20 25 30

Thr Lys Leu Met Glu Tyr Tyr Asp Arg His Phe Thr Gln Pro His Ala
35 40 45

Gln Asp Phe Leu Arg Ala Val Cys Glu Glu Lys Ile Arg Leu Met Val
50 55 60

Ser Gly Ser Ala Ala Leu Pro Leu Pro Val Leu Glu Lys Trp Lys Asn
65 70 75 80

Ile Thr Gly His Thr Leu Leu Glu Arg Tyr Gly Met Thr Glu Ile Gly
85 90 95

Met Ala Leu Ser Gly Pro Leu Thr Thr Ala Val Arg Leu Pro Gly Ser
100 105 110

Val Gly Thr Pro Leu Pro Gly Val Gln Val Arg Ile Val Ser Glu Asn
115 120 125

```
Pro Gln Arg Glu Ala Cys Ser Tyr Thr Ile His Ala Glu Gly Asp Glu
    130                 135                 140

Arg Gly Thr Lys Val Thr Pro Gly Phe Glu Glu Lys Glu Gly Glu Leu
145                 150                 155                 160

Leu Val Arg Gly Pro Ser Val Phe Arg Glu Tyr Trp Asn Lys Pro Glu
                165                 170                 175

Glu Thr Lys Ser Ala Phe Thr Leu Asp Gly Trp Phe Lys Thr
            180                 185                 190


<210> 1945
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Name:
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      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445870"

<400> 1945
Leu Val His Lys Trp Ala Trp Thr Lys Asp Asp Val Ile Leu His Val
1               5                   10                  15

Leu Pro Leu His His Val His Gly Val Val Asn Ala Leu Leu Cys Pro
            20                  25                  30

Leu Trp Val Gly Ala Thr Cys Val Met Met Pro Glu Phe Ser Pro Gln
        35                  40                  45

Gln Val Trp Glu Lys Phe Leu Ser Ser Glu Thr Pro Arg Ile Asn Val
    50                  55                  60
```

```
Phe Met Ala Val Pro Thr Ile Tyr Thr Lys Leu Met Glu Tyr Tyr Asp
65                  70                  75                  80


Arg His Phe Thr Gln Pro His Ala Gln Asp Phe Leu Arg Ala Val Cys
                85                  90                  95


Glu Glu Lys Ile Arg Phe Arg Gly Asp Pro Thr Ala Trp Ser Thr Gly
            100                 105                 110


Ala His Cys Leu Arg Lys Pro Thr Glu Gly Ser Leu Leu Leu His His
        115                 120                 125


Pro Arg Arg Gly Arg Arg Glu Gly Asp Gln Gly Pro Gln Pro Met Leu
    130                 135                 140


<210> 1946
<211> 368
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446281"

<400> 1946
Met Leu Pro His Val Val Leu Thr Phe Arg Arg Leu Gly Cys Ala Leu
1               5                   10                  15


Ala Ser Cys Arg Leu Ala Pro Ala Arg His Arg Gly Ser Gly Leu Leu
            20                  25                  30


His Thr Ala Pro Val Ala Arg Ser Asp Arg Ser Ala Pro Val Phe Thr
        35                  40                  45
```

```
Arg Ala Leu Ala Phe Gly Asp Arg Ile Ala Leu Val Asp Gln His Gly
    50                  55                  60

Arg His Thr Tyr Arg Glu Leu Tyr Ser Arg Ser Leu Arg Leu Ser Gln
65                  70                  75                  80

Glu Ile Cys Arg Leu Cys Gly Cys Val Gly Gly Asp Leu Arg Glu Glu
                85                  90                  95

Arg Val Ser Phe Leu Cys Ala Asn Asp Ala Ser Tyr Val Val Ala Gln
            100                 105                 110

Trp Ala Ser Trp Met Ser Gly Gly Val Ala Val Pro Leu Tyr Arg Lys
        115                 120                 125

His Pro Ala Ala Gln Leu Glu Tyr Val Ile Cys Asp Ser Gln Ser Ser
    130                 135                 140

Val Val Leu Ala Ser Gln Glu Tyr Leu Glu Leu Leu Ser Pro Val Val
145                 150                 155                 160

Arg Lys Leu Gly Val Pro Leu Leu Pro Leu Thr Pro Ala Ile Tyr Thr
                165                 170                 175

Gly Ala Val Glu Glu Pro Ala Glu Val Pro Val Pro Glu Gln Gly Trp
            180                 185                 190

Arg Asn Lys Gly Ala Met Ile Ile Tyr Thr Ser Gly Thr Thr Gly Arg
        195                 200                 205

Pro Lys Gly Val Leu Ser Thr His Gln Asn Ile Arg Ala Val Val Thr
    210                 215                 220

Gly Leu Val His Lys Trp Ala Trp Thr Lys Asp Asp Val Ile Leu His
225                 230                 235                 240

Val Leu Pro Leu His His Val His Gly Val Val Asn Ala Leu Leu Cys
                245                 250                 255

Pro Leu Trp Val Gly Ala Thr Cys Val Met Met Pro Glu Phe Ser Pro
            260                 265                 270

Gln Gln Val Trp Glu Lys Phe Leu Ser Ser Glu Thr Pro Arg Ile Asn
```

```
        275                 280                 285

Val Phe Met Ala Val Pro Thr Ile Tyr Thr Lys Leu Met Glu Tyr Tyr
    290                 295                 300

Asp Arg His Phe Thr Gln Pro His Ala Gln Asp Phe Leu Arg Ala Val
305                 310                 315                 320

Cys Glu Glu Lys Ile Arg Phe Arg Gly Asp Pro Thr Ala Trp Ser Thr
                325                 330                 335

Gly Ala His Cys Leu Arg Lys Pro Thr Glu Gly Ser Leu Leu Leu His
            340                 345                 350

His Pro Arg Arg Gly Arg Arg Glu Gly Asp Gln Gly Asp Pro Arg Val
        355                 360                 365


<210> 1947
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase family
      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457301"

<400> 1947
Met Leu Pro His Val Val Leu Thr Phe Arg Arg Leu Gly Cys Ala Leu
1               5                   10                  15

Ala Ser Cys Arg Leu Ala Pro Ala Arg His Arg Gly
            20                  25


<210> 1948
<211> 576
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<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 503; "

<220>
<221> source
<223> /note="Gene Symbol: ACSF3; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase family
member 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q4G176; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479130"

<400> 1948
Met Leu Pro His Val Val Leu Thr Phe Arg Arg Leu Gly Cys Ala Leu
1   5   10   15

Ala Ser Cys Arg Leu Ala Pro Ala Arg His Arg Gly Ser Gly Leu Leu
            20   25   30

His Thr Ala Pro Val Ala Arg Ser Asp Arg Ser Ala Pro Val Phe Thr
        35   40   45

Arg Ala Leu Ala Phe Gly Asp Arg Ile Ala Leu Val Asp Gln His Gly
    50   55   60

Arg His Thr Tyr Arg Glu Leu Tyr Ser Arg Ser Leu Arg Leu Ser Gln
65   70   75   80

Glu Ile Cys Arg Leu Cys Gly Cys Val Gly Gly Asp Leu Arg Glu Glu
                85   90   95

Arg Val Ser Phe Leu Cys Ala Asn Asp Ala Ser Tyr Val Val Ala Gln
            100   105   110

Trp Ala Ser Trp Met Ser Gly Gly Val Ala Val Pro Leu Tyr Arg Lys
        115   120   125

```
His Pro Ala Ala Gln Leu Glu Tyr Val Ile Cys Asp Ser Gln Ser Ser
    130                 135                 140

Val Val Leu Ala Ser Gln Glu Tyr Leu Glu Leu Leu Ser Pro Val Val
145                 150                 155                 160

Arg Lys Leu Gly Val Pro Leu Leu Pro Leu Thr Pro Ala Ile Tyr Thr
                165                 170                 175

Gly Ala Val Glu Glu Pro Ala Glu Val Pro Val Pro Glu Gln Gly Trp
            180                 185                 190

Arg Asn Lys Gly Ala Met Ile Ile Tyr Thr Ser Gly Thr Thr Gly Arg
        195                 200                 205

Pro Lys Gly Val Leu Ser Thr His Gln Asn Ile Arg Ala Val Val Thr
    210                 215                 220

Gly Leu Val His Lys Trp Ala Trp Thr Lys Asp Asp Val Ile Leu His
225                 230                 235                 240

Val Leu Pro Leu His His Val His Gly Val Val Asn Ala Leu Leu Cys
                245                 250                 255

Pro Leu Trp Val Gly Ala Thr Cys Val Met Met Pro Glu Phe Ser Pro
            260                 265                 270

Gln Gln Val Trp Glu Lys Phe Leu Ser Ser Glu Thr Pro Arg Ile Asn
        275                 280                 285

Val Phe Met Ala Val Pro Thr Ile Tyr Thr Lys Leu Met Glu Tyr Tyr
    290                 295                 300

Asp Arg His Phe Thr Gln Pro His Ala Gln Asp Phe Leu Arg Ala Val
305                 310                 315                 320

Cys Glu Glu Lys Ile Arg Leu Met Val Ser Gly Ser Ala Ala Leu Pro
                325                 330                 335

Leu Pro Val Leu Glu Lys Trp Lys Asn Ile Thr Gly His Thr Leu Leu
            340                 345                 350
```

```
Glu Arg Tyr Gly Met Thr Glu Ile Gly Met Ala Leu Ser Gly Pro Leu
        355                 360                 365

Thr Thr Ala Val Arg Leu Pro Gly Ser Val Gly Thr Pro Leu Pro Gly
    370                 375                 380

Val Gln Val Arg Ile Val Ser Glu Asn Pro Gln Arg Glu Ala Cys Ser
385                 390                 395                 400

Tyr Thr Ile His Ala Glu Gly Asp Glu Arg Gly Thr Lys Val Thr Pro
                405                 410                 415

Gly Phe Glu Glu Lys Glu Gly Glu Leu Leu Val Arg Gly Pro Ser Val
            420                 425                 430

Phe Arg Glu Tyr Trp Asn Lys Pro Glu Glu Thr Lys Ser Ala Phe Thr
        435                 440                 445

Leu Asp Gly Trp Phe Lys Thr Gly Asp Thr Val Val Phe Lys Asp Gly
    450                 455                 460

Gln Tyr Trp Ile Arg Gly Arg Thr Ser Val Asp Ile Ile Lys Thr Gly
465                 470                 475                 480

Gly Tyr Lys Val Ser Ala Leu Glu Val Glu Trp His Leu Leu Ala His
                485                 490                 495

Pro Ser Ile Thr Asp Val Ala Val Ile Gly Val Pro Asp Met Thr Trp
            500                 505                 510

Gly Gln Arg Val Thr Ala Val Val Thr Leu Arg Glu Gly His Ser Leu
        515                 520                 525

Ser His Arg Glu Leu Lys Glu Trp Ala Arg Asn Val Leu Ala Pro Tyr
    530                 535                 540

Ala Val Pro Ser Glu Leu Val Leu Val Glu Glu Ile Pro Arg Asn Gln
545                 550                 555                 560

Met Gly Lys Ile Asp Lys Lys Ala Leu Ile Arg His Phe His Pro Ser
                565                 570                 575
```

<210> 1949

<211> 698
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 1; "

<220>
<221> source
<223> /note="Uniprot ID: P33121; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000281455"

<400> 1949
Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1   5   10   15

Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
            20   25   30

Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
        35   40   45

Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
    50   55   60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
65   70   75   80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
                85   90   95

Gln Arg Gly Ile Gln Val Ser Asn Asn Gly Pro Cys Leu Gly Ser Arg
            100   105   110

Lys Pro Asp Gln Pro Tyr Glu Trp Leu Ser Tyr Lys Gln Val Ala Glu
        115   120   125

```
Leu Ser Glu Cys Ile Gly Ser Ala Leu Ile Gln Lys Gly Phe Lys Thr
    130                 135                 140

Ala Pro Asp Gln Phe Ile Gly Ile Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Val Ile Ile Glu Gln Gly Cys Phe Ala Tyr Ser Met Val Ile Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr Tyr Ile Val Asn Lys
            180                 185                 190

Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro Glu Lys Ala Lys Leu
        195                 200                 205

Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro Gly Leu Lys Ile Ile
    210                 215                 220

Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val Glu Arg Gly Gln Arg
225                 230                 235                 240

Cys Gly Val Glu Val Thr Ser Met Lys Ala Met Glu Asp Leu Gly Arg
                245                 250                 255

Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu Asp Leu Ala Val
            260                 265                 270

Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Val
        275                 280                 285

Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala Phe Val Lys Ala Thr
    290                 295                 300

Glu Asn Thr Val Asn Pro Cys Pro Asp Asp Thr Leu Ile Ser Phe Leu
305                 310                 315                 320

Pro Leu Ala His Met Phe Glu Arg Val Val Glu Cys Val Met Leu Cys
                325                 330                 335

His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Met
            340                 345                 350
```

```
Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe Pro Val Val Pro Arg
        355                 360                 365

Leu Leu Asn Arg Met Phe Asp Arg Ile Phe Gly Gln Ala Asn Thr Thr
    370                 375                 380

Leu Lys Arg Trp Leu Leu Asp Phe Ala Ser Lys Arg Lys Glu Ala Glu
385                 390                 395                 400

Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser Leu Trp Asp Arg Leu Ile
                405                 410                 415

Phe His Lys Val Gln Ser Ser Leu Gly Gly Arg Val Arg Leu Met Val
            420                 425                 430

Thr Gly Ala Ala Pro Val Ser Ala Thr Val Leu Thr Phe Leu Arg Ala
        435                 440                 445

Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
    450                 455                 460

Ala Gly Cys Cys Leu Thr Met Pro Gly Asp Trp Thr Ala Gly His Val
465                 470                 475                 480

Gly Ala Pro Met Pro Cys Asn Leu Ile Lys Leu Val Asp Val Glu Glu
                485                 490                 495

Met Asn Tyr Met Ala Ala Glu Gly Glu Gly Glu Val Cys Val Lys Gly
            500                 505                 510

Pro Asn Val Phe Gln Gly Tyr Leu Lys Asp Pro Ala Lys Thr Ala Glu
        515                 520                 525

Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
    530                 535                 540

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545                 550                 555                 560

Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Ile
                565                 570                 575
```

```
Tyr Met Arg Ser Glu Pro Val Ala Gln Val Phe Val His Gly Glu Ser
            580                 585                 590

Leu Gln Ala Phe Leu Ile Ala Ile Val Val Pro Asp Val Glu Thr Leu
        595                 600                 605

Cys Ser Trp Ala Gln Lys Arg Gly Phe Glu Gly Ser Phe Glu Glu Leu
    610                 615                 620

Cys Arg Asn Lys Asp Val Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625                 630                 635                 640

Leu Gly Lys Asp Ser Gly Leu Lys Pro Phe Glu Gln Val Lys Gly Ile
                645                 650                 655

Thr Leu His Pro Glu Leu Phe Ser Ile Asp Asn Gly Leu Leu Thr Pro
            660                 665                 670

Thr Met Lys Ala Lys Arg Pro Glu Leu Arg Asn Tyr Phe Arg Ser Gln
        675                 680                 685

Ile Asp Asp Leu Tyr Ser Thr Ile Lys Val
    690                 695


<210> 1950
<211> 527
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000407165"

<400> 1950
Met Val Ile Val Pro Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr
```

```
1               5                   10                  15

Tyr Ile Val Asn Lys Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro
            20                  25                  30

Glu Lys Ala Lys Leu Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro
        35                  40                  45

Gly Leu Lys Ile Ile Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val
    50                  55                  60

Glu Arg Gly Gln Arg Cys Gly Val Glu Val Thr Ser Met Lys Ala Met
65                  70                  75                  80

Glu Asp Leu Gly Arg Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro
                85                  90                  95

Glu Asp Leu Ala Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro
            100                 105                 110

Lys Gly Ala Met Val Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala
        115                 120                 125

Phe Val Lys Ala Thr Glu Asn Thr Val Asn Pro Cys Pro Asp Asp Thr
    130                 135                 140

Leu Ile Ser Phe Leu Pro Leu Ala His Met Phe Glu Arg Val Val Glu
145                 150                 155                 160

Cys Val Met Leu Cys His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp
                165                 170                 175

Ile Arg Leu Leu Met Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe
            180                 185                 190

Pro Val Val Pro Arg Leu Leu Asn Arg Met Phe Asp Arg Ile Phe Gly
        195                 200                 205

Gln Ala Asn Thr Thr Leu Lys Arg Trp Leu Leu Asp Phe Ala Ser Lys
    210                 215                 220

Arg Lys Glu Ala Glu Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser Leu
225                 230                 235                 240
```

```
Trp Asp Arg Leu Ile Phe His Lys Val Gln Ser Ser Leu Gly Gly Arg
                245                 250                 255

Val Arg Leu Met Val Thr Gly Ala Ala Pro Val Ser Ala Thr Val Leu
            260                 265                 270

Thr Phe Leu Arg Ala Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr Gly
        275                 280                 285

Gln Thr Glu Cys Thr Ala Gly Cys Cys Leu Thr Met Pro Gly Asp Trp
    290                 295                 300

Thr Ala Gly His Val Gly Ala Pro Met Pro Cys Asn Leu Ile Lys Leu
305                 310                 315                 320

Val Asp Val Glu Glu Met Asn Tyr Met Ala Ala Glu Gly Glu Gly Glu
                325                 330                 335

Val Cys Val Lys Gly Pro Asn Val Phe Gln Gly Tyr Leu Lys Asp Pro
            340                 345                 350

Ala Lys Thr Ala Glu Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly
        355                 360                 365

Asp Ile Gly Lys Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg
    370                 375                 380

Lys Lys His Ile Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu
385                 390                 395                 400

Lys Ile Glu Asn Ile Tyr Met Arg Ser Glu Pro Val Ala Gln Val Phe
                405                 410                 415

Val His Gly Glu Ser Leu Gln Ala Phe Leu Ile Ala Ile Val Val Pro
            420                 425                 430

Asp Val Glu Thr Leu Cys Ser Trp Ala Gln Lys Arg Gly Phe Glu Gly
        435                 440                 445

Ser Phe Glu Glu Leu Cys Arg Asn Lys Asp Val Lys Lys Ala Ile Leu
    450                 455                 460
```

```
Glu Asp Met Val Arg Leu Gly Lys Asp Ser Gly Leu Lys Pro Phe Glu
465                 470                 475                 480


Gln Val Lys Gly Ile Thr Leu His Pro Glu Leu Phe Ser Ile Asp Asn
                485                 490                 495


Gly Leu Leu Thr Pro Thr Met Lys Ala Lys Arg Pro Glu Leu Arg Asn
            500                 505                 510


Tyr Phe Arg Ser Gln Ile Asp Asp Leu Tyr Ser Thr Ile Lys Val
        515                 520                 525


<210> 1951
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P33121; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422607"

<400> 1951
Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1               5                   10                  15


Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
            20                  25                  30


Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
        35                  40                  45
```

```
Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
    50                  55                  60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
65                  70                  75                  80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
                85                  90                  95

Gln Arg Gly Ile Gln Val Ser Asn Asn Gly Pro Cys Leu Gly Ser Arg
            100                 105                 110

Lys Pro Asp Gln Pro Tyr Glu Trp Leu Ser Tyr Lys Gln Val Ala Glu
        115                 120                 125

Leu Ser Glu Cys Ile Gly Ser Ala Leu Ile Gln Lys Gly Phe Lys Thr
    130                 135                 140

Ala Pro Asp Gln Phe Ile Gly Ile Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Val Ile Ile Glu Gln Gly Cys Phe Ala Tyr Ser Met Val Ile Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr Tyr Ile Val Asn Lys
            180                 185                 190

Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro Glu Lys Ala Lys Leu
        195                 200                 205

Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro Gly Leu Lys Ile Ile
    210                 215                 220

Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val Glu Arg Gly Gln Arg
225                 230                 235                 240

Cys Gly Val Glu Val Thr Ser Met Lys Ala Met Glu Asp Leu Gly Arg
                245                 250                 255

Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu Asp Leu Ala Val
            260                 265                 270

Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Val
```

275 280 285

Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala Phe Val Lys Ala Thr
290 295 300

Glu Asn Thr Val Asn Pro Cys Pro Asp Asp Thr Leu Ile Ser Phe Leu
305 310 315 320

Pro Leu Ala His Met Phe Glu Arg Val Val Glu Cys Val Met Leu Cys
325 330 335

His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Met
340 345 350

Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe Pro Val Val Pro Arg
355 360 365

Leu Leu Asn Arg Met Phe Asp Arg Ile Phe Gly Gln Ala Asn Thr Thr
370 375 380

Leu Lys Arg Trp Leu Leu Asp Phe Ala Ser Lys Arg Lys Glu Ala Glu
385 390 395 400

Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser Leu Trp Asp Arg Leu Ile
405 410 415

Phe His Lys Val Gln Ser Ser Leu Gly Gly Arg Val Arg Leu Met Val
420 425 430

Thr Gly Ala Ala Pro Val Ser Ala Thr Val Leu Thr Phe Leu Arg Ala
435 440 445

Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
450 455 460

Ala Gly Cys Cys Leu Thr Met Pro Gly Asp Trp Thr Ala Gly His Val
465 470 475 480

Gly Ala Pro Met Pro Cys Asn Leu Ile Lys Leu Val Asp Val Glu Glu
485 490 495

Met Asn Tyr Met Ala Ala Glu Gly Glu Gly Glu Val Cys Val Lys Gly
500 505 510

Pro Asn Val Phe Gln Gly Tyr Leu Lys Asp Pro Ala Lys Thr Ala Glu
515 520 525

Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
530 535 540

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545 550 555 560

Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Ile
565 570 575

Tyr Met Arg Ser Glu Pro Val Ala Gln Val Phe Val His Gly Glu Ser
580 585 590

Leu Gln Ala Phe Leu Ile Ala Ile Val Val Pro Asp Val Glu Thr Leu
595 600 605

Cys Ser Trp Ala Gln Lys Arg Gly Phe Glu Gly Ser Phe Glu Glu Leu
610 615 620

Cys Arg Asn Lys Asp Val Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625 630 635 640

Leu Gly Lys Asp Ser Gly Leu Lys Pro Phe Glu Gln Val Lys Gly Ile
645 650 655

Thr Leu His Pro Glu Leu Phe Ser Ile Asp Asn Gly Leu Leu Thr Pro
660 665 670

Thr Met Lys Ala Lys Arg Pro Glu Leu Arg Asn Tyr Phe Arg Ser Gln
675 680 685

Ile Asp Asp Leu Tyr Ser Thr Ile Lys Val
690 695

<210> 1952
<211> 388
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424935"

<400> 1952

```
Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1               5                  10                  15

Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
            20                  25                  30

Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
        35                  40                  45

Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
    50                  55                  60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
65                  70                  75                  80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
                85                  90                  95

Gln Arg Gly Ile Gln Val Ser Asn Asn Gly Pro Cys Leu Gly Ser Arg
            100                 105                 110

Lys Pro Asp Gln Pro Tyr Glu Trp Leu Ser Tyr Lys Gln Val Ala Glu
        115                 120                 125

Leu Ser Glu Cys Ile Gly Ser Ala Leu Ile Gln Lys Gly Phe Lys Thr
    130                 135                 140

Ala Pro Asp Gln Phe Ile Gly Ile Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160
```

```
Val Ile Ile Glu Gln Gly Cys Phe Ala Tyr Ser Met Val Ile Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr Tyr Ile Val Asn Lys
            180                 185                 190

Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro Glu Lys Ala Lys Leu
        195                 200                 205

Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro Gly Leu Lys Ile Ile
    210                 215                 220

Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val Glu Arg Gly Gln Arg
225                 230                 235                 240

Cys Gly Val Glu Val Thr Ser Met Lys Ala Met Glu Asp Leu Gly Arg
                245                 250                 255

Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu Asp Leu Ala Val
            260                 265                 270

Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Val
        275                 280                 285

Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala Phe Val Lys Ala Thr
    290                 295                 300

Glu Asn Thr Val Asn Pro Cys Pro Asp Asp Thr Leu Ile Ser Phe Leu
305                 310                 315                 320

Pro Leu Ala His Met Phe Glu Arg Val Val Glu Cys Val Met Leu Cys
                325                 330                 335

His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Met
            340                 345                 350

Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe Pro Val Val Pro Arg
        355                 360                 365

Leu Leu Asn Arg Met Phe Asp Arg Val Ser Ser Lys Gln Arg Ser Pro
    370                 375                 380

Arg Thr Glu His
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385

<210> 1953
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 1; "

<220>
<221> source
<223> /note="Uniprot ID: P33121; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425006"

<400> 1953
Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1   5   10   15

Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
            20   25   30

Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
        35   40   45

Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
    50   55   60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
65   70   75   80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
                85   90   95

Gln Arg Gly Ile Gln Val Ser Asn Asn Gly Pro Cys Leu Gly Ser Arg
            100   105   110

```
Lys Pro Asp Gln Pro Tyr Glu Trp Leu Ser Tyr Lys Gln Val Ala Glu
        115                 120                 125

Leu Ser Glu Cys Ile Gly Ser Ala Leu Ile Gln Lys Gly Phe Lys Thr
    130                 135                 140

Ala Pro Asp Gln Phe Ile Gly Ile Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Val Ile Ile Glu Gln Gly Cys Phe Ala Tyr Ser Met Val Ile Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr Tyr Ile Val Asn Lys
            180                 185                 190

Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro Glu Lys Ala Lys Leu
        195                 200                 205

Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro Gly Leu Lys Ile Ile
    210                 215                 220

Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val Glu Arg Gly Gln Arg
225                 230                 235                 240

Cys Gly Val Glu Val Thr Ser Met Lys Ala Met Glu Asp Leu Gly Arg
                245                 250                 255

Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu Asp Leu Ala Val
            260                 265                 270

Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Val
        275                 280                 285

Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala Phe Val Lys Ala Thr
    290                 295                 300

Glu Asn Thr Val Asn Pro Cys Pro Asp Asp Thr Leu Ile Ser Phe Leu
305                 310                 315                 320

Pro Leu Ala His Met Phe Glu Arg Val Val Glu Cys Val Met Leu Cys
                325                 330                 335
```

```
His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Met
            340                 345                 350

Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe Pro Val Val Pro Arg
        355                 360                 365

Leu Leu Asn Arg Met Phe Asp Arg Ile Phe Gly Gln Ala Asn Thr Thr
    370                 375                 380

Leu Lys Arg Trp Leu Leu Asp Phe Ala Ser Lys Arg Lys Glu Ala Glu
385                 390                 395                 400

Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser Leu Trp Asp Arg Leu Ile
                405                 410                 415

Phe His Lys Val Gln Ser Ser Leu Gly Gly Arg Val Arg Leu Met Val
            420                 425                 430

Thr Gly Ala Ala Pro Val Ser Ala Thr Val Leu Thr Phe Leu Arg Ala
        435                 440                 445

Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
    450                 455                 460

Ala Gly Cys Cys Leu Thr Met Pro Gly Asp Trp Thr Ala Gly His Val
465                 470                 475                 480

Gly Ala Pro Met Pro Cys Asn Leu Ile Lys Leu Val Asp Val Glu Glu
                485                 490                 495

Met Asn Tyr Met Ala Ala Glu Gly Glu Gly Glu Val Cys Val Lys Gly
            500                 505                 510

Pro Asn Val Phe Gln Gly Tyr Leu Lys Asp Pro Ala Lys Thr Ala Glu
        515                 520                 525

Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
    530                 535                 540

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545                 550                 555                 560
```

```
Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Ile
                565                 570                 575

Tyr Met Arg Ser Glu Pro Val Ala Gln Val Phe Val His Gly Glu Ser
            580                 585                 590

Leu Gln Ala Phe Leu Ile Ala Ile Val Val Pro Asp Val Glu Thr Leu
        595                 600                 605

Cys Ser Trp Ala Gln Lys Arg Gly Phe Glu Gly Ser Phe Glu Glu Leu
    610                 615                 620

Cys Arg Asn Lys Asp Val Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625                 630                 635                 640

Leu Gly Lys Asp Ser Gly Leu Lys Pro Phe Glu Gln Val Lys Gly Ile
                645                 650                 655

Thr Leu His Pro Glu Leu Phe Ser Ile Asp Asn Gly Leu Leu Thr Pro
            660                 665                 670

Thr Met Lys Ala Lys Arg Pro Glu Leu Arg Asn Tyr Phe Arg Ser Gln
        675                 680                 685

Ile Asp Asp Leu Tyr Ser Thr Ile Lys Val
    690                 695


<210> 1954
<211> 294
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
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<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 1; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000425098"

<400> 1954

```
Lys Arg Lys Glu Ala Glu Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser
1               5                  10                  15

Leu Trp Asp Arg Leu Ile Phe His Lys Val Gln Ser Ser Leu Gly Gly
            20                  25                  30

Arg Val Arg Leu Met Val Thr Gly Ala Ala Pro Val Ser Ala Thr Val
        35                  40                  45

Leu Thr Phe Leu Arg Ala Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr
    50                  55                  60

Gly Gln Thr Glu Cys Thr Ala Gly Cys Cys Leu Thr Met Pro Gly Asp
65                  70                  75                  80

Trp Thr Ala Gly His Val Gly Ala Pro Met Pro Cys Asn Leu Ile Lys
                85                  90                  95

Leu Val Asp Val Glu Glu Met Asn Tyr Met Ala Ala Glu Gly Glu Gly
            100                 105                 110

Glu Gly Tyr Leu Lys Asp Pro Ala Lys Thr Ala Glu Ala Leu Asp Lys
        115                 120                 125

Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp Leu Pro Asn Gly
    130                 135                 140

Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe Lys Leu Ala Gln
145                 150                 155                 160

Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Ile Tyr Met Arg Ser
                165                 170                 175

Glu Pro Val Ala Gln Val Phe Val His Gly Glu Ser Leu Gln Ala Phe
            180                 185                 190

Leu Ile Ala Ile Val Val Pro Asp Val Glu Thr Leu Cys Ser Trp Ala
        195                 200                 205

Gln Lys Arg Gly Phe Glu Gly Ser Phe Glu Glu Leu Cys Arg Asn Lys
    210                 215                 220
```

```
Asp Val Lys Lys Ala Ile Leu Glu Asp Met Val Arg Leu Gly Lys Asp
225                 230                 235                 240


Ser Gly Leu Lys Pro Phe Glu Gln Val Lys Gly Ile Thr Leu His Pro
                245                 250                 255


Glu Leu Phe Ser Ile Asp Asn Gly Leu Leu Thr Pro Thr Met Lys Ala
            260                 265                 270


Lys Arg Pro Glu Leu Arg Asn Tyr Phe Arg Ser Gln Ile Asp Asp Leu
        275                 280                 285


Tyr Ser Thr Ile Lys Val
    290


<210> 1955
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425640"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1955
Xaa Leu Gly Arg Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu
1               5                   10                  15


Asp Leu Ala Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys
```

```
            20                  25                  30

Gly Ala Met Val Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala Phe
        35                  40                  45

Val Lys Ala Thr Glu Cys Val Met Leu Cys His Gly Ala Lys Ile Gly
    50                  55                  60

Phe Phe Gln Gly Asp Ile Arg Leu Leu Met Asp Asp Leu Lys Val Leu
65                  70                  75                  80

Gln Pro Thr Val Phe Pro Val Val Pro Arg Leu Leu Asn Arg
                85                  90


<210> 1956
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 1; "

<220>
<221> source
<223> /note="Uniprot ID:  P33121; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426150"

<400> 1956
Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1               5                   10                  15

Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
            20                  25                  30

Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
        35                  40                  45
```

```
Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
    50                  55                  60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
65                  70                  75                  80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
                85                  90                  95

Gln Arg Gly Ile Gln Val Ser Asn Asn Gly Pro Cys Leu Gly Ser Arg
            100                 105                 110

Lys Pro Asp Gln Pro Tyr Glu Trp Leu Ser Tyr Lys Gln Val Ala Glu
        115                 120                 125

Leu Ser Glu Cys Ile Gly Ser Ala Leu Ile Gln Lys Gly Phe Lys Thr
    130                 135                 140

Ala Pro Asp Gln Phe Ile Gly Ile Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Val Ile Ile Glu Gln Gly Cys Phe Ala Tyr Ser Met Val Ile Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr Tyr Ile Val Asn Lys
            180                 185                 190

Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro Glu Lys Ala Lys Leu
        195                 200                 205

Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro Gly Leu Lys Ile Ile
    210                 215                 220

Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val Glu Arg Gly Gln Arg
225                 230                 235                 240

Cys Gly Val Glu Val Thr Ser Met Lys Ala Met Glu Asp Leu Gly Arg
                245                 250                 255

Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu Asp Leu Ala Val
            260                 265                 270
```

```
Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Val
        275                 280                 285

Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala Phe Val Lys Ala Thr
    290                 295                 300

Glu Lys Ala Leu Pro Leu Ser Ala Ser Asp Thr His Ile Ser Tyr Leu
305                 310                 315                 320

Pro Leu Ala His Ile Tyr Glu Gln Leu Leu Lys Cys Val Met Leu Cys
                325                 330                 335

His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Met
            340                 345                 350

Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe Pro Val Val Pro Arg
        355                 360                 365

Leu Leu Asn Arg Met Phe Asp Arg Ile Phe Gly Gln Ala Asn Thr Thr
    370                 375                 380

Leu Lys Arg Trp Leu Leu Asp Phe Ala Ser Lys Arg Lys Glu Ala Glu
385                 390                 395                 400

Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser Leu Trp Asp Arg Leu Ile
                405                 410                 415

Phe His Lys Val Gln Ser Ser Leu Gly Gly Arg Val Arg Leu Met Val
            420                 425                 430

Thr Gly Ala Ala Pro Val Ser Ala Thr Val Leu Thr Phe Leu Arg Ala
        435                 440                 445

Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
    450                 455                 460

Ala Gly Cys Cys Leu Thr Met Pro Gly Asp Trp Thr Ala Gly His Val
465                 470                 475                 480

Gly Ala Pro Met Pro Cys Asn Leu Ile Lys Leu Val Asp Val Glu Glu
                485                 490                 495
```

```
Met Asn Tyr Met Ala Ala Glu Gly Glu Gly Glu Val Cys Val Lys Gly
            500                 505                 510

Pro Asn Val Phe Gln Gly Tyr Leu Lys Asp Pro Ala Lys Thr Ala Glu
        515                 520                 525

Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
    530                 535                 540

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545                 550                 555                 560

Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Ile
                565                 570                 575

Tyr Met Arg Ser Glu Pro Val Ala Gln Val Phe Val His Gly Glu Ser
            580                 585                 590

Leu Gln Ala Phe Leu Ile Ala Ile Val Val Pro Asp Val Glu Thr Leu
        595                 600                 605

Cys Ser Trp Ala Gln Lys Arg Gly Phe Glu Gly Ser Phe Glu Glu Leu
    610                 615                 620

Cys Arg Asn Lys Asp Val Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625                 630                 635                 640

Leu Gly Lys Asp Ser Gly Leu Lys Pro Phe Glu Gln Val Lys Gly Ile
                645                 650                 655

Thr Leu His Pro Glu Leu Phe Ser Ile Asp Asn Gly Leu Leu Thr Pro
            660                 665                 670

Thr Met Lys Ala Lys Arg Pro Glu Leu Arg Asn Tyr Phe Arg Ser Gln
        675                 680                 685

Ile Asp Asp Leu Tyr Ser Thr Ile Lys Val
    690                 695
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<210> 1957
<211> 664
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426244"

<400> 1957
Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1 5 10 15

Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
20 25 30

Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
35 40 45

Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
50 55 60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
65 70 75 80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
85 90 95

Gln Arg Gly Ile Gln Val Ser Asn Asn Gly Pro Cys Leu Gly Ser Arg
100 105 110

Lys Pro Asp Gln Pro Tyr Glu Trp Leu Ser Tyr Lys Gln Trp Val Ile
115 120 125

Ile Glu Gln Gly Cys Phe Ala Tyr Ser Met Val Ile Val Pro Leu Tyr
130 135 140

Asp Thr Leu Gly Asn Glu Ala Ile Thr Tyr Ile Val Asn Lys Ala Glu
145 150 155 160

```
Leu Ser Leu Val Phe Val Asp Lys Pro Glu Lys Ala Lys Leu Leu Leu
                165                 170                 175

Glu Gly Val Glu Asn Lys Leu Ile Pro Gly Leu Lys Ile Ile Val Val
            180                 185                 190

Met Asp Ala Tyr Gly Ser Glu Leu Val Glu Arg Gly Gln Arg Cys Gly
        195                 200                 205

Val Glu Val Thr Ser Met Lys Ala Met Glu Asp Leu Gly Arg Ala Asn
    210                 215                 220

Arg Arg Lys Pro Lys Pro Pro Ala Pro Glu Asp Leu Ala Val Ile Cys
225                 230                 235                 240

Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Val Thr His
                245                 250                 255

Arg Asn Ile Val Ser Asp Cys Ser Ala Phe Val Lys Ala Thr Glu Asn
            260                 265                 270

Thr Val Asn Pro Cys Pro Asp Asp Thr Leu Ile Ser Phe Leu Pro Leu
        275                 280                 285

Ala His Met Phe Glu Arg Val Val Glu Cys Val Met Leu Cys His Gly
    290                 295                 300

Ala Lys Ile Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Met Asp Asp
305                 310                 315                 320

Leu Lys Val Leu Gln Pro Thr Val Phe Pro Val Val Pro Arg Leu Leu
                325                 330                 335

Asn Arg Met Phe Asp Arg Ile Phe Gly Gln Ala Asn Thr Thr Leu Lys
            340                 345                 350

Arg Trp Leu Leu Asp Phe Ala Ser Lys Arg Lys Glu Ala Glu Leu Arg
        355                 360                 365

Ser Gly Ile Ile Arg Asn Asn Ser Leu Trp Asp Arg Leu Ile Phe His
    370                 375                 380
```

```
Lys Val Gln Ser Ser Leu Gly Gly Arg Val Arg Leu Met Val Thr Gly
385                 390                 395                 400

Ala Ala Pro Val Ser Ala Thr Val Leu Thr Phe Leu Arg Ala Ala Leu
                405                 410                 415

Gly Cys Gln Phe Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr Ala Gly
            420                 425                 430

Cys Cys Leu Thr Met Pro Gly Asp Trp Thr Ala Gly His Val Gly Ala
        435                 440                 445

Pro Met Pro Cys Asn Leu Ile Lys Leu Val Asp Val Glu Glu Met Asn
    450                 455                 460

Tyr Met Ala Ala Glu Gly Glu Gly Glu Val Cys Val Lys Gly Pro Asn
465                 470                 475                 480

Val Phe Gln Gly Tyr Leu Lys Asp Pro Ala Lys Thr Ala Glu Ala Leu
                485                 490                 495

Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp Leu Pro
            500                 505                 510

Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe Lys Leu
        515                 520                 525

Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn Ile Tyr Met
    530                 535                 540

Arg Ser Glu Pro Val Ala Gln Val Phe Val His Gly Glu Ser Leu Gln
545                 550                 555                 560

Ala Phe Leu Ile Ala Ile Val Val Pro Asp Val Glu Thr Leu Cys Ser
                565                 570                 575

Trp Ala Gln Lys Arg Gly Phe Glu Gly Ser Phe Glu Glu Leu Cys Arg
            580                 585                 590

Asn Lys Asp Val Lys Lys Ala Ile Leu Glu Asp Met Val Arg Leu Gly
        595                 600                 605
```

```
Lys Asp Ser Gly Leu Lys Pro Phe Glu Gln Val Lys Gly Ile Thr Leu
    610                 615                 620

His Pro Glu Leu Phe Ser Ile Asp Asn Gly Leu Leu Thr Pro Thr Met
625                 630                 635                 640

Lys Ala Lys Arg Pro Glu Leu Arg Asn Tyr Phe Arg Ser Gln Ile Asp
                645                 650                 655

Asp Leu Tyr Ser Thr Ile Lys Val
            660
```

<210> 1958
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000426491"

<400> 1958

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Met Gln Ala His Glu Leu Phe Arg Tyr Phe Arg Met Pro Glu Leu Val
1               5                   10                  15

Asp Phe Arg Gln Tyr Val Arg Thr Leu Pro Thr Asn Thr Leu Met Gly
            20                  25                  30

Phe Gly Ala Phe Ala Ala Leu Thr Thr Phe Trp Tyr Ala Thr Arg Pro
        35                  40                  45

Lys Pro Leu Lys Pro Pro Cys Asp Leu Ser Met Gln Ser Val Glu Val
    50                  55                  60

Ala Gly Ser Gly Gly Ala Arg Arg Ser Ala Leu Leu Asp Ser Asp Glu
```

65 70 75 80

Pro Leu Val Tyr Phe Tyr Asp Asp Val Thr Thr Leu Tyr Glu Gly Phe
85 90 95

Gln Arg Gly Ile Gln Val Ser Arg Ser Leu Arg Pro Leu Cys Val His
100 105 110

Cys Asn Phe Pro Arg Val Gly Pro Lys Ala His Trp Thr Leu
115 120 125

<210> 1959
<211> 527
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 504; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485264"

<400> 1959
Met Val Ile Val Pro Leu Tyr Asp Thr Leu Gly Asn Glu Ala Ile Thr
1 5 10 15

Tyr Ile Val Asn Lys Ala Glu Leu Ser Leu Val Phe Val Asp Lys Pro
20 25 30

Glu Lys Ala Lys Leu Leu Leu Glu Gly Val Glu Asn Lys Leu Ile Pro
35 40 45

Gly Leu Lys Ile Ile Val Val Met Asp Ala Tyr Gly Ser Glu Leu Val
50 55 60

Glu Arg Gly Gln Arg Cys Gly Val Glu Val Thr Ser Met Lys Ala Met
65 70 75 80

```
Glu Asp Leu Gly Arg Ala Asn Arg Arg Lys Pro Lys Pro Pro Ala Pro
                85                  90                  95

Glu Asp Leu Ala Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro
            100                 105                 110

Lys Gly Ala Met Val Thr His Arg Asn Ile Val Ser Asp Cys Ser Ala
        115                 120                 125

Phe Val Lys Ala Thr Glu Asn Thr Val Asn Pro Cys Pro Asp Asp Thr
    130                 135                 140

Leu Ile Ser Phe Leu Pro Leu Ala His Met Phe Glu Arg Val Val Glu
145                 150                 155                 160

Cys Val Met Leu Cys His Gly Ala Lys Ile Gly Phe Phe Gln Gly Asp
                165                 170                 175

Ile Arg Leu Leu Met Asp Asp Leu Lys Val Leu Gln Pro Thr Val Phe
            180                 185                 190

Pro Val Val Pro Arg Leu Leu Asn Arg Met Phe Asp Arg Ile Phe Gly
        195                 200                 205

Gln Ala Asn Thr Thr Leu Lys Arg Trp Leu Leu Asp Phe Ala Ser Lys
    210                 215                 220

Arg Lys Glu Ala Glu Leu Arg Ser Gly Ile Ile Arg Asn Asn Ser Leu
225                 230                 235                 240

Trp Asp Arg Leu Ile Phe His Lys Val Gln Ser Ser Leu Gly Gly Arg
                245                 250                 255

Val Arg Leu Met Val Thr Gly Ala Ala Pro Val Ser Ala Thr Val Leu
            260                 265                 270

Thr Phe Leu Arg Ala Ala Leu Gly Cys Gln Phe Tyr Glu Gly Tyr Gly
        275                 280                 285

Gln Thr Glu Cys Thr Ala Gly Cys Cys Leu Thr Met Pro Gly Asp Trp
    290                 295                 300
```

Thr Ala Gly His Val Gly Ala Pro Met Pro Cys Asn Leu Ile Lys Leu
305 310 315 320

Val Asp Val Glu Glu Met Asn Tyr Met Ala Ala Glu Gly Glu Gly Glu
325 330 335

Val Cys Val Lys Gly Pro Asn Val Phe Gln Gly Tyr Leu Lys Asp Pro
340 345 350

Ala Lys Thr Ala Glu Ala Leu Asp Lys Asp Gly Trp Leu His Thr Gly
355 360 365

Asp Ile Gly Lys Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg
370 375 380

Lys Lys His Ile Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu
385 390 395 400

Lys Ile Glu Asn Ile Tyr Met Arg Ser Glu Pro Val Ala Gln Val Phe
405 410 415

Val His Gly Glu Ser Leu Gln Ala Phe Leu Ile Ala Ile Val Val Pro
420 425 430

Asp Val Glu Thr Leu Cys Ser Trp Ala Gln Lys Arg Gly Phe Glu Gly
435 440 445

Ser Phe Glu Glu Leu Cys Arg Asn Lys Asp Val Lys Lys Ala Ile Leu
450 455 460

Glu Asp Met Val Arg Leu Gly Lys Asp Ser Gly Leu Lys Pro Phe Glu
465 470 475 480

Gln Val Lys Gly Ile Thr Leu His Pro Glu Leu Phe Ser Ile Asp Asn
485 490 495

Gly Leu Leu Thr Pro Thr Met Lys Ala Lys Arg Pro Glu Leu Arg Asn
500 505 510

Tyr Phe Arg Ser Gln Ile Asp Asp Leu Tyr Ser Thr Ile Lys Val
515 520 525

<210> 1960
<211> 720
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 505; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 3; "

<220>
<221> source
<223> /note="Uniprot ID: O95573; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000350012"

<400> 1960
Met Asn Asn His Val Ser Ser Lys Pro Ser Thr Met Lys Leu Lys His
1   5   10   15

Thr Ile Asn Pro Ile Leu Leu Tyr Phe Ile His Phe Leu Ile Ser Leu
            20   25   30

Tyr Thr Ile Leu Thr Tyr Ile Pro Phe Tyr Phe Phe Ser Glu Ser Arg
        35   40   45

Gln Glu Lys Ser Asn Arg Ile Lys Ala Lys Pro Val Asn Ser Lys Pro
    50   55   60

Asp Ser Ala Tyr Arg Ser Val Asn Ser Leu Asp Gly Leu Ala Ser Val
65   70   75   80

Leu Tyr Pro Gly Cys Asp Thr Leu Asp Lys Val Phe Thr Tyr Ala Lys
                85   90   95

Asn Lys Phe Lys Asn Lys Arg Leu Leu Gly Thr Arg Glu Val Leu Asn
            100   105   110

Glu Glu Asp Glu Val Gln Pro Asn Gly Lys Ile Phe Lys Lys Val Ile

```
        115                 120                 125

Leu Gly Gln Tyr Asn Trp Leu Ser Tyr Glu Asp Val Phe Val Arg Ala
    130                 135                 140

Phe Asn Phe Gly Asn Gly Leu Gln Met Leu Gly Gln Lys Pro Lys Thr
145                 150                 155                 160

Asn Ile Ala Ile Phe Cys Glu Thr Arg Ala Glu Trp Met Ile Ala Ala
                165                 170                 175

Gln Ala Cys Phe Met Tyr Asn Phe Gln Leu Val Thr Leu Tyr Ala Thr
            180                 185                 190

Leu Gly Gly Pro Ala Ile Val His Ala Leu Asn Glu Thr Glu Val Thr
        195                 200                 205

Asn Ile Ile Thr Ser Lys Glu Leu Leu Gln Thr Lys Leu Lys Asp Ile
    210                 215                 220

Val Ser Leu Val Pro Arg Leu Arg His Ile Ile Thr Val Asp Gly Lys
225                 230                 235                 240

Pro Pro Thr Trp Ser Glu Phe Pro Lys Gly Ile Ile Val His Thr Met
                245                 250                 255

Ala Ala Val Glu Ala Leu Gly Ala Lys Ala Ser Met Glu Asn Gln Pro
            260                 265                 270

His Ser Lys Pro Leu Pro Ser Asp Ile Ala Val Ile Met Tyr Thr Ser
        275                 280                 285

Gly Ser Thr Gly Leu Pro Lys Gly Val Met Ile Ser His Ser Asn Ile
    290                 295                 300

Ile Ala Gly Ile Thr Gly Met Ala Glu Arg Ile Pro Glu Leu Gly Glu
305                 310                 315                 320

Glu Asp Val Tyr Ile Gly Tyr Leu Pro Leu Ala His Val Leu Glu Leu
                325                 330                 335

Ser Ala Glu Leu Val Cys Leu Ser His Gly Cys Arg Ile Gly Tyr Ser
            340                 345                 350
```

```
Ser Pro Gln Thr Leu Ala Asp Gln Ser Ser Lys Ile Lys Lys Gly Ser
        355                 360                 365

Lys Gly Asp Thr Ser Met Leu Lys Pro Thr Leu Met Ala Ala Val Pro
    370                 375                 380

Glu Ile Met Asp Arg Ile Tyr Lys Asn Val Met Asn Lys Val Ser Glu
385                 390                 395                 400

Met Ser Ser Phe Gln Arg Asn Leu Phe Ile Leu Ala Tyr Asn Tyr Lys
                405                 410                 415

Met Glu Gln Ile Ser Lys Gly Arg Asn Thr Pro Leu Cys Asp Ser Phe
            420                 425                 430

Val Phe Arg Lys Val Arg Ser Leu Leu Gly Gly Asn Ile Arg Leu Leu
        435                 440                 445

Leu Cys Gly Gly Ala Pro Leu Ser Ala Thr Thr Gln Arg Phe Met Asn
    450                 455                 460

Ile Cys Phe Cys Cys Pro Val Gly Gln Gly Tyr Gly Leu Thr Glu Ser
465                 470                 475                 480

Ala Gly Ala Gly Thr Ile Ser Glu Val Trp Asp Tyr Asn Thr Gly Arg
                485                 490                 495

Val Gly Ala Pro Leu Val Cys Cys Glu Ile Lys Leu Lys Asn Trp Glu
            500                 505                 510

Glu Gly Gly Tyr Phe Asn Thr Asp Lys Pro His Pro Arg Gly Glu Ile
        515                 520                 525

Leu Ile Gly Gly Gln Ser Val Thr Met Gly Tyr Tyr Lys Asn Glu Ala
    530                 535                 540

Lys Thr Lys Ala Asp Phe Phe Glu Asp Glu Asn Gly Gln Arg Trp Leu
545                 550                 555                 560

Cys Thr Gly Asp Ile Gly Glu Phe Glu Pro Asp Gly Cys Leu Lys Ile
                565                 570                 575
```

```
Ile Asp Arg Lys Lys Asp Leu Val Lys Leu Gln Ala Gly Glu Tyr Val
            580                 585                 590

Ser Leu Gly Lys Val Glu Ala Ala Leu Lys Asn Leu Pro Leu Val Asp
        595                 600                 605

Asn Ile Cys Ala Tyr Ala Asn Ser Tyr His Ser Tyr Val Ile Gly Phe
    610                 615                 620

Val Val Pro Asn Gln Lys Glu Leu Thr Glu Leu Ala Arg Lys Lys Gly
625                 630                 635                 640

Leu Lys Gly Thr Trp Glu Glu Leu Cys Asn Ser Cys Glu Met Glu Asn
                645                 650                 655

Glu Val Leu Lys Val Leu Ser Glu Ala Ala Ile Ser Ala Ser Leu Glu
            660                 665                 670

Lys Phe Glu Ile Pro Val Lys Ile Arg Leu Ser Pro Glu Pro Trp Thr
        675                 680                 685

Pro Glu Thr Gly Leu Val Thr Asp Ala Phe Lys Leu Lys Arg Lys Glu
    690                 695                 700

Leu Lys Thr His Tyr Gln Ala Asp Ile Glu Arg Met Tyr Gly Arg Lys
705                 710                 715                 720
```

<210> 1961
<211> 720
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 505; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL3; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 3; "

<220>

<221> source
<223> /note="Uniprot ID: O95573; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000375918"

<400> 1961
Met Asn Asn His Val Ser Ser Lys Pro Ser Thr Met Lys Leu Lys His
1   5   10   15

Thr Ile Asn Pro Ile Leu Leu Tyr Phe Ile His Phe Leu Ile Ser Leu
            20   25   30

Tyr Thr Ile Leu Thr Tyr Ile Pro Phe Tyr Phe Phe Ser Glu Ser Arg
        35   40   45

Gln Glu Lys Ser Asn Arg Ile Lys Ala Lys Pro Val Asn Ser Lys Pro
    50   55   60

Asp Ser Ala Tyr Arg Ser Val Asn Ser Leu Asp Gly Leu Ala Ser Val
65   70   75   80

Leu Tyr Pro Gly Cys Asp Thr Leu Asp Lys Val Phe Thr Tyr Ala Lys
                85   90   95

Asn Lys Phe Lys Asn Lys Arg Leu Leu Gly Thr Arg Glu Val Leu Asn
            100   105   110

Glu Glu Asp Glu Val Gln Pro Asn Gly Lys Ile Phe Lys Lys Val Ile
        115   120   125

Leu Gly Gln Tyr Asn Trp Leu Ser Tyr Glu Asp Val Phe Val Arg Ala
    130   135   140

Phe Asn Phe Gly Asn Gly Leu Gln Met Leu Gly Gln Lys Pro Lys Thr
145   150   155   160

Asn Ile Ala Ile Phe Cys Glu Thr Arg Ala Glu Trp Met Ile Ala Ala
                165   170   175

Gln Ala Cys Phe Met Tyr Asn Phe Gln Leu Val Thr Leu Tyr Ala Thr
            180   185   190

Leu Gly Gly Pro Ala Ile Val His Ala Leu Asn Glu Thr Glu Val Thr

```
        195                 200                 205

Asn Ile Ile Thr Ser Lys Glu Leu Leu Gln Thr Lys Leu Lys Asp Ile
    210                 215                 220

Val Ser Leu Val Pro Arg Leu Arg His Ile Ile Thr Val Asp Gly Lys
225                 230                 235                 240

Pro Pro Thr Trp Ser Glu Phe Pro Lys Gly Ile Ile Val His Thr Met
                245                 250                 255

Ala Ala Val Glu Ala Leu Gly Ala Lys Ala Ser Met Glu Asn Gln Pro
            260                 265                 270

His Ser Lys Pro Leu Pro Ser Asp Ile Ala Val Ile Met Tyr Thr Ser
        275                 280                 285

Gly Ser Thr Gly Leu Pro Lys Gly Val Met Ile Ser His Ser Asn Ile
    290                 295                 300

Ile Ala Gly Ile Thr Gly Met Ala Glu Arg Ile Pro Glu Leu Gly Glu
305                 310                 315                 320

Glu Asp Val Tyr Ile Gly Tyr Leu Pro Leu Ala His Val Leu Glu Leu
                325                 330                 335

Ser Ala Glu Leu Val Cys Leu Ser His Gly Cys Arg Ile Gly Tyr Ser
            340                 345                 350

Ser Pro Gln Thr Leu Ala Asp Gln Ser Ser Lys Ile Lys Lys Gly Ser
        355                 360                 365

Lys Gly Asp Thr Ser Met Leu Lys Pro Thr Leu Met Ala Ala Val Pro
    370                 375                 380

Glu Ile Met Asp Arg Ile Tyr Lys Asn Val Met Asn Lys Val Ser Glu
385                 390                 395                 400

Met Ser Ser Phe Gln Arg Asn Leu Phe Ile Leu Ala Tyr Asn Tyr Lys
                405                 410                 415

Met Glu Gln Ile Ser Lys Gly Arg Asn Thr Pro Leu Cys Asp Ser Phe
            420                 425                 430
```

```
Val Phe Arg Lys Val Arg Ser Leu Leu Gly Gly Asn Ile Arg Leu Leu
        435                 440                 445

Leu Cys Gly Gly Ala Pro Leu Ser Ala Thr Thr Gln Arg Phe Met Asn
    450                 455                 460

Ile Cys Phe Cys Cys Pro Val Gly Gln Gly Tyr Gly Leu Thr Glu Ser
465                 470                 475                 480

Ala Gly Ala Gly Thr Ile Ser Glu Val Trp Asp Tyr Asn Thr Gly Arg
                485                 490                 495

Val Gly Ala Pro Leu Val Cys Cys Glu Ile Lys Leu Lys Asn Trp Glu
            500                 505                 510

Glu Gly Gly Tyr Phe Asn Thr Asp Lys Pro His Pro Arg Gly Glu Ile
        515                 520                 525

Leu Ile Gly Gly Gln Ser Val Thr Met Gly Tyr Tyr Lys Asn Glu Ala
    530                 535                 540

Lys Thr Lys Ala Asp Phe Phe Glu Asp Glu Asn Gly Gln Arg Trp Leu
545                 550                 555                 560

Cys Thr Gly Asp Ile Gly Glu Phe Glu Pro Asp Gly Cys Leu Lys Ile
                565                 570                 575

Ile Asp Arg Lys Lys Asp Leu Val Lys Leu Gln Ala Gly Glu Tyr Val
            580                 585                 590

Ser Leu Gly Lys Val Glu Ala Ala Leu Lys Asn Leu Pro Leu Val Asp
        595                 600                 605

Asn Ile Cys Ala Tyr Ala Asn Ser Tyr His Ser Tyr Val Ile Gly Phe
    610                 615                 620

Val Val Pro Asn Gln Lys Glu Leu Thr Glu Leu Ala Arg Lys Lys Gly
625                 630                 635                 640

Leu Lys Gly Thr Trp Glu Glu Leu Cys Asn Ser Cys Glu Met Glu Asn
                645                 650                 655
```

Glu Val Leu Lys Val Leu Ser Glu Ala Ala Ile Ser Ala Ser Leu Glu
660 665 670

Lys Phe Glu Ile Pro Val Lys Ile Arg Leu Ser Pro Glu Pro Trp Thr
675 680 685

Pro Glu Thr Gly Leu Val Thr Asp Ala Phe Lys Leu Lys Arg Lys Glu
690 695 700

Leu Lys Thr His Tyr Gln Ala Asp Ile Glu Arg Met Tyr Gly Arg Lys
705 710 715 720

<210> 1962
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 505; "

<220>
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<223> /note="Gene Symbol: ACSL3; "

<220>
<221> source
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acyl-CoA synthetase long-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000385157"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1962
Xaa Glu Gln Ile Ser Lys Gly Arg Asn Thr Pro Leu Cys Asp Arg Trp
1 5 10 15

Ile Leu

<210> 1963
<211> 88

<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
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acyl-CoA synthetase long-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416913"

<400> 1963
Met Asn Asn His Val Ser Ser Lys Pro Ser Thr Met Lys Leu Lys His
1 5 10 15

Thr Ile Asn Pro Ile Leu Leu Tyr Phe Ile His Phe Leu Ile Ser Leu
20 25 30

Tyr Thr Ile Leu Thr Tyr Ile Pro Phe Tyr Phe Phe Ser Glu Ser Arg
35 40 45

Gln Glu Lys Ser Asn Arg Ile Lys Ala Lys Pro Val Asn Ser Lys Pro
50 55 60

Asp Ser Ala Tyr Arg Ser Val Asn Ser Leu Asp Gly Leu Ala Ser Val
65 70 75 80

Leu Tyr Pro Gly Cys Asp Thr Leu
85

<210> 1964
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 505; "

<220>
<221> source

<223> /note="Gene Symbol: ACSL3; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000438342"

<400> 1964
Met Asn Asn His Val Ser Ser Lys Pro Ser Thr Met Lys Leu Lys His
1 5 10 15

Thr Ile Asn Pro Ile Leu Leu Tyr Phe Ile His Phe Leu Ile Ser Leu
20 25 30

Tyr Thr Ile Leu Thr Tyr Ile Pro Phe Tyr Phe Phe Ser Glu Ser Arg
35 40 45

Gln Glu Lys Ser Asn Arg Ile Lys Ala Lys Pro Val Asn Ser Lys Pro
50 55 60

Asp Ser Ala Tyr Arg Ser Val Asn Ser Leu Asp Gly Leu Ala Ser Val
65 70 75 80

Leu Tyr Pro Gly Cys Asp Thr Leu Asp Lys Val Phe Thr Tyr Ala
85 90 95

<210> 1965
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 505; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 3; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000441643"

<400> 1965
Met Leu Gly Gln Lys Pro Lys Thr Asn Ile Ala Ile Phe Cys Glu Thr
1   5   10   15

Arg Ala Glu Trp Met Ile Ala Ala Gln Ala Cys Phe Met Tyr Asn Phe
            20   25   30

Gln Leu Val Thr Leu Tyr Ala Thr Leu Gly Gly Pro Ala Ile Val His
        35   40   45

Ala Leu Asn Glu Thr Glu Val Thr Asn Ile Ile Thr Ser Lys Glu Leu
    50   55   60

Leu Gln Thr Lys Leu Lys Asp Ile Val Ser Leu Val Pro Arg Leu Arg
65   70   75   80

His Ile Ile Thr Val Asp Gly Lys Pro Pro Thr Trp Ser Glu Phe Pro
                85   90   95

Lys Gly Ile Ile Val His Thr Met Ala Ala Val Glu Ala Leu Gly Ala
            100   105   110

Lys Ala Ser Met Glu Asn Gln Pro His Ser Lys Pro Leu Pro Ser Asp
        115   120   125

Ile Ala Val Ile Met Tyr Thr Ser Gly Ser Thr Gly Leu
    130   135   140

<210> 1966
<211> 670
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
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<223> /note="Gene Symbol: ACSL4; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family

member 4; "

<220>
<221> source
<223> /note="Uniprot ID: O60488; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000262835"

<400> 1966
Met Ala Lys Arg Ile Lys Ala Lys Pro Thr Ser Asp Lys Pro Gly Ser
1   5   10   15

Pro Tyr Arg Ser Val Thr His Phe Asp Ser Leu Ala Val Ile Asp Ile
            20   25   30

Pro Gly Ala Asp Thr Leu Asp Lys Leu Phe Asp His Ala Val Ser Lys
        35   40   45

Phe Gly Lys Lys Asp Ser Leu Gly Thr Arg Glu Ile Leu Ser Glu Glu
    50   55   60

Asn Glu Met Gln Pro Asn Gly Lys Val Phe Lys Lys Leu Ile Leu Gly
65   70   75   80

Asn Tyr Lys Trp Met Asn Tyr Leu Glu Val Asn Arg Arg Val Asn Asn
                85   90   95

Phe Gly Ser Gly Leu Thr Ala Leu Gly Leu Lys Pro Lys Asn Thr Ile
            100   105   110

Ala Ile Phe Cys Glu Thr Arg Ala Glu Trp Met Ile Ala Ala Gln Thr
        115   120   125

Cys Phe Lys Tyr Asn Phe Pro Leu Val Thr Leu Tyr Ala Thr Leu Gly
    130   135   140

Lys Glu Ala Val Val His Gly Leu Asn Glu Ser Glu Ala Ser Tyr Leu
145   150   155   160

Ile Thr Ser Val Glu Leu Leu Glu Ser Lys Leu Lys Thr Ala Leu Leu
                165   170   175

Asp Ile Ser Cys Val Lys His Ile Ile Tyr Val Asp Asn Lys Ala Ile
            180   185   190

```
Asn Lys Ala Glu Tyr Pro Glu Gly Phe Glu Ile His Ser Met Gln Ser
        195                 200                 205

Val Glu Glu Leu Gly Ser Asn Pro Glu Asn Leu Gly Ile Pro Pro Ser
    210                 215                 220

Arg Pro Thr Pro Ser Asp Met Ala Ile Val Met Tyr Thr Ser Gly Ser
225                 230                 235                 240

Thr Gly Arg Pro Lys Gly Val Met Met His His Ser Asn Leu Ile Ala
                245                 250                 255

Gly Met Thr Gly Gln Cys Glu Arg Ile Pro Gly Leu Gly Pro Lys Asp
            260                 265                 270

Thr Tyr Ile Gly Tyr Leu Pro Leu Ala His Val Leu Glu Leu Thr Ala
        275                 280                 285

Glu Ile Ser Cys Phe Thr Tyr Gly Cys Arg Ile Gly Tyr Ser Ser Pro
    290                 295                 300

Leu Thr Leu Ser Asp Gln Ser Ser Lys Ile Lys Lys Gly Ser Lys Gly
305                 310                 315                 320

Asp Cys Thr Val Leu Lys Pro Thr Leu Met Ala Ala Val Pro Glu Ile
                325                 330                 335

Met Asp Arg Ile Tyr Lys Asn Val Met Ser Lys Val Gln Glu Met Asn
            340                 345                 350

Tyr Ile Gln Lys Thr Leu Phe Lys Ile Gly Tyr Asp Tyr Lys Leu Glu
        355                 360                 365

Gln Ile Lys Lys Gly Tyr Asp Ala Pro Leu Cys Asn Leu Leu Leu Phe
    370                 375                 380

Lys Lys Val Lys Ala Leu Leu Gly Gly Asn Val Arg Met Met Leu Ser
385                 390                 395                 400

Gly Gly Ala Pro Leu Ser Pro Gln Thr His Arg Phe Met Asn Val Cys
                405                 410                 415
```

```
Phe Cys Cys Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Ser Cys Gly
            420                 425                 430

Ala Gly Thr Val Thr Glu Val Thr Asp Tyr Thr Thr Gly Arg Val Gly
        435                 440                 445

Ala Pro Leu Ile Cys Cys Glu Ile Lys Leu Lys Asp Trp Gln Glu Gly
    450                 455                 460

Gly Tyr Thr Ile Asn Asp Lys Pro Asn Pro Arg Gly Glu Ile Val Ile
465                 470                 475                 480

Gly Gly Gln Asn Ile Ser Met Gly Tyr Phe Lys Asn Glu Glu Lys Thr
                485                 490                 495

Ala Glu Asp Tyr Ser Val Asp Glu Asn Gly Gln Arg Trp Phe Cys Thr
            500                 505                 510

Gly Asp Ile Gly Glu Phe His Pro Asp Gly Cys Leu Gln Ile Ile Asp
        515                 520                 525

Arg Lys Lys Asp Leu Val Lys Leu Gln Ala Gly Glu Tyr Val Ser Leu
    530                 535                 540

Gly Lys Val Glu Ala Ala Leu Lys Asn Cys Pro Leu Ile Asp Asn Ile
545                 550                 555                 560

Cys Ala Phe Ala Lys Ser Asp Gln Ser Tyr Val Ile Ser Phe Val Val
                565                 570                 575

Pro Asn Gln Lys Arg Leu Thr Leu Leu Ala Gln Gln Lys Gly Val Glu
            580                 585                 590

Gly Thr Trp Val Asp Ile Cys Asn Asn Pro Ala Met Glu Ala Glu Ile
        595                 600                 605

Leu Lys Glu Ile Arg Glu Ala Ala Asn Ala Met Lys Leu Glu Arg Phe
    610                 615                 620

Glu Ile Pro Ile Lys Val Arg Leu Ser Pro Glu Pro Trp Thr Pro Glu
625                 630                 635                 640
```

```
Thr Gly Leu Val Thr Asp Ala Phe Lys Leu Lys Arg Lys Glu Leu Arg
                645                 650                 655

Asn His Tyr Leu Lys Asp Ile Glu Arg Met Tyr Gly Gly Lys
            660                 665                 670


<210> 1967
<211> 711
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="Uniprot ID:  O60488; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000339787"

<400> 1967
Met Lys Leu Lys Leu Asn Val Leu Thr Ile Ile Leu Leu Pro Val His
1               5                   10                  15

Leu Leu Ile Thr Ile Tyr Ser Ala Leu Ile Phe Ile Pro Trp Tyr Phe
            20                  25                  30

Leu Thr Asn Ala Lys Lys Lys Asn Ala Met Ala Lys Arg Ile Lys Ala
        35                  40                  45

Lys Pro Thr Ser Asp Lys Pro Gly Ser Pro Tyr Arg Ser Val Thr His
    50                  55                  60

Phe Asp Ser Leu Ala Val Ile Asp Ile Pro Gly Ala Asp Thr Leu Asp
65                  70                  75                  80

Lys Leu Phe Asp His Ala Val Ser Lys Phe Gly Lys Lys Asp Ser Leu
```

```
                85                  90                  95

Gly Thr Arg Glu Ile Leu Ser Glu Glu Asn Glu Met Gln Pro Asn Gly
            100                 105                 110

Lys Val Phe Lys Lys Leu Ile Leu Gly Asn Tyr Lys Trp Met Asn Tyr
        115                 120                 125

Leu Glu Val Asn Arg Arg Val Asn Asn Phe Gly Ser Gly Leu Thr Ala
    130                 135                 140

Leu Gly Leu Lys Pro Lys Asn Thr Ile Ala Ile Phe Cys Glu Thr Arg
145                 150                 155                 160

Ala Glu Trp Met Ile Ala Ala Gln Thr Cys Phe Lys Tyr Asn Phe Pro
                165                 170                 175

Leu Val Thr Leu Tyr Ala Thr Leu Gly Lys Glu Ala Val Val His Gly
            180                 185                 190

Leu Asn Glu Ser Glu Ala Ser Tyr Leu Ile Thr Ser Val Glu Leu Leu
        195                 200                 205

Glu Ser Lys Leu Lys Thr Ala Leu Leu Asp Ile Ser Cys Val Lys His
    210                 215                 220

Ile Ile Tyr Val Asp Asn Lys Ala Ile Asn Lys Ala Glu Tyr Pro Glu
225                 230                 235                 240

Gly Phe Glu Ile His Ser Met Gln Ser Val Glu Glu Leu Gly Ser Asn
                245                 250                 255

Pro Glu Asn Leu Gly Ile Pro Pro Ser Arg Pro Thr Pro Ser Asp Met
            260                 265                 270

Ala Ile Val Met Tyr Thr Ser Gly Ser Thr Gly Arg Pro Lys Gly Val
        275                 280                 285

Met Met His His Ser Asn Leu Ile Ala Gly Met Thr Gly Gln Cys Glu
    290                 295                 300

Arg Ile Pro Gly Leu Gly Pro Lys Asp Thr Tyr Ile Gly Tyr Leu Pro
305                 310                 315                 320
```

```
Leu Ala His Val Leu Glu Leu Thr Ala Glu Ile Ser Cys Phe Thr Tyr
                325                 330                 335

Gly Cys Arg Ile Gly Tyr Ser Ser Pro Leu Thr Leu Ser Asp Gln Ser
            340                 345                 350

Ser Lys Ile Lys Lys Gly Ser Lys Gly Asp Cys Thr Val Leu Lys Pro
        355                 360                 365

Thr Leu Met Ala Ala Val Pro Glu Ile Met Asp Arg Ile Tyr Lys Asn
    370                 375                 380

Val Met Ser Lys Val Gln Glu Met Asn Tyr Ile Gln Lys Thr Leu Phe
385                 390                 395                 400

Lys Ile Gly Tyr Asp Tyr Lys Leu Glu Gln Ile Lys Lys Gly Tyr Asp
                405                 410                 415

Ala Pro Leu Cys Asn Leu Leu Leu Phe Lys Lys Val Lys Ala Leu Leu
            420                 425                 430

Gly Gly Asn Val Arg Met Met Leu Ser Gly Gly Ala Pro Leu Ser Pro
        435                 440                 445

Gln Thr His Arg Phe Met Asn Val Cys Phe Cys Cys Pro Ile Gly Gln
    450                 455                 460

Gly Tyr Gly Leu Thr Glu Ser Cys Gly Ala Gly Thr Val Thr Glu Val
465                 470                 475                 480

Thr Asp Tyr Thr Thr Gly Arg Val Gly Ala Pro Leu Ile Cys Cys Glu
                485                 490                 495

Ile Lys Leu Lys Asp Trp Gln Glu Gly Gly Tyr Thr Ile Asn Asp Lys
            500                 505                 510

Pro Asn Pro Arg Gly Glu Ile Val Ile Gly Gly Gln Asn Ile Ser Met
        515                 520                 525

Gly Tyr Phe Lys Asn Glu Glu Lys Thr Ala Glu Asp Tyr Ser Val Asp
    530                 535                 540
```

```
Glu Asn Gly Gln Arg Trp Phe Cys Thr Gly Asp Ile Gly Glu Phe His
545                 550                 555                 560

Pro Asp Gly Cys Leu Gln Ile Ile Asp Arg Lys Lys Asp Leu Val Lys
                565                 570                 575

Leu Gln Ala Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu
            580                 585                 590

Lys Asn Cys Pro Leu Ile Asp Asn Ile Cys Ala Phe Ala Lys Ser Asp
        595                 600                 605

Gln Ser Tyr Val Ile Ser Phe Val Val Pro Asn Gln Lys Arg Leu Thr
    610                 615                 620

Leu Leu Ala Gln Gln Lys Gly Val Glu Gly Thr Trp Val Asp Ile Cys
625                 630                 635                 640

Asn Asn Pro Ala Met Glu Ala Glu Ile Leu Lys Glu Ile Arg Glu Ala
                645                 650                 655

Ala Asn Ala Met Lys Leu Glu Arg Phe Glu Ile Pro Ile Lys Val Arg
            660                 665                 670

Leu Ser Pro Glu Pro Trp Thr Pro Glu Thr Gly Leu Val Thr Asp Ala
        675                 680                 685

Phe Lys Leu Lys Arg Lys Glu Leu Arg Asn His Tyr Leu Lys Asp Ile
    690                 695                 700

Glu Arg Met Tyr Gly Gly Lys
705                 710
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<210> 1968
<211> 711
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 4; "

<220>
<221> source
<223> /note="Uniprot ID: O60488; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419171"

<400> 1968

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Met Lys Leu Lys Leu Asn Val Leu Thr Ile Ile Leu Leu Pro Val His
1               5                  10                  15

Leu Leu Ile Thr Ile Tyr Ser Ala Leu Ile Phe Ile Pro Trp Tyr Phe
            20                  25                  30

Leu Thr Asn Ala Lys Lys Lys Asn Ala Met Ala Lys Arg Ile Lys Ala
        35                  40                  45

Lys Pro Thr Ser Asp Lys Pro Gly Ser Pro Tyr Arg Ser Val Thr His
    50                  55                  60

Phe Asp Ser Leu Ala Val Ile Asp Ile Pro Gly Ala Asp Thr Leu Asp
65                  70                  75                  80

Lys Leu Phe Asp His Ala Val Ser Lys Phe Gly Lys Lys Asp Ser Leu
                85                  90                  95

Gly Thr Arg Glu Ile Leu Ser Glu Glu Asn Glu Met Gln Pro Asn Gly
            100                 105                 110

Lys Val Phe Lys Lys Leu Ile Leu Gly Asn Tyr Lys Trp Met Asn Tyr
        115                 120                 125

Leu Glu Val Asn Arg Arg Val Asn Asn Phe Gly Ser Gly Leu Thr Ala
    130                 135                 140

Leu Gly Leu Lys Pro Lys Asn Thr Ile Ala Ile Phe Cys Glu Thr Arg
145                 150                 155                 160

Ala Glu Trp Met Ile Ala Ala Gln Thr Cys Phe Lys Tyr Asn Phe Pro
```

```
                165                 170                 175

Leu Val Thr Leu Tyr Ala Thr Leu Gly Lys Glu Ala Val Val His Gly
            180                 185                 190

Leu Asn Glu Ser Glu Ala Ser Tyr Leu Ile Thr Ser Val Glu Leu Leu
        195                 200                 205

Glu Ser Lys Leu Lys Thr Ala Leu Leu Asp Ile Ser Cys Val Lys His
    210                 215                 220

Ile Ile Tyr Val Asp Asn Lys Ala Ile Asn Lys Ala Glu Tyr Pro Glu
225                 230                 235                 240

Gly Phe Glu Ile His Ser Met Gln Ser Val Glu Glu Leu Gly Ser Asn
                245                 250                 255

Pro Glu Asn Leu Gly Ile Pro Pro Ser Arg Pro Thr Pro Ser Asp Met
            260                 265                 270

Ala Ile Val Met Tyr Thr Ser Gly Ser Thr Gly Arg Pro Lys Gly Val
        275                 280                 285

Met Met His His Ser Asn Leu Ile Ala Gly Met Thr Gly Gln Cys Glu
    290                 295                 300

Arg Ile Pro Gly Leu Gly Pro Lys Asp Thr Tyr Ile Gly Tyr Leu Pro
305                 310                 315                 320

Leu Ala His Val Leu Glu Leu Thr Ala Glu Ile Ser Cys Phe Thr Tyr
                325                 330                 335

Gly Cys Arg Ile Gly Tyr Ser Ser Pro Leu Thr Leu Ser Asp Gln Ser
            340                 345                 350

Ser Lys Ile Lys Lys Gly Ser Lys Gly Asp Cys Thr Val Leu Lys Pro
        355                 360                 365

Thr Leu Met Ala Ala Val Pro Glu Ile Met Asp Arg Ile Tyr Lys Asn
    370                 375                 380

Val Met Ser Lys Val Gln Glu Met Asn Tyr Ile Gln Lys Thr Leu Phe
385                 390                 395                 400
```

```
Lys Ile Gly Tyr Asp Tyr Lys Leu Glu Gln Ile Lys Lys Gly Tyr Asp
                405                 410                 415

Ala Pro Leu Cys Asn Leu Leu Leu Phe Lys Lys Val Lys Ala Leu Leu
            420                 425                 430

Gly Gly Asn Val Arg Met Met Leu Ser Gly Gly Ala Pro Leu Ser Pro
        435                 440                 445

Gln Thr His Arg Phe Met Asn Val Cys Phe Cys Cys Pro Ile Gly Gln
    450                 455                 460

Gly Tyr Gly Leu Thr Glu Ser Cys Gly Ala Gly Thr Val Thr Glu Val
465                 470                 475                 480

Thr Asp Tyr Thr Thr Gly Arg Val Gly Ala Pro Leu Ile Cys Cys Glu
                485                 490                 495

Ile Lys Leu Lys Asp Trp Gln Glu Gly Gly Tyr Thr Ile Asn Asp Lys
            500                 505                 510

Pro Asn Pro Arg Gly Glu Ile Val Ile Gly Gly Gln Asn Ile Ser Met
        515                 520                 525

Gly Tyr Phe Lys Asn Glu Glu Lys Thr Ala Glu Asp Tyr Ser Val Asp
    530                 535                 540

Glu Asn Gly Gln Arg Trp Phe Cys Thr Gly Asp Ile Gly Glu Phe His
545                 550                 555                 560

Pro Asp Gly Cys Leu Gln Ile Ile Asp Arg Lys Lys Asp Leu Val Lys
                565                 570                 575

Leu Gln Ala Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu
            580                 585                 590

Lys Asn Cys Pro Leu Ile Asp Asn Ile Cys Ala Phe Ala Lys Ser Asp
        595                 600                 605

Gln Ser Tyr Val Ile Ser Phe Val Val Pro Asn Gln Lys Arg Leu Thr
    610                 615                 620
```

```
Leu Leu Ala Gln Gln Lys Gly Val Glu Gly Thr Trp Val Asp Ile Cys
625                 630                 635                 640


Asn Asn Pro Ala Met Glu Ala Glu Ile Leu Lys Glu Ile Arg Glu Ala
                645                 650                 655


Ala Asn Ala Met Lys Leu Glu Arg Phe Glu Ile Pro Ile Lys Val Arg
            660                 665                 670


Leu Ser Pro Glu Pro Trp Thr Pro Glu Thr Gly Leu Val Thr Asp Ala
        675                 680                 685


Phe Lys Leu Lys Arg Lys Glu Leu Arg Asn His Tyr Leu Lys Asp Ile
    690                 695                 700


Glu Arg Met Tyr Gly Gly Lys
705                 710


<210> 1969
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421425"

<400> 1969
Met Lys Leu Lys Leu Asn Val Leu Thr Ile Ile Leu Leu Pro Val His
1               5                   10                  15


Leu Leu Ile Thr Ile Tyr Ser Ala Leu Ile Phe Ile Pro Trp Tyr Phe
            20                  25                  30
```

```
Leu Thr Asn Ala Lys Lys Lys Asn Ala Met Ala Lys Arg Ile Lys Ala
        35                  40                  45

Lys Pro Thr Ser Asp Lys Pro Gly Ser Pro Tyr Arg Ser Val Thr His
    50                  55                  60

Phe Asp Ser Leu Ala Val Ile Asp Ile Pro Gly Ala Asp Thr Leu Asp
65                  70                  75                  80

Lys Leu Phe Asp His Ala Val Ser Lys Phe Gly Lys Lys Asp Ser Leu
                85                  90                  95

Gly Thr Arg Glu Ile Leu Ser Glu Glu Asn Glu Met Gln Pro Asn Gly
            100                 105                 110

Lys Val Phe Lys Lys Leu Ile Leu Gly Asn Tyr Lys Trp Met
        115                 120                 125


<210> 1970
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423077"

<400> 1970
Met Lys Leu Lys Leu Asn Val Leu Thr Ile Ile Leu Leu Pro Val His
1               5                   10                  15

Leu Leu Ile Thr Ile Tyr Ser Ala Leu Ile Phe Ile Pro Trp Tyr Phe
            20                  25                  30

Leu Thr Asn Ala Lys Lys Lys Asn Ala Met Ala Lys Arg Ile Lys Ala
```

```
        35                  40                  45

Lys Pro Thr Ser Asp Lys
    50


<210> 1971
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423539"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1971
Xaa Thr Leu Phe Lys Ile Gly Tyr Asp Tyr Lys Leu Glu Gln Ile Lys
1               5                   10                  15


Lys Gly Tyr Asp Ala Pro Leu Cys Asn Leu Leu Leu Phe Lys Lys Val
            20                  25                  30


Lys Ala Leu Leu Gly Gly Asn Val Arg Met Met Leu Ser Gly Gly Ala
        35                  40                  45


Pro Leu Ser Pro Gln Thr His Arg Phe Met Asn Val Cys Phe Cys Cys
    50                  55                  60


Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Ser Cys Gly Ala Gly Thr
65                  70                  75                  80
```

```
Val Thr Glu Val Thr Asp Tyr Thr Thr Gly Arg Val Gly Ala Pro Leu
                85                  90                  95

Ile Cys Cys Glu Ile Lys Leu Lys Asp Trp Gln Glu Gly Gly Tyr Thr
            100                 105                 110

Ile Asn Asp Lys Pro Asn Pro Arg Gly Glu Ile Val Ile Gly Gly Gln
        115                 120                 125

Asn Ile Ser Met Gly Tyr Phe Lys Asn Glu Glu Lys Thr Ala Glu Asp
    130                 135                 140

Tyr Ser Val Asp Glu Asn Gly Gln Arg Asn Leu Gly
145                 150                 155


<210> 1972
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000424808"

<400> 1972
Met Ala Lys Arg Ile Lys Ala Lys Pro Thr Ser Asp Lys Pro Gly Ser
1               5                   10                  15

Pro Tyr Arg Ser Val Thr His Phe Asp Ser Leu Ala Val Ile Asp Ile
            20                  25                  30

Pro Gly Ala Asp Thr Leu Asp Lys Leu Phe Asp His Ala Val Ser Lys
        35                  40                  45

Phe Gly Lys Lys Asp Ser Leu Gly Thr Arg Glu Ile Leu Ser Glu Glu
```

```
    50                  55                  60

Asn Glu Met Gln Pro Asn Gly Lys Val Phe Lys Lys Leu Ile Leu Gly
65                  70                  75                  80

Asn Tyr Lys Trp Met Asn Tyr Leu Glu Val Asn Arg Arg Val Asn Asn
                85                  90                  95

Phe Gly Ser Gly Leu Thr Ala Leu Gly Leu Lys Pro Lys Asn Thr Ile
            100                 105                 110

Ala Ile Phe Cys Glu Thr Arg Ala Glu Trp Met Ile Ala Ala Gln Thr
        115                 120                 125

Cys Phe Lys Tyr Asn Phe Pro Leu Val Thr Leu Tyr Ala Thr Leu Gly
    130                 135                 140

Lys Glu Ala Val Val His Gly Leu Asn Glu
145                 150


<210> 1973
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425378"

<400> 1973
Met Lys Leu Lys Leu Asn Val Leu Thr Ile Ile Leu Leu Pro Val His
1               5                  10                  15

Leu Leu Ile Thr Ile Tyr Ser Ala Leu Ile Phe Ile Pro Trp Tyr Phe
            20                  25                  30
```

```
Leu Thr Asn Ala Lys Lys Lys Asn Ala Met Ala Lys Arg Ile Lys Ala
        35                  40                  45

Lys Pro Thr Ser Asp Lys Pro Gly Ser Pro Tyr Arg Ser Val Thr His
    50                  55                  60

Phe Asp Ser Leu Ala Val Ile Asp Ile Pro Gly Ala Asp Thr Leu Asp
65                  70                  75                  80

Lys Leu Phe Asp His Ala Val Ser Lys Phe Gly Lys Lys Asp Ser Leu
                85                  90                  95

Gly Thr Arg Glu Ile Leu Ser Glu Glu Asn Glu Met Gln Pro Asn Gly
            100                 105                 110

Lys Val Phe Lys Lys Leu Ile Leu Gly Asn Tyr Lys Trp Met Asn Tyr
        115                 120                 125


<210> 1974
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 506; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000425408"

<400> 1974
Met Lys Leu Lys Leu Asn Val Leu Thr Ile Ile Leu Leu Pro Val His
1               5                   10                  15

Leu Leu Ile Thr Ile Tyr Ser Ala Leu Ile Phe Ile Pro Trp Tyr Phe
            20                  25                  30
```

```
Leu Thr Asn Ala Lys Lys Lys Asn Ala Met Ala Lys Arg Ile Lys Ala
        35                  40                  45

Lys Pro Thr Ser Asp Lys Pro Gly Ser Pro Tyr Arg Ser Val Thr His
    50                  55                  60

Phe Asp Ser Leu Ala Val Ile Asp Ile Pro Gly Ala Asp Thr Leu Asp
65                  70                  75                  80

Lys Leu Phe Asp His Ala Val Ser Lys Phe Gly Lys Lys Asp Ser Leu
                85                  90                  95

Gly Thr Arg Glu Ile Leu Ser Glu Glu Asn Glu Met Gln Pro Asn Gly
            100                 105                 110

Lys Val Phe Lys Lys Leu Ile Leu Gly Asn Tyr Lys Trp Met Asn Tyr
        115                 120                 125

Leu Glu Val Asn Arg Arg Val Asn Asn Phe Gly Ser Gly Leu Thr Ala
    130                 135                 140

Leu
145


<210> 1975
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 507; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9ULC5; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000346223"

<400> 1975
Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
1 5 10 15

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
20 25 30

Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser
35 40 45

Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
50 55 60

Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu Val
65 70 75 80

Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly Tyr
85 90 95

Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val Ser
100 105 110

Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr Lys
115 120 125

Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro Glu
130 135 140

Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Ala Val
145 150 155 160

Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val Asn
165 170 175

Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala Leu
180 185 190

Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys Val
195 200 205

Ile Ile Leu Met Asp Pro Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu

210 215 220

Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly
225 230 235 240

Lys Glu His Phe Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser
245 250 255

Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met
260 265 270

Ile Thr His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys
275 280 285

Val Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
290 295 300

Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val Tyr
305 310 315 320

Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu
325 330 335

Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val Pro
340 345 350

Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys Thr
355 360 365

Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val Ser Ser Lys Phe Lys
370 375 380

Glu Leu Gln Lys Gly Ile Ile Arg His Asp Ser Phe Trp Asp Lys Leu
385 390 395 400

Ile Phe Ala Lys Ile Gln Asp Ser Leu Gly Gly Arg Val Arg Val Ile
405 410 415

Val Thr Gly Ala Ala Pro Met Ser Thr Ser Val Met Thr Phe Phe Arg
420 425 430

Ala Ala Met Gly Cys Gln Val Tyr Glu Ala Tyr Gly Gln Thr Glu Cys
435 440 445

```
Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly His
    450                 455                 460

Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala
465                 470                 475                 480

Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys
                485                 490                 495

Gly Thr Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln
            500                 505                 510

Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg
        515                 520                 525

Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
    530                 535                 540

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn
545                 550                 555                 560

Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His Gly Glu
                565                 570                 575

Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp Thr Asp Val
            580                 585                 590

Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly Ser Phe Glu Glu
        595                 600                 605

Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile Leu Glu Asp Leu Gln
    610                 615                 620

Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr Phe Glu Gln Val Lys Ala
625                 630                 635                 640

Ile Phe Leu His Pro Glu Pro Phe Ser Ile Glu Asn Gly Leu Leu Thr
                645                 650                 655

Pro Thr Leu Lys Ala Lys Arg Gly Glu Leu Ser Lys Tyr Phe Arg Thr
            660                 665                 670
```

Gln Ile Asp Ser Leu Tyr Glu His Ile Gln Asp
675 680

<210> 1976
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 507; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL5; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 5; "

<220>
<221> source
<223> /note="Uniprot ID: Q9ULC5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000346680"

<400> 1976
Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
1 5 10 15

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
20 25 30

Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser
35 40 45

Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
50 55 60

Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu Val
65 70 75 80

Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly Tyr
85 90 95

```
Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val Ser
            100                 105                 110

Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr Lys
        115                 120                 125

Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro Glu
    130                 135                 140

Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Ala Val
145                 150                 155                 160

Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val Asn
                165                 170                 175

Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala Leu
            180                 185                 190

Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys Val
        195                 200                 205

Ile Ile Leu Met Asp Pro Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu
    210                 215                 220

Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly
225                 230                 235                 240

Lys Glu His Phe Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser
                245                 250                 255

Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met
            260                 265                 270

Ile Thr His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys
        275                 280                 285

Val Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
    290                 295                 300

Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val Tyr
305                 310                 315                 320

Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu
```

```
                325                 330                 335

Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val Pro
            340                 345                 350

Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys Thr
        355                 360                 365

Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val Ser Ser Lys Phe Lys
    370                 375                 380

Glu Leu Gln Lys Gly Ile Ile Arg His Asp Ser Phe Trp Asp Lys Leu
385                 390                 395                 400

Ile Phe Ala Lys Ile Gln Asp Ser Leu Gly Gly Arg Val Arg Val Ile
                405                 410                 415

Val Thr Gly Ala Ala Pro Met Ser Thr Ser Val Met Thr Phe Phe Arg
            420                 425                 430

Ala Ala Met Gly Cys Gln Val Tyr Glu Ala Tyr Gly Gln Thr Glu Cys
        435                 440                 445

Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly His
    450                 455                 460

Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala
465                 470                 475                 480

Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys
                485                 490                 495

Gly Thr Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln
            500                 505                 510

Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg
        515                 520                 525

Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
    530                 535                 540

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn
545                 550                 555                 560
```

```
Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His Gly Glu
                565                 570                 575

Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp Thr Asp Val
            580                 585                 590

Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly Ser Phe Glu Glu
        595                 600                 605

Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile Leu Glu Asp Leu Gln
    610                 615                 620

Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr Phe Glu Gln Val Lys Ala
625                 630                 635                 640

Ile Phe Leu His Pro Glu Pro Phe Ser Ile Glu Asn Gly Leu Leu Thr
                645                 650                 655

Pro Thr Leu Lys Ala Lys Arg Gly Glu Leu Ser Lys Tyr Phe Arg Thr
            660                 665                 670

Gln Ile Asp Ser Leu Tyr Glu His Ile Gln Asp
        675                 680


<210> 1977
<211> 739
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 507; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9ULC5; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000348429"

<400> 1977
Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg Gly
1   5   10   15

Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro Gly Ser
            20   25   30

Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser Gln Gly Leu
        35   40   45

Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile Phe Asn Phe Leu
    50   55   60

Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys Ile Leu Thr Phe Gly
65   70   75   80

Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg Pro Gln Pro Val Leu Pro
                85   90   95

Leu Leu Asp Leu Asn Asn Gln Ser Val Gly Ile Glu Gly Gly Ala Arg
            100   105   110

Lys Gly Val Ser Gln Lys Asn Asn Asp Leu Thr Ser Cys Cys Phe Ser
        115   120   125

Asp Ala Lys Thr Met Tyr Glu Val Phe Gln Arg Gly Leu Ala Val Ser
    130   135   140

Asp Asn Gly Pro Cys Leu Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg
145   150   155   160

Trp Leu Ser Tyr Lys Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser
                165   170   175

Cys Leu Leu His Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly
            180   185   190

Ile Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys
        195   200   205

```
Tyr Thr Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro
    210                 215                 220

Glu Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
225                 230                 235                 240

Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu Lys
                245                 250                 255

Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro Phe Asp
            260                 265                 270

Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu Ile Leu Ser
        275                 280                 285

Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe Arg Lys Pro Val
    290                 295                 300

Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys Phe Thr Ser Gly Thr
305                 310                 315                 320

Thr Gly Asp Pro Lys Gly Ala Met Ile Thr His Gln Asn Ile Val Ser
                325                 330                 335

Asn Ala Ala Ala Phe Leu Lys Cys Val Glu His Ala Tyr Glu Pro Thr
            340                 345                 350

Pro Asp Asp Val Ala Ile Ser Tyr Leu Pro Leu Ala His Met Phe Glu
        355                 360                 365

Arg Ile Val Gln Ala Val Val Tyr Ser Cys Gly Ala Arg Val Gly Phe
    370                 375                 380

Phe Gln Gly Asp Ile Arg Leu Leu Ala Asp Asp Met Lys Thr Leu Lys
385                 390                 395                 400

Pro Thr Leu Phe Pro Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp
                405                 410                 415

Lys Val Gln Asn Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys
            420                 425                 430

Leu Ala Val Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg
```

```
        435                 440                 445

His Asp Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser
    450                 455                 460

Leu Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser
465                 470                 475                 480

Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val Tyr
                485                 490                 495

Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe Thr Leu
            500                 505                 510

Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu Ala Cys Asn
        515                 520                 525

Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr Phe Thr Val Asn
    530                 535                 540

Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn Val Phe Lys Gly Tyr
545                 550                 555                 560

Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala Leu Asp Ser Asp Gly Trp
                565                 570                 575

Leu His Thr Gly Asp Ile Gly Arg Trp Leu Pro Asn Gly Thr Leu Lys
            580                 585                 590

Ile Ile Asp Arg Lys Lys Asn Ile Phe Lys Leu Ala Gln Gly Glu Tyr
        595                 600                 605

Ile Ala Pro Glu Lys Ile Glu Asn Ile Tyr Asn Arg Ser Gln Pro Val
    610                 615                 620

Leu Gln Ile Phe Val His Gly Glu Ser Leu Arg Ser Ser Leu Val Gly
625                 630                 635                 640

Val Val Val Pro Asp Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu
                645                 650                 655

Gly Val Lys Gly Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg
            660                 665                 670
```

```
Glu Ala Ile Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu
        675                 680                 685

Lys Thr Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe
    690                 695                 700

Ser Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
705                 710                 715                 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu His
                725                 730                 735

Ile Gln Asp
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<210> 1978
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 507; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL5; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 5; "

<220>
<221> source
<223> /note="Uniprot ID: Q9ULC5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376796"

<400> 1978

```
Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
1               5                  10                  15

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
            20                  25                  30
```

```
Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser
        35                  40                  45

Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
    50                  55                  60

Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu Val
65                  70                  75                  80

Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly Tyr
                85                  90                  95

Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val Ser
            100                 105                 110

Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr Lys
        115                 120                 125

Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro Glu
    130                 135                 140

Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Ala Val
145                 150                 155                 160

Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val Asn
                165                 170                 175

Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala Leu
            180                 185                 190

Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys Val
        195                 200                 205

Ile Ile Leu Met Asp Pro Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu
    210                 215                 220

Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly
225                 230                 235                 240

Lys Glu His Phe Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser
                245                 250                 255
```

```
Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met
            260                 265                 270

Ile Thr His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys
        275                 280                 285

Val Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
    290                 295                 300

Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val Tyr
305                 310                 315                 320

Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu
                325                 330                 335

Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val Pro
            340                 345                 350

Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys Thr
        355                 360                 365

Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val Ser Ser Lys Phe Lys
    370                 375                 380

Glu Leu Gln Lys Gly Ile Ile Arg His Asp Ser Phe Trp Asp Lys Leu
385                 390                 395                 400

Ile Phe Ala Lys Ile Gln Asp Ser Leu Gly Gly Arg Val Arg Val Ile
                405                 410                 415

Val Thr Gly Ala Ala Pro Met Ser Thr Ser Val Met Thr Phe Phe Arg
            420                 425                 430

Ala Ala Met Gly Cys Gln Val Tyr Glu Ala Tyr Gly Gln Thr Glu Cys
        435                 440                 445

Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly His
    450                 455                 460

Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala
465                 470                 475                 480

Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys
```

485 490 495

Gly Thr Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln
500 505 510

Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg
515 520 525

Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
530 535 540

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn
545 550 555 560

Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His Gly Glu
565 570 575

Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp Thr Asp Val
580 585 590

Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly Ser Phe Glu Glu
595 600 605

Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile Leu Glu Asp Leu Gln
610 615 620

Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr Phe Glu Gln Val Lys Ala
625 630 635 640

Ile Phe Leu His Pro Glu Pro Phe Ser Ile Glu Asn Gly Leu Leu Thr
645 650 655

Pro Thr Leu Lys Ala Lys Arg Gly Glu Leu Ser Lys Tyr Phe Arg Thr
660 665 670

Gln Ile Asp Ser Leu Tyr Glu His Ile Gln Asp
675 680

<210> 1979
<211> 659
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 507; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL5; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 5; "

<220>
<221> source
<223> /note="Uniprot ID: Q9ULC5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403647"

<400> 1979

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Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
1               5                   10                  15


Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
            20                  25                  30


Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser
        35                  40                  45


Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
    50                  55                  60


Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu Val
65                  70                  75                  80


Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly Tyr
                85                  90                  95


Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val Ser
            100                 105                 110


Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr Lys
        115                 120                 125


Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro Glu
    130                 135                 140
```

```
Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Ala Val
145                 150                 155                 160

Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val Asn
                165                 170                 175

Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala Leu
            180                 185                 190

Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys Val
        195                 200                 205

Ile Ile Leu Met Asp Pro Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu
    210                 215                 220

Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly
225                 230                 235                 240

Lys Glu His Phe Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser
                245                 250                 255

Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met
            260                 265                 270

Ile Thr His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys
        275                 280                 285

Val Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
    290                 295                 300

Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val Tyr
305                 310                 315                 320

Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu
                325                 330                 335

Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val Pro
            340                 345                 350

Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys Thr
        355                 360                 365
```

```
Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val Ser Ser Lys Phe Lys
    370                 375                 380

Glu Leu Gln Lys Gly Ile Ile Arg His Asp Ser Phe Trp Asp Lys Leu
385                 390                 395                 400

Ile Phe Ala Lys Ile Gln Asp Ser Leu Gly Gly Arg Val Arg Val Ile
                405                 410                 415

Val Thr Gly Ala Ala Pro Met Ser Thr Ser Val Met Thr Phe Phe Arg
            420                 425                 430

Ala Ala Met Gly Cys Gln Val Tyr Glu Ala Tyr Gly Gln Thr Glu Cys
        435                 440                 445

Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly His
    450                 455                 460

Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala
465                 470                 475                 480

Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys
                485                 490                 495

Gly Thr Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln
            500                 505                 510

Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg
        515                 520                 525

Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
    530                 535                 540

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn
545                 550                 555                 560

Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His Gly Glu
                565                 570                 575

Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp Thr Asp Val
            580                 585                 590

Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly Ser Phe Glu Glu
```

595 600 605

Leu Cys Gln Asn Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe
610 615 620

Ser Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
625 630 635 640

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu His
645 650 655

Ile Gln Asp

<210> 1980
<211> 722
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 508; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL6; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKU0; "

<220>
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<223> /note="ENSP ID: ENSP00000296869"

<400> 1980
Met Leu Thr Phe Phe Leu Val Ser Gly Gly Ser Leu Trp Leu Phe Val
1 5 10 15

Glu Phe Val Leu Ser Leu Leu Glu Lys Met Gln Thr Gln Glu Ile Leu
20 25 30

Arg Ile Leu Arg Leu Pro Glu Leu Gly Asp Leu Gly Gln Phe Phe Arg
35 40 45

```
Ser Leu Ser Ala Thr Thr Leu Val Ser Met Gly Ala Leu Ala Ala Ile
    50                  55                  60

Leu Ala Tyr Trp Phe Thr His Arg Pro Lys Ala Leu Gln Pro Pro Cys
65                  70                  75                  80

Asn Leu Leu Met Gln Ser Glu Glu Val Glu Asp Ser Gly Gly Ala Arg
                85                  90                  95

Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr His Tyr Tyr Asp
            100                 105                 110

Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly Leu Ser Ile Ser
        115                 120                 125

Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys Gln Pro Tyr Gln
    130                 135                 140

Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu Phe Leu Gly Ser
145                 150                 155                 160

Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp Gln Phe Ile Gly
                165                 170                 175

Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val Glu Leu Ala Cys
            180                 185                 190

Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp Thr Leu Gly Pro
        195                 200                 205

Gly Ala Ile Arg Tyr Ile Ile Asn Thr Ala Asp Ile Ser Thr Val Ile
    210                 215                 220

Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu His Val Glu Arg
225                 230                 235                 240

Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met Asp Pro Phe Glu
                245                 250                 255

Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val Val Ile Lys Ser
            260                 265                 270
```

```
Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His Gln Ala Pro Val
        275                 280                 285

Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe Thr Ser Gly Thr
    290                 295                 300

Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly Asn Val Val Ala
305                 310                 315                 320

Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Ser Gln Trp Ala Pro Thr
                325                 330                 335

Cys Ala Asp Val His Ile Ser Tyr Leu Pro Leu Ala His Met Phe Glu
            340                 345                 350

Arg Met Val Gln Ser Val Val Tyr Cys His Gly Gly Arg Val Gly Phe
        355                 360                 365

Phe Gln Gly Asp Ile Arg Leu Leu Ser Asp Asp Met Lys Ala Leu Cys
    370                 375                 380

Pro Thr Ile Phe Pro Val Val Pro Arg Leu Leu Asn Arg Met Tyr Asp
385                 390                 395                 400

Lys Ile Phe Ser Gln Ala Asn Thr Pro Leu Lys Arg Trp Leu Leu Glu
                405                 410                 415

Phe Ala Ala Lys Arg Lys Gln Ala Glu Val Arg Ser Gly Ile Ile Arg
            420                 425                 430

Asn Asp Ser Ile Trp Asp Glu Leu Phe Phe Asn Lys Ile Gln Ala Ser
        435                 440                 445

Leu Gly Gly Cys Val Arg Met Ile Val Thr Gly Ala Ala Pro Ala Ser
    450                 455                 460

Pro Thr Val Leu Gly Phe Leu Arg Ala Ala Leu Gly Cys Gln Val Tyr
465                 470                 475                 480

Glu Gly Tyr Gly Gln Thr Glu Cys Thr Ala Gly Cys Thr Phe Thr Thr
                485                 490                 495
```

```
Pro Gly Asp Trp Thr Ser Gly His Val Gly Ala Pro Leu Pro Cys Asn
            500                 505                 510

His Ile Lys Leu Val Asp Val Glu Glu Leu Asn Tyr Trp Ala Cys Lys
        515                 520                 525

Gly Glu Gly Glu Ile Cys Val Arg Gly Pro Asn Val Phe Lys Gly Tyr
    530                 535                 540

Leu Lys Asp Pro Asp Arg Thr Lys Glu Ala Leu Asp Ser Asp Gly Trp
545                 550                 555                 560

Leu His Thr Gly Asp Ile Gly Lys Trp Leu Pro Ala Gly Thr Leu Lys
                565                 570                 575

Ile Ile Asp Arg Lys Lys His Ile Phe Lys Leu Ala Gln Gly Glu Tyr
            580                 585                 590

Val Ala Pro Glu Lys Ile Glu Asn Ile Tyr Ile Arg Ser Gln Pro Val
        595                 600                 605

Ala Gln Ile Tyr Val His Gly Asp Ser Leu Lys Ala Phe Leu Val Gly
    610                 615                 620

Ile Val Val Pro Asp Pro Glu Val Met Pro Ser Trp Ala Gln Lys Arg
625                 630                 635                 640

Gly Ile Glu Gly Thr Tyr Ala Asp Leu Cys Thr Asn Lys Asp Leu Lys
                645                 650                 655

Lys Ala Ile Leu Glu Asp Met Val Arg Leu Gly Lys Glu Ser Gly Leu
            660                 665                 670

His Ser Phe Glu Gln Val Lys Ala Ile His Ile His Ser Asp Met Phe
        675                 680                 685

Ser Val Gln Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Pro
    690                 695                 700

Glu Leu Arg Glu Tyr Phe Lys Lys Gln Ile Glu Glu Leu Tyr Ser Ile
705                 710                 715                 720

Ser Met
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<210> 1981
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 508; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL6; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKU0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000349608"

<400> 1981
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1   5   10   15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Asp Ser
            20   25   30

Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr
        35   40   45

His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly
    50   55   60

Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys
65   70   75   80

Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu
                85   90   95

Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp
            100   105   110

```
Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val
        115                 120                 125

Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp
    130                 135                 140

Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr Ala Asp Ile
145                 150                 155                 160

Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu
                165                 170                 175

His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met
            180                 185                 190

Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val
        195                 200                 205

Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His
    210                 215                 220

Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe
225                 230                 235                 240

Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly
                245                 250                 255

Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Gly Asp
            260                 265                 270

Ile Arg Leu Leu Ser Asp Asp Met Lys Ala Leu Cys Pro Thr Ile Phe
        275                 280                 285

Pro Val Val Pro Arg Leu Leu Asn Arg Met Tyr Asp Lys Ile Phe Ser
    290                 295                 300

Gln Ala Asn Thr Pro Leu Lys Arg Trp Leu Leu Glu Phe Ala Ala Lys
305                 310                 315                 320

Arg Lys Gln Ala Glu Val Arg Ser Gly Ile Ile Arg Asn Asp Ser Ile
                325                 330                 335
```

```
Trp Asp Glu Leu Phe Phe Asn Lys Ile Gln Ala Ser Leu Gly Gly Cys
            340                 345                 350

Val Arg Met Ile Val Thr Gly Ala Ala Pro Ala Ser Pro Thr Val Leu
        355                 360                 365

Gly Phe Leu Arg Ala Ala Leu Gly Cys Gln Val Tyr Glu Gly Tyr Gly
    370                 375                 380

Gln Thr Glu Cys Thr Ala Gly Cys Thr Phe Thr Thr Pro Gly Asp Trp
385                 390                 395                 400

Thr Ser Gly His Val Gly Ala Pro Leu Pro Cys Asn His Ile Lys Leu
                405                 410                 415

Val Asp Val Glu Glu Leu Asn Tyr Trp Ala Cys Lys Gly Glu Gly Glu
            420                 425                 430

Ile Cys Val Arg Gly Pro Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro
        435                 440                 445

Asp Arg Thr Lys Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly
    450                 455                 460

Asp Ile Gly Lys Trp Leu Pro Ala Gly Thr Leu Lys Ile Ile Asp Arg
465                 470                 475                 480

Lys Lys His Ile Phe Lys Leu Ala Gln Gly Glu Tyr Val Ala Pro Glu
                485                 490                 495

Lys Ile Glu Asn Ile Tyr Ile Arg Ser Gln Pro Val Ala Gln Ile Tyr
            500                 505                 510

Val His Gly Asp Ser Leu Lys Ala Phe Leu Val Gly Ile Val Val Pro
        515                 520                 525

Asp Pro Glu Val Met Pro Ser Trp Ala Gln Lys Arg Gly Ile Glu Gly
    530                 535                 540

Thr Tyr Ala Asp Leu Cys Thr Asn Lys Asp Leu Lys Lys Ala Ile Leu
545                 550                 555                 560
```

```
Glu Asp Met Val Arg Leu Gly Lys Glu Ser Gly Leu His Ser Phe Glu
                565                 570                 575


Gln Val Lys Ala Ile His Ile His Ser Asp Met Phe Ser Val Gln Asn
            580                 585                 590


Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Pro Glu Leu Arg Glu
        595                 600                 605


Tyr Phe Lys Lys Gln Ile Glu Glu Leu Tyr Ser Ile Ser Met
    610                 615                 620


<210> 1982
<211> 697
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 508; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL6; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 6; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UKU0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000368542"

<400> 1982
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1               5                  10                  15


Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
            20                  25                  30


Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
        35                  40                  45


Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
```

```
    50                  55                  60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65                  70                  75                  80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
                85                  90                  95

Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
            100                 105                 110

Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
        115                 120                 125

Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
    130                 135                 140

Cys Thr Asp Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Ile Ile Val Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr
            180                 185                 190

Ala Asp Ile Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu
        195                 200                 205

Leu Leu Glu His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile
    210                 215                 220

Ile Leu Met Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys
225                 230                 235                 240

Cys Gly Val Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln
                245                 250                 255

Glu Asn His Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile
            260                 265                 270

Val Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu
        275                 280                 285
```

```
Thr His Gly Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr
    290                 295                 300

Glu Lys Val Ile Phe Pro Arg Gln Asp Asp Val Leu Ile Ser Phe Leu
305                 310                 315                 320

Pro Leu Ala His Met Phe Glu Arg Val Ile Gln Ser Val Val Tyr Cys
                325                 330                 335

His Gly Gly Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser
            340                 345                 350

Asp Asp Met Lys Ala Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg
        355                 360                 365

Leu Leu Asn Arg Met Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro
    370                 375                 380

Leu Lys Arg Trp Leu Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu
385                 390                 395                 400

Val Arg Ser Gly Ile Ile Arg Asn Asp Ser Ile Trp Asp Glu Leu Phe
                405                 410                 415

Phe Asn Lys Ile Gln Ala Ser Leu Gly Gly Cys Val Arg Met Ile Val
            420                 425                 430

Thr Gly Ala Ala Pro Ala Ser Pro Thr Val Leu Gly Phe Leu Arg Ala
        435                 440                 445

Ala Leu Gly Cys Gln Val Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
    450                 455                 460

Ala Gly Cys Thr Phe Thr Thr Pro Gly Asp Trp Thr Ser Gly His Val
465                 470                 475                 480

Gly Ala Pro Leu Pro Cys Asn His Ile Lys Leu Val Asp Val Glu Glu
                485                 490                 495

Leu Asn Tyr Trp Ala Cys Lys Gly Glu Gly Glu Ile Cys Val Arg Gly
            500                 505                 510
```

```
Pro Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Asp Arg Thr Lys Glu
        515                 520                 525

Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
    530                 535                 540

Leu Pro Ala Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545                 550                 555                 560

Lys Leu Ala Gln Gly Glu Tyr Val Ala Pro Glu Lys Ile Glu Asn Ile
                565                 570                 575

Tyr Ile Arg Ser Gln Pro Val Ala Gln Ile Tyr Val His Gly Asp Ser
            580                 585                 590

Leu Lys Ala Phe Leu Val Gly Ile Val Val Pro Asp Pro Glu Val Met
        595                 600                 605

Pro Ser Trp Ala Gln Lys Arg Gly Ile Glu Gly Thr Tyr Ala Asp Leu
    610                 615                 620

Cys Thr Asn Lys Asp Leu Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625                 630                 635                 640

Leu Gly Lys Glu Ser Gly Leu His Ser Phe Glu Gln Val Lys Ala Ile
                645                 650                 655

His Ile His Ser Asp Met Phe Ser Val Gln Asn Gly Leu Leu Thr Pro
            660                 665                 670

Thr Leu Lys Ala Lys Arg Pro Glu Leu Arg Glu Tyr Phe Lys Lys Gln
        675                 680                 685

Ile Glu Glu Leu Tyr Ser Ile Ser Met
    690                 695


<210> 1983
<211> 697
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 508; "
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<220>
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<223> /note="Gene Symbol: ACSL6; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKU0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000368546"

<400> 1983
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1   5   10   15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
            20   25   30

Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
        35   40   45

Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
    50   55   60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65   70   75   80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
                85   90   95

Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
            100   105   110

Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
        115   120   125

Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
    130   135   140

Cys Thr Asp Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp

145 150 155 160

Ile Ile Val Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro
165 170 175

Leu Tyr Asp Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr
180 185 190

Ala Asp Ile Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu
195 200 205

Leu Leu Glu His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile
210 215 220

Ile Leu Met Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys
225 230 235 240

Cys Gly Val Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln
245 250 255

Glu Asn His Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile
260 265 270

Val Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu
275 280 285

Thr His Gly Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr
290 295 300

Glu Ser Gln Trp Ala Pro Thr Cys Ala Asp Val His Ile Ser Tyr Leu
305 310 315 320

Pro Leu Ala His Met Phe Glu Arg Met Val Gln Ser Val Val Tyr Cys
325 330 335

His Gly Gly Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser
340 345 350

Asp Asp Met Lys Ala Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg
355 360 365

Leu Leu Asn Arg Met Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro
370 375 380

```
Leu Lys Arg Trp Leu Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu
385                 390                 395                 400

Val Arg Ser Gly Ile Ile Arg Asn Asp Ser Ile Trp Asp Glu Leu Phe
                405                 410                 415

Phe Asn Lys Ile Gln Ala Ser Leu Gly Gly Cys Val Arg Met Ile Val
            420                 425                 430

Thr Gly Ala Ala Pro Ala Ser Pro Thr Val Leu Gly Phe Leu Arg Ala
        435                 440                 445

Ala Leu Gly Cys Gln Val Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
    450                 455                 460

Ala Gly Cys Thr Phe Thr Thr Pro Gly Asp Trp Thr Ser Gly His Val
465                 470                 475                 480

Gly Ala Pro Leu Pro Cys Asn His Ile Lys Leu Val Asp Val Glu Glu
                485                 490                 495

Leu Asn Tyr Trp Ala Cys Lys Gly Glu Gly Glu Ile Cys Val Arg Gly
            500                 505                 510

Pro Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Asp Arg Thr Lys Glu
        515                 520                 525

Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
    530                 535                 540

Leu Pro Ala Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545                 550                 555                 560

Lys Leu Ala Gln Gly Glu Tyr Val Ala Pro Glu Lys Ile Glu Asn Ile
                565                 570                 575

Tyr Ile Arg Ser Gln Pro Val Ala Gln Ile Tyr Val His Gly Asp Ser
            580                 585                 590

Leu Lys Ala Phe Leu Val Gly Ile Val Val Pro Asp Pro Glu Val Met
        595                 600                 605
```

```
Pro Ser Trp Ala Gln Lys Arg Gly Ile Glu Gly Thr Tyr Ala Asp Leu
    610                 615                 620

Cys Thr Asn Lys Asp Leu Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625                 630                 635                 640

Leu Gly Lys Glu Ser Gly Leu His Ser Phe Glu Gln Val Lys Ala Ile
                645                 650                 655

His Ile His Ser Asp Met Phe Ser Val Gln Asn Gly Leu Leu Thr Pro
            660                 665                 670

Thr Leu Lys Ala Lys Arg Pro Glu Leu Arg Glu Tyr Phe Lys Lys Gln
        675                 680                 685

Ile Glu Glu Leu Tyr Ser Ile Ser Met
    690                 695
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<210> 1984
<211> 708
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 508; "

<220>
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<223> /note="Gene Symbol: ACSL6; "

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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
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<223> /note="Uniprot ID: Q9UKU0; "

<220>
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<223> /note="ENSP ID: ENSP00000368548"

<400> 1984

```
Met Pro Glu Phe Val Leu Ser Leu Leu Glu Lys Met Gln Thr Gln Glu
1               5                  10                  15
```

```
Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly Asp Leu Gly Gln Phe
            20                  25                  30

Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser Met Gly Ala Leu Ala
        35                  40                  45

Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro Lys Ala Leu Gln Pro
    50                  55                  60

Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val Glu Asp Ser Gly Gly
65                  70                  75                  80

Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr His Tyr
                85                  90                  95

Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly Leu Ser
            100                 105                 110

Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys Gln Pro
        115                 120                 125

Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu Phe Leu
    130                 135                 140

Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp Gln Phe
145                 150                 155                 160

Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val Glu Leu
                165                 170                 175

Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp Thr Leu
            180                 185                 190

Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr Ala Asp Ile Ser Thr
        195                 200                 205

Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu His Val
    210                 215                 220

Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met Asp Pro
225                 230                 235                 240

Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val Val Ile
```

```
                245                 250                 255

Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His Gln Ala
            260                 265                 270

Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe Thr Ser
        275                 280                 285

Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly Asn Val
    290                 295                 300

Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Lys Val Ile Phe
305                 310                 315                 320

Pro Arg Gln Asp Asp Val Leu Ile Ser Phe Leu Pro Leu Ala His Met
                325                 330                 335

Phe Glu Arg Val Ile Gln Ser Val Val Tyr Cys His Gly Gly Arg Val
            340                 345                 350

Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser Asp Asp Met Lys Ala
        355                 360                 365

Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg Leu Leu Asn Arg Met
    370                 375                 380

Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro Leu Lys Arg Trp Leu
385                 390                 395                 400

Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu Val Arg Ser Gly Ile
                405                 410                 415

Ile Arg Asn Asp Ser Ile Trp Asp Glu Leu Phe Phe Asn Lys Ile Gln
            420                 425                 430

Ala Ser Leu Gly Gly Cys Val Arg Met Ile Val Thr Gly Ala Ala Pro
        435                 440                 445

Ala Ser Pro Thr Val Leu Gly Phe Leu Arg Ala Ala Leu Gly Cys Gln
    450                 455                 460

Val Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr Ala Gly Cys Thr Phe
465                 470                 475                 480
```

Thr Thr Pro Gly Asp Trp Thr Ser Gly His Val Gly Ala Pro Leu Pro
485 490 495

Cys Asn His Ile Lys Leu Val Asp Val Glu Glu Leu Asn Tyr Trp Ala
500 505 510

Cys Lys Gly Glu Gly Glu Ile Cys Val Arg Gly Pro Asn Val Phe Lys
515 520 525

Gly Tyr Leu Lys Asp Pro Asp Arg Thr Lys Glu Ala Leu Asp Ser Asp
530 535 540

Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp Leu Pro Ala Gly Thr
545 550 555 560

Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe Lys Leu Ala Gln Gly
565 570 575

Glu Tyr Val Ala Pro Glu Lys Ile Glu Asn Ile Tyr Ile Arg Ser Gln
580 585 590

Pro Val Ala Gln Ile Tyr Val His Gly Asp Ser Leu Lys Ala Phe Leu
595 600 605

Val Gly Ile Val Val Pro Asp Pro Glu Val Met Pro Ser Trp Ala Gln
610 615 620

Lys Arg Gly Ile Glu Gly Thr Tyr Ala Asp Leu Cys Thr Asn Lys Asp
625 630 635 640

Leu Lys Lys Ala Ile Leu Glu Asp Met Val Arg Leu Gly Lys Glu Ser
645 650 655

Gly Leu His Ser Phe Glu Gln Val Lys Ala Ile His Ile His Ser Asp
660 665 670

Met Phe Ser Val Gln Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys
675 680 685

Arg Pro Glu Leu Arg Glu Tyr Phe Lys Lys Gln Ile Glu Glu Leu Tyr
690 695 700

Ser Ile Ser Met
705

<210> 1985
<211> 622
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 508; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL6; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKU0; "

<220>
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<400> 1985
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1   5   10   15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Asp Ser
            20   25   30

Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr
        35   40   45

His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly
    50   55   60

Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys
65   70   75   80

Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu
                85   90   95

```
Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp
            100                 105                 110

Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val
        115                 120                 125

Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp
    130                 135                 140

Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr Ala Asp Ile
145                 150                 155                 160

Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu
                165                 170                 175

His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met
            180                 185                 190

Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val
        195                 200                 205

Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His
    210                 215                 220

Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe
225                 230                 235                 240

Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly
                245                 250                 255

Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Gly Asp
            260                 265                 270

Ile Arg Leu Leu Ser Asp Asp Met Lys Ala Leu Cys Pro Thr Ile Phe
        275                 280                 285

Pro Val Val Pro Arg Leu Leu Asn Arg Met Tyr Asp Lys Ile Phe Ser
    290                 295                 300

Gln Ala Asn Thr Pro Leu Lys Arg Trp Leu Leu Glu Phe Ala Ala Lys
305                 310                 315                 320

Arg Lys Gln Ala Glu Val Arg Ser Gly Ile Ile Arg Asn Asp Ser Ile
```

325 330 335

Trp Asp Glu Leu Phe Phe Asn Lys Ile Gln Ala Ser Leu Gly Gly Cys
340 345 350

Val Arg Met Ile Val Thr Gly Ala Ala Pro Ala Ser Pro Thr Val Leu
355 360 365

Gly Phe Leu Arg Ala Ala Leu Gly Cys Gln Val Tyr Glu Gly Tyr Gly
370 375 380

Gln Thr Glu Cys Thr Ala Gly Cys Thr Phe Thr Thr Pro Gly Asp Trp
385 390 395 400

Thr Ser Gly His Val Gly Ala Pro Leu Pro Cys Asn His Ile Lys Leu
405 410 415

Val Asp Val Glu Glu Leu Asn Tyr Trp Ala Cys Lys Gly Glu Gly Glu
420 425 430

Ile Cys Val Arg Gly Pro Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro
435 440 445

Asp Arg Thr Lys Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly
450 455 460

Asp Ile Gly Lys Trp Leu Pro Ala Gly Thr Leu Lys Ile Ile Asp Arg
465 470 475 480

Lys Lys His Ile Phe Lys Leu Ala Gln Gly Glu Tyr Val Ala Pro Glu
485 490 495

Lys Ile Glu Asn Ile Tyr Ile Arg Ser Gln Pro Val Ala Gln Ile Tyr
500 505 510

Val His Gly Asp Ser Leu Lys Ala Phe Leu Val Gly Ile Val Val Pro
515 520 525

Asp Pro Glu Val Met Pro Ser Trp Ala Gln Lys Arg Gly Ile Glu Gly
530 535 540

Thr Tyr Ala Asp Leu Cys Thr Asn Lys Asp Leu Lys Lys Ala Ile Leu
545 550 555 560

```
Glu Asp Met Val Arg Leu Gly Lys Glu Ser Gly Leu His Ser Phe Glu
                565                 570                 575


Gln Val Lys Ala Ile His Ile His Ser Asp Met Phe Ser Val Gln Asn
            580                 585                 590


Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Pro Glu Leu Arg Glu
        595                 600                 605


Tyr Phe Lys Lys Gln Ile Glu Glu Leu Tyr Ser Ile Ser Met
    610                 615                 620


<210> 1986
<211> 722
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ACSL6; "

<220>
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<223> /note="Gene Name:
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      member 6; "

<220>
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<223> /note="Uniprot ID:  Q9UKU0; "

<220>
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<223> /note="ENSP ID: ENSP00000368566"

<400> 1986
Met Leu Thr Phe Phe Leu Val Ser Gly Gly Ser Leu Trp Leu Phe Val
1               5                   10                  15


Glu Phe Val Leu Ser Leu Leu Glu Lys Met Gln Thr Gln Glu Ile Leu
            20                  25                  30


Arg Ile Leu Arg Leu Pro Glu Leu Gly Asp Leu Gly Gln Phe Phe Arg
        35                  40                  45
```

```
Ser Leu Ser Ala Thr Thr Leu Val Ser Met Gly Ala Leu Ala Ala Ile
    50                  55                  60

Leu Ala Tyr Trp Phe Thr His Arg Pro Lys Ala Leu Gln Pro Pro Cys
65                  70                  75                  80

Asn Leu Leu Met Gln Ser Glu Glu Val Glu Asp Ser Gly Gly Ala Arg
                85                  90                  95

Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr His Tyr Tyr Asp
            100                 105                 110

Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly Leu Ser Ile Ser
        115                 120                 125

Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys Gln Pro Tyr Gln
    130                 135                 140

Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu Phe Leu Gly Ser
145                 150                 155                 160

Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp Gln Phe Ile Gly
                165                 170                 175

Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val Glu Leu Ala Cys
            180                 185                 190

Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp Thr Leu Gly Pro
        195                 200                 205

Gly Ala Ile Arg Tyr Ile Ile Asn Thr Ala Asp Ile Ser Thr Val Ile
    210                 215                 220

Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu His Val Glu Arg
225                 230                 235                 240

Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met Asp Pro Phe Glu
                245                 250                 255

Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val Val Ile Lys Ser
            260                 265                 270
```

```
Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His Gln Ala Pro Val
        275                 280                 285

Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe Thr Ser Gly Thr
    290                 295                 300

Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly Asn Val Val Ala
305                 310                 315                 320

Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Lys Val Ile Phe Pro Arg
                325                 330                 335

Gln Asp Asp Val Leu Ile Ser Phe Leu Pro Leu Ala His Met Phe Glu
            340                 345                 350

Arg Val Ile Gln Ser Val Val Tyr Cys His Gly Gly Arg Val Gly Phe
        355                 360                 365

Phe Gln Gly Asp Ile Arg Leu Leu Ser Asp Asp Met Lys Ala Leu Cys
    370                 375                 380

Pro Thr Ile Phe Pro Val Val Pro Arg Leu Leu Asn Arg Met Tyr Asp
385                 390                 395                 400

Lys Ile Phe Ser Gln Ala Asn Thr Pro Leu Lys Arg Trp Leu Leu Glu
                405                 410                 415

Phe Ala Ala Lys Arg Lys Gln Ala Glu Val Arg Ser Gly Ile Ile Arg
            420                 425                 430

Asn Asp Ser Ile Trp Asp Glu Leu Phe Phe Asn Lys Ile Gln Ala Ser
        435                 440                 445

Leu Gly Gly Cys Val Arg Met Ile Val Thr Gly Ala Ala Pro Ala Ser
    450                 455                 460

Pro Thr Val Leu Gly Phe Leu Arg Ala Ala Leu Gly Cys Gln Val Tyr
465                 470                 475                 480

Glu Gly Tyr Gly Gln Thr Glu Cys Thr Ala Gly Cys Thr Phe Thr Thr
                485                 490                 495

Pro Gly Asp Trp Thr Ser Gly His Val Gly Ala Pro Leu Pro Cys Asn
```

```
            500                 505                 510

His Ile Lys Leu Val Asp Val Glu Glu Leu Asn Tyr Trp Ala Cys Lys
        515                 520                 525

Gly Glu Gly Glu Ile Cys Val Arg Gly Pro Asn Val Phe Lys Gly Tyr
    530                 535                 540

Leu Lys Asp Pro Asp Arg Thr Lys Glu Ala Leu Asp Ser Asp Gly Trp
545                 550                 555                 560

Leu His Thr Gly Asp Ile Gly Lys Trp Leu Pro Ala Gly Thr Leu Lys
                565                 570                 575

Ile Ile Asp Arg Lys Lys His Ile Phe Lys Leu Ala Gln Gly Glu Tyr
            580                 585                 590

Val Ala Pro Glu Lys Ile Glu Asn Ile Tyr Ile Arg Ser Gln Pro Val
        595                 600                 605

Ala Gln Ile Tyr Val His Gly Asp Ser Leu Lys Ala Phe Leu Val Gly
    610                 615                 620

Ile Val Val Pro Asp Pro Glu Val Met Pro Ser Trp Ala Gln Lys Arg
625                 630                 635                 640

Gly Ile Glu Gly Thr Tyr Ala Asp Leu Cys Thr Asn Lys Asp Leu Lys
                645                 650                 655

Lys Ala Ile Leu Glu Asp Met Val Arg Leu Gly Lys Glu Ser Gly Leu
            660                 665                 670

His Ser Phe Glu Gln Val Lys Ala Ile His Ile His Ser Asp Met Phe
        675                 680                 685

Ser Val Gln Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Pro
    690                 695                 700

Glu Leu Arg Glu Tyr Phe Lys Lys Gln Ile Glu Glu Leu Tyr Ser Ile
705                 710                 715                 720

Ser Met
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<210> 1987
<211> 152
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388424"

<400> 1987
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1 5 10 15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
20 25 30

Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
35 40 45

Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
50 55 60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65 70 75 80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
85 90 95

Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
100 105 110

Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
115 120 125

```
Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
    130                 135                 140

Cys Thr Asp Gln Phe Ile Gly Val
145                 150
```

<210> 1988
<211> 99
<212> PRT
<213> Homo sapiens

<220>
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member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000389189"

<400> 1988

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Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1               5                   10                  15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Asp Ser
            20                  25                  30

Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr
        35                  40                  45

His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly
    50                  55                  60

Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys
65                  70                  75                  80

Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu
                85                  90                  95
```

Phe Leu Gly

<210> 1989
<211> 134
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394810"

<400> 1989
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1 5 10 15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
20 25 30

Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
35 40 45

Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
50 55 60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65 70 75 80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
85 90 95

Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
100 105 110

Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp

115 120 125

Arg Ala Glu Phe Leu Gly
130

<210> 1990
<211> 365
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000397507"

<400> 1990
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1 5 10 15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Asp Ser
20 25 30

Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr
35 40 45

His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly
50 55 60

Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys
65 70 75 80

Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu
85 90 95

Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp
100 105 110

```
Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val
        115                 120                 125

Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp
    130                 135                 140

Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr Ala Asp Ile
145                 150                 155                 160

Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu
                165                 170                 175

His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met
            180                 185                 190

Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val
        195                 200                 205

Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His
    210                 215                 220

Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe
225                 230                 235                 240

Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly
                245                 250                 255

Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Ser Gln
            260                 265                 270

Trp Ala Pro Thr Cys Ala Asp Val His Ile Ser Tyr Leu Pro Leu Ala
        275                 280                 285

His Met Phe Glu Arg Met Val Gln Ser Val Val Tyr Cys His Gly Gly
    290                 295                 300

Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser Asp Asp Met
305                 310                 315                 320

Lys Ala Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg Leu Leu Asn
                325                 330                 335
```

```
Arg Met Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro Leu Lys Arg
            340                 345                 350

Trp Leu Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu
        355                 360                 365


<210> 1991
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 508; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase long-chain family
      member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398381"

<400> 1991
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1               5                   10                  15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
            20                  25                  30

Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
        35                  40                  45

Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
    50                  55                  60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65                  70                  75                  80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
                85                  90                  95
```

```
Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
            100                 105                 110

Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
        115                 120                 125

Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
    130                 135                 140


<210> 1992
<211> 213
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 508; "

<220>
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<223> /note="Gene Name:
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      member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000398423"

<400> 1992
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1               5                  10                  15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
            20                  25                  30

Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
        35                  40                  45

Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
    50                  55                  60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65                  70                  75                  80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
```

```
                85                  90                  95

Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
            100                 105                 110

Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
        115                 120                 125

Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
    130                 135                 140

Cys Thr Asp Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Ile Ile Val Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr
            180                 185                 190

Ala Asp Ile Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu
        195                 200                 205

Leu Leu Glu His Val
    210


<210> 1993
<211> 677
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ACSL6; "

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<223> /note="Gene Name:
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      member 6; "

<220>
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<223> /note="ENSP ID: ENSP00000413329"
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<400> 1993
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1 5 10 15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Asp Ser
20 25 30

Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln Leu Leu Thr
35 40 45

His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe Arg Arg Gly
50 55 60

Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg Lys Pro Lys
65 70 75 80

Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp Arg Ala Glu
85 90 95

Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala Cys Thr Asp
100 105 110

Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp Ile Ile Val
115 120 125

Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro Leu Tyr Asp
130 135 140

Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr Gly Leu Ser
145 150 155 160

Cys Gln Glu Gly Ala Ser Ala Thr Ala Ser Thr Gln Ala Asp Ile Ser
165 170 175

Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu Leu Leu Glu His
180 185 190

Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile Leu Met Asp
195 200 205

Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys Gly Val Val
210 215 220

```
Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln Glu Asn His Gln
225                 230                 235                 240

Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile Val Cys Phe Thr
                245                 250                 255

Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu Thr His Gly Asn
            260                 265                 270

Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr Glu Lys Val Ile
        275                 280                 285

Phe Pro Arg Gln Asp Asp Val Leu Ile Ser Phe Leu Pro Leu Ala His
    290                 295                 300

Met Phe Glu Arg Val Ile Gln Ser Val Val Tyr Cys His Gly Gly Arg
305                 310                 315                 320

Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser Asp Asp Met Lys
                325                 330                 335

Ala Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg Leu Leu Asn Arg
            340                 345                 350

Met Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro Leu Lys Arg Trp
        355                 360                 365

Leu Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu Val Arg Ser Gly
    370                 375                 380

Ile Ile Arg Asn Asp Ser Ile Trp Asp Glu Leu Phe Phe Asn Lys Ile
385                 390                 395                 400

Gln Ala Ser Leu Gly Gly Cys Val Arg Met Ile Val Thr Gly Ala Ala
                405                 410                 415

Pro Ala Ser Pro Thr Val Leu Gly Phe Leu Arg Ala Ala Leu Gly Cys
            420                 425                 430

Gln Val Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr Ala Gly Cys Thr
        435                 440                 445
```

```
Phe Thr Thr Pro Gly Asp Trp Thr Ser Gly His Val Gly Ala Pro Leu
    450                 455                 460

Pro Cys Asn His Ile Lys Leu Val Asp Val Glu Glu Leu Asn Tyr Trp
465                 470                 475                 480

Ala Cys Lys Gly Glu Gly Glu Ile Cys Val Arg Gly Pro Asn Val Phe
                485                 490                 495

Lys Gly Tyr Leu Lys Asp Pro Asp Arg Thr Lys Glu Ala Leu Asp Ser
            500                 505                 510

Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp Leu Pro Ala Gly
        515                 520                 525

Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe Lys Leu Ala Gln
    530                 535                 540

Gly Glu Tyr Val Ala Pro Glu Lys Ile Glu Asn Ile Tyr Ile Arg Ser
545                 550                 555                 560

Gln Pro Val Ala Gln Ile Tyr Val His Gly Asp Ser Leu Lys Ala Phe
                565                 570                 575

Leu Val Gly Ile Val Val Pro Asp Pro Glu Val Met Pro Ser Trp Ala
            580                 585                 590

Gln Lys Arg Gly Ile Glu Gly Thr Tyr Ala Asp Leu Cys Thr Asn Lys
        595                 600                 605

Asp Leu Lys Lys Ala Ile Leu Glu Asp Met Val Arg Leu Gly Lys Glu
    610                 615                 620

Ser Gly Leu His Ser Phe Glu Gln Val Lys Ala Ile His Ile His Ser
625                 630                 635                 640

Asp Met Phe Ser Val Gln Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala
                645                 650                 655

Lys Arg Pro Glu Leu Arg Glu Tyr Phe Lys Lys Gln Ile Glu Glu Leu
            660                 665                 670

Tyr Ser Ile Ser Met
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675

<210> 1994
<211> 712
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 508; "

<220>
<221> source
<223> /note="Gene Symbol: ACSL6; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase long-chain family
member 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKU0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000442124"

<400> 1994
Met Gln Thr Gln Glu Ile Leu Arg Ile Leu Arg Leu Pro Glu Leu Gly
1   5   10   15

Asp Leu Gly Gln Phe Phe Arg Ser Leu Ser Ala Thr Thr Leu Val Ser
            20   25   30

Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
        35   40   45

Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
    50   55   60

Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65   70   75   80

Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
                85   90   95

Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
            100   105   110

```
Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
        115                 120                 125

Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
    130                 135                 140

Cys Thr Asp Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp
145                 150                 155                 160

Ile Ile Val Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro
                165                 170                 175

Leu Tyr Asp Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr
            180                 185                 190

Gly Leu Ser Cys Gln Glu Gly Ala Ser Ala Thr Ala Ser Thr Gln Ala
        195                 200                 205

Asp Ile Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu Leu
    210                 215                 220

Leu Glu His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile Ile
225                 230                 235                 240

Leu Met Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys Cys
                245                 250                 255

Gly Val Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln Glu
            260                 265                 270

Asn His Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile Val
        275                 280                 285

Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu Thr
    290                 295                 300

His Gly Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr Glu
305                 310                 315                 320

Lys Val Ile Phe Pro Arg Gln Asp Asp Val Leu Ile Ser Phe Leu Pro
                325                 330                 335
```

```
Leu Ala His Met Phe Glu Arg Val Ile Gln Ser Val Val Tyr Cys His
            340                 345                 350

Gly Gly Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser Asp
        355                 360                 365

Asp Met Lys Ala Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg Leu
    370                 375                 380

Leu Asn Arg Met Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro Leu
385                 390                 395                 400

Lys Arg Trp Leu Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu Val
                405                 410                 415

Arg Ser Gly Ile Ile Arg Asn Asp Ser Ile Trp Asp Glu Leu Phe Phe
            420                 425                 430

Asn Lys Ile Gln Ala Ser Leu Gly Gly Cys Val Arg Met Ile Val Thr
        435                 440                 445

Gly Ala Ala Pro Ala Ser Pro Thr Val Leu Gly Phe Leu Arg Ala Ala
    450                 455                 460

Leu Gly Cys Gln Val Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr Ala
465                 470                 475                 480

Gly Cys Thr Phe Thr Thr Pro Gly Asp Trp Thr Ser Gly His Val Gly
                485                 490                 495

Ala Pro Leu Pro Cys Asn His Ile Lys Leu Val Asp Val Glu Glu Leu
            500                 505                 510

Asn Tyr Trp Ala Cys Lys Gly Glu Gly Glu Ile Cys Val Arg Gly Pro
        515                 520                 525

Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Asp Arg Thr Lys Glu Ala
    530                 535                 540

Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp Leu
545                 550                 555                 560
```

```
Pro Ala Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe Lys
                565                 570                 575

Leu Ala Gln Gly Glu Tyr Val Ala Pro Glu Lys Ile Glu Asn Ile Tyr
            580                 585                 590

Ile Arg Ser Gln Pro Val Ala Gln Ile Tyr Val His Gly Asp Ser Leu
        595                 600                 605

Lys Ala Phe Leu Val Gly Ile Val Val Pro Asp Pro Glu Val Met Pro
    610                 615                 620

Ser Trp Ala Gln Lys Arg Gly Ile Glu Gly Thr Tyr Ala Asp Leu Cys
625                 630                 635                 640

Thr Asn Lys Asp Leu Lys Lys Ala Ile Leu Glu Asp Met Val Arg Leu
                645                 650                 655

Gly Lys Glu Ser Gly Leu His Ser Phe Glu Gln Val Lys Ala Ile His
            660                 665                 670

Ile His Ser Asp Met Phe Ser Val Gln Asn Gly Leu Leu Thr Pro Thr
        675                 680                 685

Leu Lys Ala Lys Arg Pro Glu Leu Arg Glu Tyr Phe Lys Lys Gln Ile
    690                 695                 700

Glu Glu Leu Tyr Ser Ile Ser Met
705                 710


<210> 1995
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 509; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
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member 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q08AH1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000301956"

<400> 1995
Met Gln Trp Leu Met Arg Phe Arg Thr Leu Trp Gly Ile His Lys Ser
1   5   10   15

Phe His Asn Ile His Pro Ala Pro Ser Gln Leu Arg Cys Arg Ser Leu
            20   25   30

Ser Glu Phe Gly Ala Pro Arg Trp Asn Asp Tyr Glu Val Pro Glu Glu
        35   40   45

Phe Asn Phe Ala Ser Tyr Val Leu Asp Tyr Trp Ala Gln Lys Glu Lys
    50   55   60

Glu Gly Lys Arg Gly Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Gln
65   70   75   80

Gly Asp Glu Val Lys Trp Ser Phe Arg Glu Met Gly Asp Leu Thr Arg
                85   90   95

Arg Val Ala Asn Val Phe Thr Gln Thr Cys Gly Leu Gln Gln Gly Asp
            100   105   110

His Leu Ala Leu Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ala
        115   120   125

Val Gly Cys Met Arg Thr Gly Ile Ile Phe Ile Pro Ala Thr Ile Leu
    130   135   140

Leu Lys Ala Lys Asp Ile Leu Tyr Arg Leu Gln Leu Ser Lys Ala Lys
145   150   155   160

Gly Ile Val Thr Ile Asp Ala Leu Ala Ser Glu Val Asp Ser Ile Ala
                165   170   175

Ser Gln Cys Pro Ser Leu Lys Thr Lys Leu Leu Val Ser Asp His Ser
            180   185   190

```
Arg Glu Gly Trp Leu Asp Phe Arg Ser Leu Val Lys Ser Ala Ser Pro
        195                 200                 205

Glu His Thr Cys Val Lys Ser Lys Thr Leu Asp Pro Met Val Ile Phe
    210                 215                 220

Phe Thr Ser Gly Thr Thr Gly Phe Pro Lys Met Ala Lys His Ser His
225                 230                 235                 240

Gly Leu Ala Leu Gln Pro Ser Phe Pro Gly Ser Arg Lys Leu Arg Ser
                245                 250                 255

Leu Lys Thr Ser Asp Val Ser Trp Cys Leu Ser Asp Ser Gly Trp Ile
            260                 265                 270

Val Ala Thr Ile Trp Thr Leu Val Glu Pro Trp Thr Ala Gly Cys Thr
        275                 280                 285

Val Phe Ile His His Leu Pro Gln Phe Asp Thr Lys Val Ile Ile Gln
    290                 295                 300

Thr Leu Leu Lys Tyr Pro Ile Asn His Phe Trp Gly Val Ser Ser Ile
305                 310                 315                 320

Tyr Arg Met Ile Leu Gln Gln Asp Phe Thr Ser Ile Arg Phe Pro Ala
                325                 330                 335

Leu Glu His Cys Tyr Thr Gly Gly Glu Val Val Leu Pro Lys Asp Gln
            340                 345                 350

Glu Glu Trp Lys Arg Arg Thr Gly Leu Leu Leu Tyr Glu Asn Tyr Gly
        355                 360                 365

Gln Ser Glu Thr Gly Leu Ile Cys Ala Thr Tyr Trp Gly Met Lys Ile
    370                 375                 380

Lys Pro Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Val
385                 390                 395                 400

Ile Asp Asp Lys Gly Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile
                405                 410                 415
```

```
Gly Ile Arg Ile Lys Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr
            420                 425                 430

Glu Gly Asp Pro Glu Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr
        435                 440                 445

Asn Thr Gly Asp Arg Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe
    450                 455                 460

Leu Gly Arg Ser Asp Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly
465                 470                 475                 480

Pro Ala Glu Val Glu Ser Ala Leu Val Glu His Pro Ala Val Ala Glu
                485                 490                 495

Ser Ala Val Val Gly Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys
            500                 505                 510

Ala Phe Ile Val Leu Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln
        515                 520                 525

Leu Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr
    530                 535                 540

Lys Tyr Pro Arg Lys Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile
545                 550                 555                 560

Thr Gly Lys Ile Glu Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln
                565                 570                 575

Met
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<210> 1996
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 509; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q08AH1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428047"

<400> 1996
Met Gln Trp Leu Met Arg Phe Arg Thr Leu Trp Gly Ile His Lys Ser
1   5   10   15

Phe His Asn Ile His Pro Ala Pro Ser Gln Leu Arg Cys Arg Ser Leu
            20   25   30

Ser Glu Phe Gly Ala Pro Arg Trp Asn Asp Tyr Glu Val Pro Glu Glu
        35   40   45

Phe Asn Phe Ala Ser Tyr Val Leu Asp Tyr Trp Ala Gln Lys Glu Lys
    50   55   60

Glu Gly Lys Arg Gly Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Gln
65   70   75   80

Gly Asp Glu Val Lys Trp Ser Phe Arg Glu Met Gly Asp Leu Thr Arg
                85   90   95

Arg Val Ala Asn Val Phe Thr Gln Thr Cys Gly Leu Gln Gln Gly Asp
            100   105   110

His Leu Ala Leu Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ala
        115   120   125

Val Gly Cys Met Arg Thr Gly Ile Ile Phe Ile Pro Ala Thr Ile Leu
    130   135   140

Leu Lys Ala Lys Asp Ile Leu Tyr Arg Leu Gln Leu Ser Lys Ala Lys
145   150   155   160

Gly Ile Val Thr Ile Asp Ala Leu Ala Ser Glu Val Asp Ser Ile Ala

```
                165                 170                 175

Ser Gln Cys Pro Ser Leu Lys Thr Lys Leu Leu Val Ser Asp His Ser
            180                 185                 190

Arg Glu Gly Trp Leu Asp Phe Arg Ser Leu Val Lys Ser Ala Ser Pro
        195                 200                 205

Glu His Thr Cys Val Lys Ser Lys Thr Leu Asp Pro Met Val Ile Phe
    210                 215                 220

Phe Thr Ser Gly Thr Thr Gly Phe Pro Lys Met Ala Lys His Ser His
225                 230                 235                 240

Gly Leu Ala Leu Gln Pro Ser Phe Pro Gly Ser Arg Lys Leu Arg Ser
                245                 250                 255

Leu Lys Thr Ser Asp Val Ser Trp Cys Leu Ser Asp Ser Gly Trp Ile
            260                 265                 270

Val Ala Thr Ile Trp Thr Leu Val Glu Pro Trp Thr Ala Gly Cys Thr
        275                 280                 285

Val Phe Ile His His Leu Pro Gln Phe Asp Thr Lys Val Ile Ile Gln
    290                 295                 300

Thr Leu Leu Lys Tyr Pro Ile Asn His Phe Trp Gly Val Ser Ser Ile
305                 310                 315                 320

Tyr Arg Met Ile Leu Gln Gln Asp Phe Thr Ser Ile Arg Phe Pro Ala
                325                 330                 335

Leu Glu His Cys Tyr Thr Gly Gly Glu Val Val Leu Pro Lys Asp Gln
            340                 345                 350

Glu Glu Trp Lys Arg Arg Thr Gly Leu Leu Leu Tyr Glu Asn Tyr Gly
        355                 360                 365

Gln Ser Glu Thr Gly Leu Ile Cys Ala Thr Tyr Trp Gly Met Lys Ile
    370                 375                 380

Lys Pro Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Val
385                 390                 395                 400
```

```
Ile Asp Asp Lys Gly Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile
                405                 410                 415

Gly Ile Arg Ile Lys Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr
            420                 425                 430

Glu Gly Asp Pro Glu Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr
        435                 440                 445

Asn Thr Gly Asp Arg Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe
    450                 455                 460

Leu Gly Arg Ser Asp Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly
465                 470                 475                 480

Pro Ala Glu Val Glu Ser Ala Leu Val Glu His Pro Ala Val Ala Glu
                485                 490                 495

Ser Ala Val Val Gly Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys
            500                 505                 510

Ala Phe Ile Val Leu Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln
        515                 520                 525

Leu Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr
    530                 535                 540

Lys Tyr Pro Arg Lys Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile
545                 550                 555                 560

Thr Gly Lys Ile Glu Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln
                565                 570                 575

Met
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<210> 1997
<211> 249
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 509; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428098"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 1997

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Xaa Gln Phe Asp Thr Lys Val Ile Ile Gln Thr Leu Leu Lys Tyr Pro
1               5                  10                  15

Ile Asn His Phe Trp Gly Val Ser Ser Ile Tyr Arg Met Ile Leu Gln
            20                  25                  30

Gln Asp Phe Thr Ser Ile Arg Phe Pro Ala Leu Glu His Cys Tyr Thr
        35                  40                  45

Gly Gly Glu Val Val Leu Pro Lys Asp Gln Glu Glu Trp Lys Arg Arg
    50                  55                  60

Thr Gly Leu Leu Leu Tyr Glu Asn Tyr Gly Gln Ser Glu Thr Gly Leu
65                  70                  75                  80

Ile Cys Ala Thr Tyr Trp Gly Met Lys Ile Lys Pro Gly Phe Met Gly
                85                  90                  95

Lys Ala Thr Pro Pro Tyr Asp Val Gln Gly Asp Pro Glu Lys Thr Ala
            100                 105                 110

Lys Val Glu Cys Gly Asp Phe Tyr Asn Thr Gly Asp Arg Gly Lys Met
        115                 120                 125

Asp Glu Glu Gly Tyr Ile Cys Phe Leu Gly Arg Ser Asp Asp Ile Ile
    130                 135                 140
```

```
Asn Ala Ser Gly Tyr Arg Ile Gly Pro Ala Glu Val Glu Ser Ala Leu
145                 150                 155                 160

Val Glu His Pro Ala Val Ala Glu Ser Ala Val Val Gly Ser Pro Asp
                165                 170                 175

Pro Ile Arg Gly Glu Val Val Lys Ala Phe Ile Val Leu Thr Pro Gln
            180                 185                 190

Phe Leu Ser His Asp Lys Asp Gln Leu Thr Lys Glu Leu Gln Gln His
        195                 200                 205

Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Val Glu Phe
    210                 215                 220

Val Ser Glu Leu Pro Lys Thr Ile Thr Gly Lys Ile Glu Arg Lys Glu
225                 230                 235                 240

Leu Arg Lys Lys Glu Thr Gly Gln Met
                245
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<210> 1998
<211> 204
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 509; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q08AH1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428650"

<400> 1998
Met Gln Trp Leu Met Arg Phe Arg Thr Leu Trp Gly Ile His Lys Ser
1 5 10 15

Phe His Asn Ile His Pro Ala Pro Ser Gln Leu Arg Cys Arg Ser Leu
20 25 30

Ser Glu Phe Gly Ala Pro Arg Trp Asn Asp Tyr Glu Val Pro Glu Glu
35 40 45

Phe Asn Phe Ala Ser Tyr Val Leu Asp Tyr Trp Ala Gln Lys Glu Lys
50 55 60

Glu Gly Lys Arg Gly Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Gln
65 70 75 80

Gly Asp Glu Val Lys Trp Ser Phe Arg Glu Met Gly Asp Leu Thr Arg
85 90 95

Arg Val Ala Asn Val Phe Thr Gln Thr Cys Gly Leu Gln Gln Gly Asp
100 105 110

His Leu Ala Leu Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ala
115 120 125

Val Gly Cys Met Arg Thr Gly Ile Ile Phe Ile Pro Ala Thr Ile Leu
130 135 140

Leu Lys Ala Lys Asp Ile Leu Tyr Arg Leu Gln Leu Ser Lys Ala Lys
145 150 155 160

Gly Ile Val Thr Ile Asp Ala Leu Ala Ser Glu Val Asp Ser Ile Ala
165 170 175

Ser Gln Cys Pro Ser Leu Lys Thr Lys Leu Leu Val Ser Asp His Ser
180 185 190

Arg Glu Gly Trp Leu Asp Phe Arg Ser Leu Val Lys
195 200

<210> 1999
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 509; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428830"

<400> 1999
Met Gln Trp Leu Met Arg Phe Arg Thr Leu Trp Gly Ile His Lys Ser
1 5 10 15

Phe His Asn Ile His Pro Ala Pro Ser Gln Leu Arg Cys Arg Ser Leu
20 25 30

Ser Glu Phe Gly Ala Pro Arg Trp Asn Asp Tyr Glu Val Pro Glu Glu
35 40 45

Phe Asn Phe Ala Ser Tyr Val Leu Asp Tyr Trp Ala Gln Lys Glu Lys
50 55 60

Glu Gly Lys Arg Gly Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Gln
65 70 75 80

Gly Asp Glu Val Lys Trp Ser Phe Arg Glu Met Gly Asp Leu Thr Arg
85 90 95

Arg Val Ala Asn Val Phe Thr Gln Thr Cys Gly Leu Gln Gln Gly Asp
100 105 110

His Leu Ala Leu Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ala
115 120 125

Val Gly Cys Met Arg Thr Gly Ile Ile Phe Ile Pro Ala Thr Ile Leu
130 135 140

Leu Lys Ala Lys Asp Ile Leu Tyr Arg Leu

145 150

<210> 2000
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 510; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2A; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2A; "

<220>
<221> source
<223> /note="Uniprot ID: Q08AH3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000219054"

<400> 2000
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1 5 10 15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
20 25 30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
35 40 45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
50 55 60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65 70 75 80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Val
85 90 95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Val
100 105 110

```
Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Cys Ser
            260                 265                 270

Leu Met Glu Pro Trp Ala Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Val Thr
                325                 330                 335
```

```
Val Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350

Thr Gly Leu Asp Ile Arg Glu Ser Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
    370                 375                 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Ile Ile Asp Asp Lys Gly Asn
385                 390                 395                 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
                405                 410                 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Asp Asn Pro Asp Lys
            420                 425                 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
        435                 440                 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asn Asp
    450                 455                 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Glu His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Val Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560
```

Ala Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
565 570 575

Gln

<210> 2001
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 510; "

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member 2A; "

<220>
<221> source
<223> /note="Uniprot ID: Q08AH3; "

<220>
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<223> /note="ENSP ID: ENSP00000379411"

<400> 2001
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1 5 10 15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
20 25 30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
35 40 45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
50 55 60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65 70 75 80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Val

```
                85                  90                  95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Val
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Cys Ser
            260                 265                 270

Leu Met Glu Pro Trp Ala Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320
```

```
Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Val Thr
                325                 330                 335

Val Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350

Thr Gly Leu Asp Ile Arg Glu Ser Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
    370                 375                 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Ile Ile Asp Asp Lys Gly Asn
385                 390                 395                 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
                405                 410                 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Asp Asn Pro Asp Lys
            420                 425                 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
        435                 440                 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asn Asp
    450                 455                 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Glu His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Val Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540
```

```
Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560


Ala Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
                565                 570                 575


Gln



<210> 2002
<211> 498
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
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      acyl-CoA synthetase medium-chain family
      member 2A; "

<220>
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<223> /note="ENSP ID: ENSP00000392169"

<400> 2002
Met Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn
1               5                   10                  15


Val Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val
            20                  25                  30


Val Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile
        35                  40                  45


Arg Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr
    50                  55                  60


Asp Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala
65                  70                  75                  80
```

```
Gly Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro
                85                  90                  95

Ser Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp
            100                 105                 110

Leu Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys
        115                 120                 125

Val Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly
    130                 135                 140

Thr Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly
145                 150                 155                 160

Leu Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp
                165                 170                 175

Ile Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Cys
            180                 185                 190

Ser Leu Met Glu Pro Trp Ala Leu Gly Ala Cys Thr Phe Val His Leu
        195                 200                 205

Leu Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr
    210                 215                 220

Pro Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu
225                 230                 235                 240

Gln Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Val
                245                 250                 255

Thr Val Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala
            260                 265                 270

Gln Thr Gly Leu Asp Ile Arg Glu Ser Tyr Gly Gln Thr Glu Thr Gly
        275                 280                 285

Leu Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met
    290                 295                 300

Gly Thr Ala Ala Ser Cys Tyr Asp Val Gln Ile Ile Asp Asp Lys Gly
```

305 310 315 320

Asn Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys
325 330 335

Pro Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Asp Asn Pro Asp
340 345 350

Lys Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg
355 360 365

Gly Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asn
370 375 380

Asp Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu
385 390 395 400

Asn Ala Leu Met Glu His Pro Ala Val Val Glu Thr Ala Val Ile Ser
405 410 415

Ser Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Val Leu
420 425 430

Ala Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu
435 440 445

Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys
450 455 460

Ile Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln
465 470 475 480

Arg Ala Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg
485 490 495

Ala Gln

<210> 2003
<211> 577
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 510; "

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<223> /note="Gene Symbol: ACSM2A; "

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member 2A; "

<220>
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<223> /note="Uniprot ID: Q08AH3; "

<220>
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<223> /note="ENSP ID: ENSP00000459451"

<400> 2003

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Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1               5                  10                  15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20                  25                  30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35                  40                  45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50                  55                  60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65                  70                  75                  80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Val
                85                  90                  95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Val
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140
```

```
Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Cys Ser
            260                 265                 270

Leu Met Glu Pro Trp Ala Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Val Thr
                325                 330                 335

Val Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350

Thr Gly Leu Asp Ile Arg Glu Ser Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365
```

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
370 375 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Ile Ile Asp Asp Lys Gly Asn
385 390 395 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
405 410 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Asp Asn Pro Asp Lys
420 425 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
435 440 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asn Asp
450 455 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465 470 475 480

Ala Leu Met Glu His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
485 490 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Val Leu Ala
500 505 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
515 520 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
530 535 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545 550 555 560

Ala Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
565 570 575

Gln

<210> 2004

<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 510; "

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<223> /note="Gene Symbol: ACSM2A; "

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<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460031"

<400> 2004

Met	His	Trp	Leu	Arg	Lys	Val	Gln	Gly	Leu	Cys	Thr	Leu	Trp	Gly	Thr
1				5				10						15	

Gln	Met	Ser	Ser	Arg	Thr	Leu	Tyr	Ile	Asn	Ser	Arg	Gln	Leu	Val	Ser
			20					25					30		

Leu	Gln	Trp	Gly	His	Gln	Glu	Val	Pro	Ala	Lys	Phe	Asn	Phe	Ala	Ser
		35					40					45			

Asp	Val	Leu	Asp	His	Trp	Ala	Asp	Met	Glu	Lys	Ala	Gly	Lys	Arg	Leu
	50					55					60				

Pro	Ser	Pro	Ala	Leu	Trp	Trp	Val	Asn	Gly	Lys	Gly	Lys	Glu	Leu	Met
65					70					75					80

Trp	Asn	Phe	Arg	Glu	Leu	Ser	Glu	Asn	Ser	Gln	Gln	Ala	Ala	Asn	Val
				85					90					95	

Leu	Ser	Gly	Ala	Cys	Gly	Leu	Gln	Arg	Gly	Asp	Arg	Val	Ala	Val	Val
			100					105					110		

Leu	Pro	Arg	Val	Pro	Glu
		115			

<210> 2005
<211> 61

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ACSM2A; "

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<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460153"

<400> 2005
Met Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn
1 5 10 15

Val Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val
20 25 30

Val Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile
35 40 45

Arg Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met
50 55 60

<210> 2006
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 510; "

<220>
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member 2A; "

<220>
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<223> /note="Uniprot ID: Q08AH3; "

<220>
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<223> /note="ENSP ID: ENSP00000460349"

<400> 2006
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1   5   10   15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20   25   30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35   40   45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50   55   60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65   70   75   80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Val
                85   90   95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Val
            100   105   110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115   120   125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130   135   140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145   150   155   160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165   170   175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180   185   190

```
Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Cys Ser
            260                 265                 270

Leu Met Glu Pro Trp Ala Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Val Thr
                325                 330                 335

Val Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350

Thr Gly Leu Asp Ile Arg Glu Ser Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
    370                 375                 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Ile Ile Asp Asp Lys Gly Asn
385                 390                 395                 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
                405                 410                 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Asp Asn Pro Asp Lys
```

```
            420                 425                 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
        435                 440                 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asn Asp
    450                 455                 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Glu His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Val Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560

Ala Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
                565                 570                 575

Gln
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<210> 2007
<211> 208
<212> PRT
<213> Homo sapiens

<220>
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<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460884"

<400> 2007

```
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1               5                  10                  15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20                  25                  30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35                  40                  45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50                  55                  60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65                  70                  75                  80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Val
                85                  90                  95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Val
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190
```

Asn Phe Lys Lys Leu Leu Lys Tyr Lys Val Arg His Arg Asp Val Lys
195 200 205

<210> 2008
<211> 105
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 510; "

<220>
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<223> /note="Gene Symbol: ACSM2A; "

<220>
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acyl-CoA synthetase medium-chain family
member 2A; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460948"

<400> 2008
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1 5 10 15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
20 25 30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
35 40 45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
50 55 60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65 70 75 80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Val
85 90 95

Leu Ser Gly Ala Cys Gly Leu Gln Arg
100 105

<210> 2009
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2B; "

<220>
<221> source
<223> /note="Uniprot ID: Q68CK6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000327453"

<400> 2009
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1   5   10   15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20   25   30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35   40   45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50   55   60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65   70   75   80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
                85   90   95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Met
            100   105   110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg

```
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Gly Ser
            260                 265                 270

Leu Leu Glu Ser Trp Thr Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Leu Ala
                325                 330                 335

Gly Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350
```

```
Thr Gly Leu Asp Ile Arg Glu Phe Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
    370                 375                 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Val Ile Asp Asp Lys Gly Asn
385                 390                 395                 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
                405                 410                 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Glu Asn Pro Asp Lys
            420                 425                 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
        435                 440                 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asp Asp
    450                 455                 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Lys His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Ile Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560

Thr Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
                565                 570                 575
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Gln

<210> 2010
<211> 577
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 511; "

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<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
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acyl-CoA synthetase medium-chain family
member 2B; "

<220>
<221> source
<223> /note="Uniprot ID: Q68CK6; "

<220>
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<400> 2010
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1   5   10   15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20   25   30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35   40   45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50   55   60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65   70   75   80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
                85   90   95

```
Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Met
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Gly Ser
            260                 265                 270

Leu Leu Glu Ser Trp Thr Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Leu Ala
```

```
                325                 330                 335

Gly Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350

Thr Gly Leu Asp Ile Arg Glu Phe Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
    370                 375                 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Val Ile Asp Asp Lys Gly Asn
385                 390                 395                 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
                405                 410                 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Glu Asn Pro Asp Lys
            420                 425                 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
        435                 440                 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asp Asp
    450                 455                 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Lys His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Ile Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560
```

Thr Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
565 570 575

Gln

<210> 2011
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454247"

<400> 2011
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1 5 10 15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
20 25 30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
35 40 45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
50 55 60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65 70 75 80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
85 90 95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Met
100 105 110

Leu Pro Arg Val Pro Glu
115

<210> 2012
<211> 208
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
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<220>
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<223> /note="Gene Name:
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member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454887"

<400> 2012
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1 5 10 15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
20 25 30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
35 40 45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
50 55 60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65 70 75 80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
85 90 95

```
Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Met
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Lys Tyr Lys Val Arg His Arg Glu Val Lys
        195                 200                 205


<210> 2013
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
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<223> /note="Gene Symbol: ACSM2B; "

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      acyl-CoA synthetase medium-chain family
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<220>
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<223> /note="Uniprot ID:  Q68CK6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454995"

<400> 2013
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
```

```
1               5                   10                  15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20                  25                  30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35                  40                  45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50                  55                  60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65                  70                  75                  80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
                85                  90                  95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Met
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240
```

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
245 250 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Gly Ser
260 265 270

Leu Leu Glu Ser Trp Thr Leu Gly Ala Cys Thr Phe Val His Leu Leu
275 280 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
290 295 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305 310 315 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Leu Ala
325 330 335

Gly Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
340 345 350

Thr Gly Leu Asp Ile Arg Glu Phe Tyr Gly Gln Thr Glu Thr Gly Leu
355 360 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
370 375 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Val Ile Asp Asp Lys Gly Asn
385 390 395 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
405 410 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Glu Asn Pro Asp Lys
420 425 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
435 440 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asp Asp
450 455 460

```
Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Lys His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495

Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Ile Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560

Thr Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
                565                 570                 575

Gln
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<210> 2014
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455137"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2014
Xaa Ser Gly Tyr Val Glu Asn Pro Asp Lys Thr Ala Ala Asn Ile Arg
1   5   10   15

Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly Ile Lys Asp Glu Asp Gly
            20   25   30

Tyr Phe Gln Phe Met Gly Arg Ala Phe Val Ile Leu Ala Ser Gln Phe
        35   40   45

Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln Gln His Val
    50   55   60

Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile Glu Phe Val
65   70   75   80

Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg Thr Lys Leu
                85   90   95

Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala Gln
            100   105   110

<210> 2015
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455190"

<400> 2015
Met Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn
1   5   10   15

Ile Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val
            20   25   30

Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile
        35   40   45

Arg Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met
    50   55   60

<210> 2016
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455658"

<400> 2016
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1   5   10   15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20   25   30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35   40   45

Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50   55   60

```
Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65                  70                  75                  80


Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
                85                  90                  95


Leu Ser Gly Ala Cys Gly Leu Gln Arg
            100                 105


<210> 2017
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456369"

<400> 2017
Trp Leu Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His
1               5                   10                  15


Cys Val Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser
            20                  25                  30


Gly Thr Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu
        35                  40                  45


Gly Leu Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser
    50                  55                  60


Asp Ile Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu
65                  70                  75                  80


Gly Ser Leu Leu Glu Ser Trp Thr Leu Gly Ala Cys Thr Phe Val His
```

```
                85                  90                  95

Leu Leu Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Val Phe Arg Ser
            100                 105                 110

Thr Gln Pro Ile Val Asn Gln Lys Lys Phe Lys Ser Thr Tyr Lys Leu
        115                 120                 125

Glu Ala Pro Ala Ser Ser Cys Pro Thr Phe Leu Asp Gln Thr Asn Val
    130                 135                 140

Phe Phe Lys Cys Val
145


<210> 2018
<211> 577
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 2B; "

<220>
<221> source
<223> /note="Uniprot ID:  Q68CK6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456378"

<400> 2018
Met His Trp Leu Arg Lys Val Gln Gly Leu Cys Thr Leu Trp Gly Thr
1               5                   10                  15

Gln Met Ser Ser Arg Thr Leu Tyr Ile Asn Ser Arg Gln Leu Val Ser
            20                  25                  30

Leu Gln Trp Gly His Gln Glu Val Pro Ala Lys Phe Asn Phe Ala Ser
        35                  40                  45
```

```
Asp Val Leu Asp His Trp Ala Asp Met Glu Lys Ala Gly Lys Arg Leu
    50                  55                  60

Pro Ser Pro Ala Leu Trp Trp Val Asn Gly Lys Gly Lys Glu Leu Met
65                  70                  75                  80

Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn Ile
                85                  90                  95

Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val Met
            100                 105                 110

Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile Arg
        115                 120                 125

Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr Asp
    130                 135                 140

Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala Gly
145                 150                 155                 160

Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro Ser
                165                 170                 175

Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp Leu
            180                 185                 190

Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys Val
        195                 200                 205

Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly Thr
    210                 215                 220

Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly Leu
225                 230                 235                 240

Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp Ile
                245                 250                 255

Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Gly Ser
            260                 265                 270
```

```
Leu Leu Glu Ser Trp Thr Leu Gly Ala Cys Thr Phe Val His Leu Leu
        275                 280                 285

Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr Pro
    290                 295                 300

Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu Gln
305                 310                 315                 320

Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Leu Ala
                325                 330                 335

Gly Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala Gln
            340                 345                 350

Thr Gly Leu Asp Ile Arg Glu Phe Tyr Gly Gln Thr Glu Thr Gly Leu
        355                 360                 365

Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met Gly
    370                 375                 380

Thr Ala Ala Ser Cys Tyr Asp Val Gln Val Ile Asp Asp Lys Gly Asn
385                 390                 395                 400

Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys Pro
                405                 410                 415

Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Glu Asn Pro Asp Lys
            420                 425                 430

Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg Gly
        435                 440                 445

Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asp Asp
    450                 455                 460

Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu Asn
465                 470                 475                 480

Ala Leu Met Lys His Pro Ala Val Val Glu Thr Ala Val Ile Ser Ser
                485                 490                 495
```

```
Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Ile Leu Ala
            500                 505                 510

Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu Gln
        515                 520                 525

Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Ile
    530                 535                 540

Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln Arg
545                 550                 555                 560

Thr Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg Ala
                565                 570                 575

Gln
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<210> 2019
<211> 498
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457377"

<400> 2019

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Met Trp Asn Phe Arg Glu Leu Ser Glu Asn Ser Gln Gln Ala Ala Asn
1               5                   10                  15

Ile Leu Ser Gly Ala Cys Gly Leu Gln Arg Gly Asp Arg Val Ala Val
            20                  25                  30

Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ile Leu Gly Cys Ile
```

```
        35                  40                  45

Arg Ala Gly Leu Ile Phe Met Pro Gly Thr Ile Gln Met Lys Ser Thr
    50                  55                  60

Asp Ile Leu Tyr Arg Leu Gln Met Ser Lys Ala Lys Ala Ile Val Ala
65                  70                  75                  80

Gly Asp Glu Val Ile Gln Glu Val Asp Thr Val Ala Ser Glu Cys Pro
                85                  90                  95

Ser Leu Arg Ile Lys Leu Leu Val Ser Glu Lys Ser Cys Asp Gly Trp
            100                 105                 110

Leu Asn Phe Lys Lys Leu Leu Asn Glu Ala Ser Thr Thr His His Cys
        115                 120                 125

Val Glu Thr Gly Ser Gln Glu Ala Ser Ala Ile Tyr Phe Thr Ser Gly
    130                 135                 140

Thr Ser Gly Leu Pro Lys Met Ala Glu His Ser Tyr Ser Ser Leu Gly
145                 150                 155                 160

Leu Lys Ala Lys Met Asp Ala Gly Trp Thr Gly Leu Gln Ala Ser Asp
                165                 170                 175

Ile Met Trp Thr Ile Ser Asp Thr Gly Trp Ile Leu Asn Ile Leu Gly
            180                 185                 190

Ser Leu Leu Glu Ser Trp Thr Leu Gly Ala Cys Thr Phe Val His Leu
        195                 200                 205

Leu Pro Lys Phe Asp Pro Leu Val Ile Leu Lys Thr Leu Ser Ser Tyr
    210                 215                 220

Pro Ile Lys Ser Met Met Gly Ala Pro Ile Val Tyr Arg Met Leu Leu
225                 230                 235                 240

Gln Gln Asp Leu Ser Ser Tyr Lys Phe Pro His Leu Gln Asn Cys Leu
                245                 250                 255

Ala Gly Gly Glu Ser Leu Leu Pro Glu Thr Leu Glu Asn Trp Arg Ala
            260                 265                 270
```

```
Gln Thr Gly Leu Asp Ile Arg Glu Phe Tyr Gly Gln Thr Glu Thr Gly
        275                 280                 285

Leu Thr Cys Met Val Ser Lys Thr Met Lys Ile Lys Pro Gly Tyr Met
    290                 295                 300

Gly Thr Ala Ala Ser Cys Tyr Asp Val Gln Val Ile Asp Asp Lys Gly
305                 310                 315                 320

Asn Val Leu Pro Pro Gly Thr Glu Gly Asp Ile Gly Ile Arg Val Lys
                325                 330                 335

Pro Ile Arg Pro Ile Gly Ile Phe Ser Gly Tyr Val Glu Asn Pro Asp
            340                 345                 350

Lys Thr Ala Ala Asn Ile Arg Gly Asp Phe Trp Leu Leu Gly Asp Arg
        355                 360                 365

Gly Ile Lys Asp Glu Asp Gly Tyr Phe Gln Phe Met Gly Arg Ala Asp
    370                 375                 380

Asp Ile Ile Asn Ser Ser Gly Tyr Arg Ile Gly Pro Ser Glu Val Glu
385                 390                 395                 400

Asn Ala Leu Met Lys His Pro Ala Val Val Glu Thr Ala Val Ile Ser
                405                 410                 415

Ser Pro Asp Pro Val Arg Gly Glu Val Val Lys Ala Phe Val Ile Leu
            420                 425                 430

Ala Ser Gln Phe Leu Ser His Asp Pro Glu Gln Leu Thr Lys Glu Leu
        435                 440                 445

Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys
    450                 455                 460

Ile Glu Phe Val Leu Asn Leu Pro Lys Thr Val Thr Gly Lys Ile Gln
465                 470                 475                 480

Arg Thr Lys Leu Arg Asp Lys Glu Trp Lys Met Ser Gly Lys Ala Arg
                485                 490                 495
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Ala Gln

<210> 2020
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 511; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM2B; "

<220>
<221> source
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acyl-CoA synthetase medium-chain family
member 2B; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478316"

<400> 2020
Glu His Ser Tyr Ser Ser Leu Gly Leu Lys Ala Lys Met Asp Ala Gly
1 5 10 15

Trp Thr Gly Leu Gln Ala Ser Asp Ile Met Trp Thr Ile Ser Asp Thr
20 25 30

Gly Trp Ile Leu Asn Ile Leu Gly Ser Leu Leu Glu Ser Trp Thr Leu
35 40 45

Gly Ala Cys Thr Phe Val His Leu Leu Pro Lys Phe Asp Pro Leu Val
50 55 60

Ile Leu Lys Thr Leu Ser Ser Tyr Pro Ile Lys Ser Met Met Gly Ala
65 70 75 80

Pro Ile Val Tyr Arg Met Leu Leu Gln Gln Asp Leu Ser Ser Tyr Lys
85 90 95

Phe Pro His Leu Gln Asn Cys Leu Ala Gly Gly Glu Ser Leu Leu Pro
100 105 110

```
Glu Thr Leu Glu Asn Trp Arg Ala Gln Thr Gly Leu Asp Ile Arg Glu
        115                 120                 125

Phe Tyr Gly Gln Thr Glu Thr Gly Leu Thr Cys Met Val Ser Lys Thr
    130                 135                 140

Met Lys Ile Lys Pro Gly Tyr Met Gly Thr Ala Ala Ser Cys Tyr Asp
145                 150                 155                 160

Val Gln Val Ile Asp Asp Lys Gly Asn Val Leu Pro Pro Gly Thr Glu
                165                 170                 175

Gly Asp Ile Gly Ile Arg Val Lys Pro Ile Arg Pro Ile Gly Ile Phe
            180                 185                 190

Ser Gly Tyr Val Val Ser Ser Pro
        195                 200


<210> 2021
<211> 586
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
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<223> /note="Gene Name:
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      member 3; "

<220>
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<223> /note="Uniprot ID:  Q53FZ2; "

<220>
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<223> /note="ENSP ID: ENSP00000289416"

<400> 2021
Met Leu Ala Arg Val Thr Arg Lys Met Leu Arg His Ala Lys Cys Phe
1               5                   10                  15

Gln Arg Leu Ala Ile Phe Gly Ser Val Arg Ala Leu His Lys Asp Asn
```

```
            20                  25                  30

Arg Thr Ala Thr Pro Gln Asn Phe Ser Asn Tyr Glu Ser Met Lys Gln
        35                  40                  45

Asp Phe Lys Leu Gly Ile Pro Glu Tyr Phe Asn Phe Ala Lys Asp Val
    50                  55                  60

Leu Asp Gln Trp Thr Asp Lys Glu Lys Ala Gly Lys Lys Pro Ser Asn
65                  70                  75                  80

Pro Ala Phe Trp Trp Ile Asn Arg Asn Gly Glu Glu Met Arg Trp Ser
                85                  90                  95

Phe Glu Glu Leu Gly Ser Leu Ser Arg Lys Phe Ala Asn Ile Leu Ser
            100                 105                 110

Glu Ala Cys Ser Leu Gln Arg Gly Asp Arg Val Ile Leu Ile Leu Pro
        115                 120                 125

Arg Val Pro Glu Trp Trp Leu Ala Asn Val Ala Cys Leu Arg Thr Gly
    130                 135                 140

Thr Val Leu Ile Pro Gly Thr Thr Gln Leu Thr Gln Lys Asp Ile Leu
145                 150                 155                 160

Tyr Arg Leu Gln Ser Ser Lys Ala Asn Cys Ile Ile Thr Asn Asp Val
                165                 170                 175

Leu Ala Pro Ala Val Asp Ala Val Ala Ser Lys Cys Glu Asn Leu His
            180                 185                 190

Ser Lys Leu Ile Val Ser Glu Asn Ser Arg Glu Gly Trp Gly Asn Leu
        195                 200                 205

Lys Glu Leu Met Lys His Ala Ser Asp Ser His Thr Cys Val Lys Thr
    210                 215                 220

Lys His Asn Glu Ile Met Ala Ile Phe Phe Thr Ser Gly Thr Ser Gly
225                 230                 235                 240

Tyr Pro Lys Met Thr Ala His Thr His Ser Ser Phe Gly Leu Gly Leu
                245                 250                 255
```

```
Ser Val Asn Gly Arg Phe Trp Leu Asp Leu Thr Pro Ser Asp Val Met
            260                 265                 270

Trp Asn Thr Ser Asp Thr Gly Trp Ala Lys Ser Ala Trp Ser Ser Val
        275                 280                 285

Phe Ser Pro Trp Ile Gln Gly Ala Cys Val Phe Thr His His Leu Pro
    290                 295                 300

Arg Phe Glu Pro Thr Ser Ile Leu Gln Thr Leu Ser Lys Tyr Pro Ile
305                 310                 315                 320

Thr Val Phe Cys Ser Ala Pro Thr Val Tyr Arg Met Leu Val Gln Asn
                325                 330                 335

Asp Ile Thr Ser Tyr Lys Phe Lys Ser Leu Lys His Cys Val Ser Ala
            340                 345                 350

Gly Glu Pro Ile Thr Pro Asp Val Thr Glu Lys Trp Arg Asn Lys Thr
        355                 360                 365

Gly Leu Asp Ile Tyr Glu Gly Tyr Gly Gln Thr Glu Thr Val Leu Ile
    370                 375                 380

Cys Gly Asn Phe Lys Gly Met Lys Ile Lys Pro Gly Ser Met Gly Lys
385                 390                 395                 400

Pro Ser Pro Ala Phe Asp Val Lys Ile Val Asp Val Asn Gly Asn Val
                405                 410                 415

Leu Pro Pro Gly Gln Glu Gly Asp Ile Gly Ile Gln Val Leu Pro Asn
            420                 425                 430

Arg Pro Phe Gly Leu Phe Thr His Tyr Val Asp Asn Pro Ser Lys Thr
        435                 440                 445

Ala Ser Thr Leu Arg Gly Asn Phe Tyr Ile Thr Gly Asp Arg Gly Tyr
    450                 455                 460

Met Asp Lys Asp Gly Tyr Phe Trp Phe Val Ala Arg Ala Asp Asp Val
465                 470                 475                 480
```

```
Ile Leu Ser Ser Gly Tyr Arg Ile Gly Pro Phe Glu Val Glu Asn Ala
                485                 490                 495

Leu Asn Glu His Pro Ser Val Ala Glu Ser Ala Val Val Ser Ser Pro
            500                 505                 510

Asp Pro Ile Arg Gly Glu Val Val Lys Ala Phe Val Val Leu Asn Pro
        515                 520                 525

Asp Tyr Lys Ser His Asp Gln Glu Gln Leu Ile Lys Glu Ile Gln Glu
    530                 535                 540

His Val Lys Lys Thr Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Val Glu
545                 550                 555                 560

Phe Ile Gln Glu Leu Pro Lys Thr Ile Ser Gly Lys Thr Lys Arg Asn
                565                 570                 575

Glu Leu Arg Lys Lys Glu Trp Lys Thr Ile
            580                 585
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<210> 2022
<211> 438
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 512; "

<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q53FZ2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000394565"

<400> 2022

```
Met Leu Ala Arg Val Thr Arg Lys Met Leu Arg His Ala Lys Cys Phe
1               5                  10                  15

Gln Arg Leu Ala Ile Phe Gly Ser Val Arg Ala Leu His Lys Asp Asn
            20                  25                  30

Arg Thr Ala Thr Pro Gln Asn Phe Ser Asn Tyr Glu Ser Met Lys Gln
        35                  40                  45

Asp Phe Lys Leu Gly Ile Pro Glu Tyr Phe Asn Phe Ala Lys Asp Val
    50                  55                  60

Leu Asp Gln Trp Thr Asp Lys Glu Lys Ala Gly Lys Lys Pro Ser Asn
65                  70                  75                  80

Pro Ala Phe Trp Trp Ile Asn Arg Asn Gly Glu Glu Met Arg Trp Ser
                85                  90                  95

Phe Glu Glu Leu Gly Ser Leu Ser Arg Lys Phe Ala Asn Ile Leu Ser
            100                 105                 110

Glu Ala Cys Ser Leu Gln Arg Gly Asp Arg Val Ile Leu Ile Leu Pro
        115                 120                 125

Arg Val Pro Glu Trp Trp Leu Ala Asn Val Ala Cys Leu Arg Thr Gly
    130                 135                 140

Thr Val Leu Ile Pro Gly Thr Thr Gln Leu Thr Gln Lys Asp Ile Leu
145                 150                 155                 160

Tyr Arg Leu Gln Ser Ser Lys Ala Asn Cys Ile Ile Thr Asn Asp Val
                165                 170                 175

Leu Ala Pro Ala Val Asp Ala Val Ala Ser Lys Cys Glu Asn Leu His
            180                 185                 190

Ser Lys Leu Ile Val Ser Glu Asn Ser Arg Glu Gly Trp Gly Asn Leu
        195                 200                 205

Lys Glu Leu Met Lys His Ala Ser Asp Ser His Thr Cys Val Lys Thr
    210                 215                 220

Lys His Asn Glu Ile Met Ala Ile Phe Phe Thr Ser Gly Thr Ser Gly
```

225 230 235 240

Tyr Pro Lys Met Thr Ala His Thr His Ser Ser Phe Gly Leu Gly Leu
245 250 255

Ser Val Asn Gly Arg Phe Trp Leu Asp Leu Thr Pro Ser Asp Val Met
260 265 270

Trp Asn Thr Ser Asp Thr Gly Trp Ala Lys Ser Ala Trp Ser Ser Val
275 280 285

Phe Ser Pro Trp Ile Gln Gly Ala Cys Val Phe Thr His His Leu Pro
290 295 300

Arg Phe Glu Pro Thr Ser Ile Leu Gln Thr Leu Ser Lys Tyr Pro Ile
305 310 315 320

Thr Val Phe Cys Ser Ala Pro Thr Val Tyr Arg Met Leu Val Gln Asn
325 330 335

Asp Ile Thr Ser Tyr Lys Phe Lys Ser Leu Lys His Cys Val Ser Ala
340 345 350

Gly Glu Pro Ile Thr Pro Asp Val Thr Glu Lys Trp Arg Asn Lys Thr
355 360 365

Gly Leu Asp Ile Tyr Glu Gly Tyr Gly Gln Thr Glu Thr Val Leu Ile
370 375 380

Cys Gly Asn Phe Lys Gly Met Lys Ile Lys Pro Gly Ser Met Gly Lys
385 390 395 400

Pro Ser Pro Ala Phe Asp Val Lys Val Cys Thr Ser Pro Ser Arg Arg
405 410 415

Met Phe Asn Asn Pro Ile Cys Thr Leu Pro Thr Tyr Arg Leu Pro Pro
420 425 430

Tyr Lys Leu Ser Leu Leu
435

<210> 2023
<211> 52

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456055"

<400> 2023
Met Leu Ala Arg Val Thr Arg Lys Met Leu Arg His Ala Lys Cys Phe
1 5 10 15

Gln Arg Leu Ala Ile Phe Gly Ser Val Arg Ala Leu His Lys Asp Asn
20 25 30

Arg Thr Ala Thr Pro Gln Asn Phe Ser Asn Tyr Glu Ser Met Lys Gln
35 40 45

Asp Phe Lys Leu
50

<210> 2024
<211> 582
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456767"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2024
Xaa Tyr Glu Ser Met Lys Gln Asp Phe Lys Leu Gly Ile Pro Glu Tyr
1 5 10 15

Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Thr Asp Lys Glu Lys
20 25 30

Ala Gly Lys Lys Pro Ser Asn Pro Ala Phe Trp Trp Ile Asn Arg Asn
35 40 45

Gly Glu Glu Met Arg Trp Ser Phe Glu Glu Leu Gly Ser Leu Ser Arg
50 55 60

Lys Phe Ala Asn Ile Leu Ser Glu Ala Cys Ser Leu Gln Arg Gly Asp
65 70 75 80

Arg Val Ile Leu Ile Leu Pro Arg Val Pro Glu Trp Trp Leu Ala Asn
85 90 95

Val Ala Cys Leu Arg Thr Gly Thr Val Leu Ile Pro Gly Thr Thr Gln
100 105 110

Leu Thr Gln Lys Asp Ile Leu Tyr Arg Leu Gln Ser Ser Lys Ala Asn
115 120 125

Cys Ile Ile Thr Asn Asp Val Leu Ala Pro Ala Val Asp Ala Val Ala
130 135 140

Ser Lys Cys Glu Asn Leu His Ser Lys Leu Ile Val Ser Glu Asn Ser
145 150 155 160

Arg Glu Gly Trp Gly Asn Leu Lys Glu Leu Met Lys Val Phe Leu Cys
165 170 175

His Pro Gly Trp Ser Thr Val Ala Arg Ser Trp Leu Thr Ala Thr Ser
180 185 190

```
Thr Ser Leu Val Gln Ala Ile Leu Ser Leu Leu Ser Ser Trp Asp Tyr
        195                 200                 205

Arg His Ala Ser Asp Ser His Thr Cys Val Lys Thr Lys His Asn Glu
    210                 215                 220

Ile Met Ala Ile Phe Phe Thr Ser Gly Thr Ser Gly Tyr Pro Lys Met
225                 230                 235                 240

Thr Ala His Thr His Ser Ser Phe Gly Leu Gly Leu Ser Val Asn Gly
                245                 250                 255

Arg Phe Trp Leu Asp Leu Thr Pro Ser Asp Val Met Trp Asn Thr Ser
            260                 265                 270

Asp Thr Gly Trp Ala Lys Ser Ala Trp Ser Ser Val Phe Ser Pro Trp
        275                 280                 285

Ile Gln Gly Ala Cys Val Phe Thr His His Leu Pro Arg Phe Glu Pro
    290                 295                 300

Thr Ser Ile Leu Gln Thr Leu Ser Lys Tyr Pro Ile Thr Val Phe Cys
305                 310                 315                 320

Ser Ala Pro Thr Val Tyr Arg Met Leu Val Gln Asn Asp Ile Thr Ser
                325                 330                 335

Tyr Lys Phe Lys Ser Leu Lys His Cys Val Ser Ala Gly Glu Pro Ile
            340                 345                 350

Thr Pro Asp Val Thr Glu Lys Trp Arg Asn Lys Thr Gly Leu Asp Ile
        355                 360                 365

Tyr Glu Gly Tyr Gly Gln Thr Glu Thr Val Leu Ile Cys Gly Asn Phe
    370                 375                 380

Lys Gly Met Lys Ile Lys Pro Gly Ser Met Gly Lys Pro Ser Pro Ala
385                 390                 395                 400

Phe Asp Val Lys Ile Val Asp Val Asn Gly Asn Val Leu Pro Pro Gly
                405                 410                 415
```

```
Gln Glu Gly Asp Ile Gly Ile Gln Val Leu Pro Asn Arg Pro Phe Gly
            420                 425                 430

Leu Phe Thr His Tyr Val Asp Asn Pro Ser Lys Thr Ala Ser Thr Leu
        435                 440                 445

Arg Gly Asn Phe Tyr Ile Thr Gly Asp Arg Gly Tyr Met Asp Lys Asp
    450                 455                 460

Gly Tyr Phe Trp Phe Val Ala Arg Ala Asp Asp Val Ile Leu Ser Ser
465                 470                 475                 480

Gly Tyr Arg Ile Gly Pro Phe Glu Val Glu Asn Ala Leu Asn Glu His
                485                 490                 495

Pro Ser Val Ala Glu Ser Ala Val Val Ser Ser Pro Asp Pro Ile Arg
            500                 505                 510

Gly Glu Val Val Lys Ala Phe Val Val Leu Asn Pro Asp Tyr Lys Ser
        515                 520                 525

His Asp Gln Glu Gln Leu Ile Lys Glu Ile Gln Glu His Val Lys Lys
    530                 535                 540

Thr Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Val Glu Phe Ile Gln Glu
545                 550                 555                 560

Leu Pro Lys Thr Ile Ser Gly Lys Thr Lys Arg Asn Glu Leu Arg Lys
                565                 570                 575

Lys Glu Trp Lys Thr Ile
            580
```

<210> 2025
<211> 100
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 512; "

<220>
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<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457003"

<400> 2025
Met Leu Ala Arg Val Thr Arg Lys Met Leu Arg His Ala Lys Cys Phe
1 5 10 15

Gln Arg Leu Ala Ile Phe Gly Ser Val Arg Ala Leu His Lys Asp Asn
20 25 30

Arg Thr Ala Thr Pro Gln Asn Phe Ser Asn Tyr Glu Ser Met Lys Gln
35 40 45

Asp Phe Lys Leu Gly Ile Pro Glu Tyr Phe Asn Phe Ala Lys Asp Val
50 55 60

Leu Asp Gln Trp Thr Asp Lys Glu Lys Ala Gly Lys Lys Pro Ser Asn
65 70 75 80

Pro Ala Phe Trp Trp Ile Asn Arg Asn Gly Glu Glu Met Arg Trp Ser
85 90 95

Phe Glu Glu Leu
100

<210> 2026
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family

member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457158"

<400> 2026
Met Leu Ala Arg Val Thr Arg Lys Met Leu Arg His Ala Lys Cys Phe
1   5   10   15

Gln Arg Leu Ala Ile Phe Gly Ser Val
            20   25

<210> 2027
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457608"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2027
Xaa Lys Trp Arg Asn Lys Thr Gly Leu Asp Ile Tyr Glu Gly Tyr Gly
1   5   10   15

Gln Thr Glu Thr Val Leu Ile Cys Gly Asn Phe Lys Gly Met Lys Ile
            20   25   30

Lys Pro Gly Ser Met Gly Lys Pro Ser Pro Ala Phe Asp Val Lys Ile
        35   40   45

```
Val Asp Val Asn Gly Asn Val Leu Pro Pro Gly Gln Glu Gly Asp Ile
    50                  55                  60

Gly Ile Gln Val Leu Pro Asn Arg Pro Phe Gly Leu Phe Thr His Tyr
65                  70                  75                  80

Val Val Val Lys Ala Phe Val Val Leu Asn Pro Asp Tyr Lys Ser His
                85                  90                  95

Asp Gln Glu Gln Leu Ile Lys Glu Ile Gln Glu His Val Lys Lys Thr
            100                 105                 110

Thr Ala Pro Tyr Lys Tyr Pro Arg Lys Val Glu Phe Ile Gln Glu Leu
        115                 120                 125

Pro Lys Thr Ile Ser Gly Lys
    130                 135


<210> 2028
<211> 235
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457926"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2028
Xaa Ser Leu Leu Ser Ser Trp Asp Tyr Arg His Ala Ser Asp Ser His
1               5                   10                  15
```

```
Thr Cys Val Lys Thr Lys His Asn Glu Ile Met Ala Ile Phe Phe Thr
            20                  25                  30

Ser Gly Thr Ser Gly Tyr Pro Lys Met Thr Ala His Thr His Ser Ser
        35                  40                  45

Phe Gly Leu Gly Leu Ser Val Asn Gly Arg Phe Trp Leu Asp Leu Thr
    50                  55                  60

Pro Ser Asp Val Met Trp Asn Thr Ser Asp Thr Gly Trp Ala Lys Ser
65                  70                  75                  80

Ala Trp Ser Ser Val Phe Ser Pro Trp Ile Gln Gly Ala Cys Val Phe
                85                  90                  95

Thr His His Leu Pro Arg Phe Glu Pro Thr Ser Ile Leu Gln Thr Leu
            100                 105                 110

Ser Lys Tyr Pro Ile Thr Val Phe Cys Ser Ala Pro Thr Val Tyr Arg
        115                 120                 125

Met Leu Val Gln Asn Asp Ile Thr Ser Tyr Lys Phe Lys Ser Leu Lys
    130                 135                 140

His Cys Val Ser Ala Gly Glu Pro Ile Thr Pro Asp Val Thr Glu Lys
145                 150                 155                 160

Trp Arg Asn Lys Thr Gly Leu Asp Ile Tyr Glu Gly Tyr Gly Gln Thr
                165                 170                 175

Glu Thr Val Leu Ile Cys Gly Asn Phe Lys Gly Met Lys Ile Lys Pro
            180                 185                 190

Gly Ser Met Gly Lys Pro Ser Pro Ala Phe Asp Val Lys Val Cys Thr
        195                 200                 205

Ser Pro Ser Arg Arg Met Phe Asn Asn Pro Ile Cys Thr Leu Pro Thr
    210                 215                 220

Tyr Arg Leu Pro Pro Tyr Lys Leu Ser Leu Leu
225                 230                 235
```

<210> 2029
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 512; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458068"

<400> 2029
Met Leu Ala Arg Val Thr Arg Lys Met Leu Arg His Ala Lys Cys Phe
1 5 10 15

Gln Arg Leu Ala Ile Phe Gly Ser Val Arg Ala Leu His Lys Asp Asn
20 25 30

Arg Thr Ala Thr Pro Gln Asn Phe Ser Asn Tyr Glu Ser Met Lys Gln
35 40 45

Asp Phe Lys Leu Gly Ile Pro Glu Tyr Phe Asn Phe Ala Lys Asp Val
50 55 60

Leu Asp Gln Trp Thr Asp Lys Glu Lys Ala Gly Lys Lys Pro Ser Asn
65 70 75 80

Pro Ala Phe Trp Trp Ile Asn Arg Asn Gly Glu Glu Met Arg Trp Ser
85 90 95

Phe Glu Glu Leu Gly Ser Leu Ser Arg Lys Phe Ala Asn Ile Leu Ser
100 105 110

Glu Ala Cys Ser Leu Gln Arg Gly Asp Arg Val Ile Leu Ile Leu Pro
115 120 125

Arg Val Pro Glu Trp Trp Leu Ala Asn Val Ala Cys Leu Arg Thr Gly

```
    130                 135                 140

Thr Val Leu Ile Pro Gly Thr Thr Gln Leu Thr Gln Lys Asp
145                 150                 155


<210> 2030
<211> 580
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 513; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 4; "

<220>
<221> source
<223> /note="Uniprot ID:  P0C7M7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000382349"

<400> 2030
Met Lys Ile Phe Phe Arg Tyr Gln Thr Phe Arg Phe Ile Trp Leu Thr
1               5                   10                  15


Lys Pro Pro Gly Arg Arg Leu His Lys Asp His Gln Leu Trp Thr Pro
            20                  25                  30


Leu Thr Leu Ala Asp Phe Glu Ala Ile Asn Arg Cys Asn Arg Pro Leu
        35                  40                  45


Pro Lys Asn Phe Asn Phe Ala Ala Asp Val Leu Asp Gln Trp Ser Gln
    50                  55                  60


Lys Glu Lys Thr Gly Glu Arg Pro Ala Asn Pro Ala Leu Trp Trp Val
65                  70                  75                  80


Asn Gly Lys Gly Asp Glu Val Lys Trp Ser Phe Arg Glu Leu Gly Ser
                85                  90                  95
```

```
Leu Ser Arg Lys Ala Ala Asn Val Leu Thr Lys Pro Cys Gly Leu Gln
            100                 105                 110

Arg Gly Asp Arg Leu Ala Val Ile Leu Pro Arg Ile Pro Glu Trp Trp
        115                 120                 125

Leu Val Asn Val Ala Cys Ile Arg Thr Gly Ile Ile Phe Met Pro Gly
    130                 135                 140

Thr Ile Gln Leu Thr Ala Lys Asp Ile Leu Tyr Arg Leu Arg Ala Ser
145                 150                 155                 160

Lys Ala Lys Cys Ile Val Ala Ser Glu Glu Val Ala Pro Ala Val Glu
                165                 170                 175

Ser Ile Val Leu Glu Cys Pro Asp Leu Lys Thr Lys Leu Leu Val Ser
            180                 185                 190

Pro Gln Ser Trp Asn Gly Trp Leu Ser Phe Gln Glu Leu Phe Gln Phe
        195                 200                 205

Ala Ser Glu Glu His Ser Cys Val Glu Thr Gly Ser Gln Glu Pro Met
    210                 215                 220

Thr Ile Tyr Phe Thr Ser Gly Thr Thr Gly Phe Pro Lys Met Ala Gln
225                 230                 235                 240

His Ser Gln Ser Ser Leu Gly Ile Gly Phe Thr Leu Cys Gly Arg Tyr
                245                 250                 255

Trp Leu Asp Leu Lys Ser Ser Asp Ile Ile Trp Asn Met Ser Asp Thr
            260                 265                 270

Gly Trp Val Lys Ala Ala Ile Gly Ser Val Phe Ser Ser Trp Leu Cys
        275                 280                 285

Gly Ala Cys Val Phe Val His Arg Met Ala Gln Phe Asp Thr Asp Thr
    290                 295                 300

Phe Leu Asp Thr Leu Thr Thr Tyr Pro Ile Thr Thr Leu Cys Ser Pro
305                 310                 315                 320
```

Pro Thr Val Tyr Arg Met Leu Val Gln Lys Asp Leu Lys Arg Tyr Lys
325 330 335

Phe Lys Ser Leu Arg His Cys Leu Thr Gly Gly Glu Pro Leu Asn Pro
340 345 350

Glu Val Leu Glu Gln Trp Arg Val Gln Thr Gly Leu Glu Leu Tyr Glu
355 360 365

Gly Tyr Gly Gln Thr Glu Val Gly Met Ile Cys Ala Asn Gln Lys Gly
370 375 380

Gln Glu Ile Lys Pro Gly Ser Met Gly Lys Gly Met Leu Pro Tyr Asp
385 390 395 400

Val Gln Ile Ile Asp Glu Asn Gly Asn Val Leu Pro Pro Gly Lys Glu
405 410 415

Gly Glu Ile Ala Leu Arg Leu Lys Pro Thr Arg Pro Phe Cys Phe Phe
420 425 430

Ser Lys Tyr Val Asp Asn Pro Gln Lys Thr Ala Ala Thr Ile Arg Gly
435 440 445

Asp Phe Tyr Val Thr Gly Asp Arg Gly Val Met Asp Ser Asp Gly Tyr
450 455 460

Phe Trp Phe Val Gly Arg Ala Asp Asp Val Ile Ile Ser Ser Gly Tyr
465 470 475 480

Arg Ile Gly Pro Phe Glu Val Glu Ser Ala Leu Ile Glu His Pro Ala
485 490 495

Val Val Glu Ser Ala Val Val Ser Ser Pro Asp Gln Ile Arg Gly Glu
500 505 510

Val Val Lys Ala Phe Val Val Leu Ala Ala Pro Phe Lys Ser Tyr Asn
515 520 525

Pro Glu Lys Leu Thr Leu Glu Leu Gln Asp His Val Lys Lys Ser Thr
530 535 540

```
Ala Pro Tyr Lys Tyr Pro Arg Lys Val Glu Phe Val Gln Glu Leu Pro
545                 550                 555                 560


Lys Thr Ile Thr Gly Lys Ile Lys Arg Asn Val Leu Arg Asp Gln Glu
                565                 570                 575


Trp Arg Gly Arg
            580


<210> 2031
<211> 579
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 514; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 5; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6NUN0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000327916"

<400> 2031
Met Arg Pro Trp Leu Arg His Leu Val Leu Gln Ala Leu Arg Asn Ser
1               5                   10                  15


Arg Ala Phe Cys Gly Ser His Gly Lys Pro Ala Pro Leu Pro Val Pro
            20                  25                  30


Gln Lys Ile Val Ala Thr Trp Glu Ala Ile Ser Leu Gly Arg Gln Leu
        35                  40                  45


Val Pro Glu Tyr Phe Asn Phe Ala His Asp Val Leu Asp Val Trp Ser
    50                  55                  60


Arg Leu Glu Glu Ala Gly His Arg Pro Pro Asn Pro Ala Phe Trp Trp
```

65 70 75 80

Val Asn Gly Thr Gly Ala Glu Ile Lys Trp Ser Phe Glu Glu Leu Gly
85 90 95

Lys Gln Ser Arg Lys Ala Ala Asn Val Leu Gly Gly Ala Cys Gly Leu
100 105 110

Gln Pro Gly Asp Arg Met Met Leu Val Leu Pro Arg Leu Pro Glu Trp
115 120 125

Trp Leu Val Ser Val Ala Cys Met Arg Thr Gly Thr Val Met Ile Pro
130 135 140

Gly Val Thr Gln Leu Thr Glu Lys Asp Leu Lys Tyr Arg Leu Gln Ala
145 150 155 160

Ser Arg Ala Lys Ser Ile Ile Thr Ser Asp Ser Leu Ala Pro Arg Val
165 170 175

Asp Ala Ile Ser Ala Glu Cys Pro Ser Leu Gln Thr Lys Leu Leu Val
180 185 190

Ser Asp Ser Ser Arg Pro Gly Trp Leu Asn Phe Arg Glu Leu Leu Arg
195 200 205

Glu Ala Ser Thr Glu His Asn Cys Met Arg Thr Lys Ser Arg Asp Pro
210 215 220

Leu Ala Ile Tyr Phe Thr Ser Gly Thr Thr Gly Ala Pro Lys Met Val
225 230 235 240

Glu His Ser Gln Ser Ser Tyr Gly Leu Gly Phe Val Ala Ser Gly Arg
245 250 255

Arg Trp Val Ala Leu Thr Glu Ser Asp Ile Phe Trp Asn Thr Thr Asp
260 265 270

Thr Gly Trp Val Lys Ala Ala Trp Thr Leu Phe Ser Ala Trp Pro Asn
275 280 285

Gly Ser Cys Ile Phe Val His Glu Leu Pro Arg Val Asp Ala Lys Val
290 295 300

```
Ile Leu Asn Thr Leu Ser Lys Phe Pro Ile Thr Thr Leu Cys Cys Val
305                 310                 315                 320

Pro Thr Ile Phe Arg Leu Leu Val Gln Glu Asp Leu Thr Arg Tyr Gln
                325                 330                 335

Phe Gln Ser Leu Arg His Cys Leu Thr Gly Gly Glu Ala Leu Asn Pro
            340                 345                 350

Asp Val Arg Glu Lys Trp Lys His Gln Thr Gly Val Glu Leu Tyr Glu
        355                 360                 365

Gly Tyr Gly Gln Ser Glu Thr Val Val Ile Cys Ala Asn Pro Lys Gly
    370                 375                 380

Met Lys Ile Lys Ser Gly Ser Met Gly Lys Ala Ser Pro Pro Tyr Asp
385                 390                 395                 400

Val Gln Ile Val Asp Asp Glu Gly Asn Val Leu Pro Pro Gly Glu Glu
                405                 410                 415

Gly Asn Val Ala Val Arg Ile Arg Pro Thr Arg Pro Phe Cys Phe Phe
            420                 425                 430

Asn Cys Tyr Leu Asp Asn Pro Glu Lys Thr Ala Ala Ser Glu Gln Gly
        435                 440                 445

Asp Phe Tyr Ile Thr Gly Asp Arg Ala Arg Met Asp Lys Asp Gly Tyr
    450                 455                 460

Phe Trp Phe Met Gly Arg Asn Asp Asp Val Ile Asn Ser Ser Ser Tyr
465                 470                 475                 480

Arg Ile Gly Pro Val Glu Val Glu Ser Ala Leu Ala Glu His Pro Ala
                485                 490                 495

Val Leu Glu Ser Ala Val Val Ser Ser Pro Asp Pro Ile Arg Gly Glu
            500                 505                 510

Val Val Lys Ala Phe Ile Val Leu Thr Pro Ala Tyr Ser Ser His Asp
        515                 520                 525
```

```
Pro Glu Ala Leu Thr Arg Glu Leu Gln Glu His Val Lys Arg Val Thr
    530                 535                 540

Ala Pro Tyr Lys Tyr Pro Arg Lys Val Ala Phe Val Ser Glu Leu Pro
545                 550                 555                 560

Lys Thr Val Ser Gly Lys Ile Gln Arg Ser Lys Leu Arg Ser Gln Glu
                565                 570                 575

Trp Gly Lys
```

<210> 2032
<211> 208
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 514; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM5; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 5; "

<220>
<221> source
<223> /note="Uniprot ID: Q6NUN0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000460112"

<400> 2032

```
Met Arg Pro Trp Leu Arg His Leu Val Leu Gln Ala Leu Arg Asn Ser
1               5                   10                  15

Arg Ala Phe Cys Gly Ser His Gly Lys Pro Ala Pro Leu Pro Val Pro
            20                  25                  30

Gln Lys Ile Val Ala Thr Trp Glu Ala Ile Ser Leu Gly Arg Gln Leu
        35                  40                  45
```

```
Val Pro Glu Tyr Phe Asn Phe Ala His Asp Val Leu Asp Val Trp Ser
    50                  55                  60

Arg Leu Glu Glu Ala Gly His Arg Pro Pro Asn Pro Ala Phe Trp Trp
65                  70                  75                  80

Val Asn Gly Thr Gly Ala Glu Ile Lys Trp Ser Phe Glu Glu Leu Gly
                85                  90                  95

Lys Gln Ser Arg Lys Ala Ala Asn Val Leu Gly Gly Ala Cys Gly Leu
            100                 105                 110

Gln Pro Gly Asp Arg Met Met Leu Val Leu Pro Arg Leu Pro Glu Trp
        115                 120                 125

Trp Leu Val Ser Val Ala Cys Met Arg Thr Gly Thr Val Met Ile Pro
    130                 135                 140

Gly Val Thr Gln Leu Thr Glu Lys Asp Leu Lys Tyr Arg Leu Gln Ala
145                 150                 155                 160

Ser Arg Ala Lys Ser Ile Ile Thr Ser Asp Ser Leu Ala Pro Arg Val
                165                 170                 175

Asp Ala Ile Ser Ala Glu Cys Pro Ser Leu Gln Thr Lys Leu Leu Val
            180                 185                 190

Ser Asp Ser Ser Arg Pro Gly Trp Leu Asn Phe Arg Glu Leu Leu Arg
        195                 200                 205


<210> 2033
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 514; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
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member 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461752"

<400> 2033
His Asn Cys Met Arg Thr Lys Ser Arg Asp Pro Leu Ala Ile Tyr Phe
1   5   10   15

Thr Ser Gly Thr Thr Gly Ala Pro Lys Met Val Glu His Ser Gln Ser
            20   25   30

Ser Tyr Gly Leu Gly Phe Val Ala Ser Gly Arg Arg Trp Val Ala Leu
        35   40   45

Thr Glu Ser Asp Ile Phe Trp Asn Thr Thr Asp Thr Gly Trp Val Lys
    50   55   60

Ala Ala Trp Thr Leu Phe Ser Ala Trp Pro Asn Gly Ser Cys Ile Phe
65   70   75   80

Val His Glu Leu Pro Arg Val Asp Ala Lys Val Ile Leu Asn Val Pro
                85   90   95

Val Ser Glu Pro Glu Ala Leu Ser Asp Arg Arg Arg Gly Pro Gln Pro
            100   105   110

<210> 2034
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 514; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM5; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478073"

<400> 2034
Met Arg Pro Trp Leu Arg His Leu Val Leu Gln Ala Leu Arg Asn Ser
1 5 10 15

Arg Ala Phe Cys Gly Ser His Gly Lys Pro Ala Pro Leu Pro Val Pro
20 25 30

Gln Lys Ile Val Ala Thr Trp Glu Ala Ile Ser Leu Gly Arg Gln Leu
35 40 45

Val Pro Glu Tyr Phe Asn Phe Ala His Asp Val Leu Asp Val Trp Ser
50 55 60

Arg Leu Glu Glu Val Lys Pro Val Leu Ser
65 70

<210> 2035
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 515; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM6; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000328491"

<400> 2035
Met Leu Gly Arg Phe Gln Pro Phe Ser Leu Val Arg Ser Phe Arg Leu
1 5 10 15

Gly Phe Glu Ala Cys Cys Tyr Pro Asn Gln Lys Cys Ala Thr Gln Thr
20 25 30

Ile Arg Pro Pro Asp Ser Arg Cys Leu Val Gln Ala Val Ser Gln Asn
35 40 45

```
Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Ser Gln Leu Glu Lys
    50                  55                  60

Asp Gly Leu Arg Gly Pro Tyr Pro Ala Leu Trp Lys Val Ser Ala Lys
65                  70                  75                  80

Gly Glu Glu Asp Lys Trp Ser Phe Glu Arg Met Thr Gln Leu Ser Lys
                85                  90                  95

Lys Ala Ala Ser Ile Leu Ser Asp Thr Cys Ala Leu Ser His Gly Asp
            100                 105                 110

Arg Leu Met Ile Ile Leu Pro Pro Thr Pro Glu Ala Tyr Trp Ile Cys
        115                 120                 125

Leu Ala Cys Glu Ser Pro Leu Cys Leu Gly Ala Pro Ser
    130                 135                 140


<210> 2036
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 515; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM6; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 6; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6P461; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000340296"

<400> 2036
Met Leu Gly Arg Phe Gln Pro Phe Ser Leu Val Arg Ser Phe Arg Leu
1               5                   10                  15
```

```
Gly Phe Glu Ala Cys Cys Tyr Pro Asn Gln Lys Cys Ala Thr Gln Thr
            20                  25                  30

Ile Arg Pro Pro Asp Ser Arg Cys Leu Val Gln Ala Val Ser Gln Asn
        35                  40                  45

Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Ser Gln Leu Glu Lys
    50                  55                  60

Asp Gly Leu Arg Gly Pro Tyr Pro Ala Leu Trp Lys Val Ser Ala Lys
65                  70                  75                  80

Gly Glu Glu Asp Lys Trp Ser Phe Glu Arg Met Thr Gln Leu Ser Lys
                85                  90                  95

Lys Ala Ala Ser Ile Leu Ser Asp Thr Cys Ala Leu Ser His Gly Asp
            100                 105                 110

Arg Leu Met Ile Ile Leu Pro Pro Thr Pro Glu Ala Tyr Trp Ile Cys
        115                 120                 125

Leu Ala Cys Val Arg Leu Gly Ile Thr Phe Val Pro Gly Ser Pro Gln
    130                 135                 140

Leu Thr Ala Lys Lys Ile Arg Tyr Gln Leu Arg Met Ser Lys Ala Gln
145                 150                 155                 160

Cys Ile Val Ala Asn Glu Ala Met Ala Pro Val Val Asn Ser Ala Val
                165                 170                 175

Ser Asp Cys Pro Thr Leu Lys Thr Lys Leu Leu Val Ser Asp Lys Ser
            180                 185                 190

Tyr Asp Gly Trp Leu Asp Phe Lys Lys Leu Ile Gln Val Ala Pro Pro
        195                 200                 205

Lys Gln Thr Tyr Met Arg Thr Lys Ser Gln Asp Pro Met Ala Ile Phe
    210                 215                 220

Phe Thr Lys Gly Thr Thr Gly Ala Pro Lys Met Val Glu Tyr Ser Gln
225                 230                 235                 240

Tyr Gly Leu Gly Met Gly Phe Ser Gln Ala Ser Arg Arg Trp Met Asp
```

245 250 255

Leu Gln Pro Thr Asp Val Leu Trp Ser Leu Gly Asp Ala Phe Gly Gly
260 265 270

Ser Leu Ser Leu Ser Ala Val Leu Gly Thr Trp Phe Gln Gly Ala Cys
275 280 285

Val Phe Leu Cys His Met Pro Thr Phe Cys Pro Glu Thr Val Leu Asn
290 295 300

Val Leu Ser Arg Phe Pro Ile Thr Thr Leu Ser Ala Asn Pro Glu Met
305 310 315 320

Tyr Gln Glu Leu Leu Gln His Lys Cys Phe Thr Ser Tyr Arg Phe Lys
325 330 335

Ser Leu Lys Gln Cys Val Ala Ala Gly Gly Pro Ile Ser Pro Gly Val
340 345 350

Ile Glu Asp Trp Lys Arg Ile Thr Lys Leu Asp Ile Tyr Glu Gly Tyr
355 360 365

Gly Gln Thr Glu Thr Gly Leu Leu Cys Ala Thr Ser Lys Thr Ile Lys
370 375 380

Leu Lys Pro Ser Ser Leu Gly Lys Pro Leu Pro Pro Tyr Ile Val Gln
385 390 395 400

Ile Val Asp Glu Asn Ser Asn Leu Leu Pro Pro Gly Glu Glu Gly Asn
405 410 415

Ile Ala Ile Arg Ile Lys Leu Asn Gln Pro Ala Ser Leu Tyr Cys Pro
420 425 430

His Met Val Ser Trp Glu Glu Tyr Ala Ser Ala Arg Gly His Met Leu
435 440 445

Tyr Leu Thr Gly Asp Arg Gly Ile Met Asp Glu Asp Gly Tyr Phe Trp
450 455 460

Trp Ser Gly Arg Val Asp Asp Val Ala Asn Ala Leu Gly Gln Arg Leu
465 470 475 480

<210> 2037
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 515; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM6; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase medium-chain family
member 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q6P461; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000377573"

<400> 2037
Met Leu Gly Arg Phe Gln Pro Phe Ser Leu Val Arg Ser Phe Arg Leu
1   5   10   15

Gly Phe Glu Ala Cys Cys Tyr Pro Asn Gln Lys Cys Ala Thr Gln Thr
            20   25   30

Ile Arg Pro Pro Asp Ser Arg Cys Leu Val Gln Ala Val Ser Gln Asn
        35   40   45

Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Ser Gln Leu Glu Lys
    50   55   60

Asp Gly Leu Arg Gly Pro Tyr Pro Ala Leu Trp Lys Val Ser Ala Lys
65   70   75   80

Gly Glu Glu Asp Lys Trp Ser Phe Glu Arg Met Thr Gln Leu Ser Lys
                85   90   95

Lys Ala Ala Ser Ile Leu Ser Asp Thr Cys Ala Leu Ser His Gly Asp
            100   105   110

```
Arg Leu Met Ile Ile Leu Pro Pro Thr Pro Glu Ala Tyr Trp Ile Cys
        115                 120                 125

Leu Ala Cys Val Arg Leu Gly Ile Thr Phe Val Pro Gly Ser Pro Gln
    130                 135                 140

Leu Thr Ala Lys Lys Ile Arg Tyr Gln Leu Arg Met Ser Lys Ala Gln
145                 150                 155                 160

Cys Ile Val Ala Asn Glu Ala Met Ala Pro Val Val Asn Ser Ala Val
                165                 170                 175

Ser Asp Cys Pro Thr Leu Lys Thr Lys Leu Leu Val Ser Asp Lys Ser
            180                 185                 190

Tyr Asp Gly Trp Leu Asp Phe Lys Lys Leu Ile Gln Val Ala Pro Pro
        195                 200                 205

Lys Gln Thr Tyr Met Arg Thr Lys Ser Gln Asp Pro Met Ala Ile Phe
    210                 215                 220

Phe Thr Lys Gly Thr Thr Gly Ala Pro Lys Met Val Glu Tyr Ser Gln
225                 230                 235                 240

Tyr Gly Leu Gly Met Gly Phe Ser Gln Ala Ser Arg Arg Trp Met Asp
                245                 250                 255

Leu Gln Pro Thr Asp Val Leu Trp Ser Leu Gly Asp Ala Phe Gly Gly
            260                 265                 270

Ser Leu Ser Leu Ser Ala Val Leu Gly Thr Trp Phe Gln Gly Ala Cys
        275                 280                 285

Val Phe Leu Cys His Met Pro Thr Phe Cys Pro Glu Thr Val Leu Asn
    290                 295                 300

Val Leu Ser Arg Phe Pro Ile Thr Thr Leu Ser Ala Asn Pro Glu Met
305                 310                 315                 320

Tyr Gln Glu Leu Leu Gln His Lys Cys Phe Thr Ser Tyr Arg Phe Lys
                325                 330                 335
```

```
Ser Leu Lys Gln Cys Val Ala Ala Gly Gly Pro Ile Ser Pro Gly Val
            340                 345                 350

Ile Glu Asp Trp Lys Arg Ile Thr Lys Leu Asp Ile Tyr Glu Gly Tyr
        355                 360                 365

Gly Gln Thr Glu Thr Gly Leu Leu Cys Ala Thr Ser Lys Thr Ile Lys
    370                 375                 380

Leu Lys Pro Ser Ser Leu Gly Lys Pro Leu Pro Pro Tyr Ile Val Gln
385                 390                 395                 400

Ile Val Asp Glu Asn Ser Asn Leu Leu Pro Pro Gly Glu Glu Gly Asn
                405                 410                 415

Ile Ala Ile Arg Ile Lys Leu Asn Gln Pro Ala Ser Leu Tyr Cys Pro
            420                 425                 430

His Met Val Ser Trp Glu Glu Tyr Ala Ser Ala Arg Gly His Met Leu
        435                 440                 445

Tyr Leu Thr Gly Asp Arg Gly Ile Met Asp Glu Asp Gly Tyr Phe Trp
    450                 455                 460

Trp Ser Gly Arg Val Asp Asp Val Ala Asn Ala Leu Gly Gln Arg Leu
465                 470                 475                 480


<210> 2038
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 515; "

<220>
<221> source
<223> /note="Gene Symbol: ACSM6; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase medium-chain family
      member 6; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000384922"

<400> 2038
Met Leu Gly Arg Phe Gln Pro Phe Ser Leu Val Arg Ser Phe Arg Leu
1   5   10   15

Gly Phe Glu Ala Cys Cys Tyr Pro Asn Gln Lys Cys Ala Thr Gln Thr
            20   25   30

Ile Arg Pro Pro Asp Ser Arg Cys Leu Val Gln Ala Val Ser Gln Asn
        35   40   45

Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Ser Gln Leu Glu Lys
    50   55   60

Asp Asn Gly Leu Gln Leu His Pro Cys Cys Cys Lys Arg Gln Asp Phe
65   70   75   80

Ile Leu Phe His Gly
                85

<210> 2039
<211> 689
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 516; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase short-chain family
      member 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUB1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000316924"

<400> 2039
Met Ala Ala Arg Thr Leu Gly Arg Gly Val Gly Arg Leu Leu Gly Ser
1   5   10   15

```
Leu Arg Gly Leu Ser Gly Gln Pro Ala Arg Pro Pro Cys Gly Val Ser
            20                  25                  30

Ala Pro Arg Arg Ala Ala Ser Gly Pro Ser Gly Ser Ala Pro Ala Val
        35                  40                  45

Ala Ala Ala Ala Ala Gln Pro Gly Ser Tyr Pro Ala Leu Ser Ala Gln
    50                  55                  60

Ala Ala Arg Glu Pro Ala Ala Phe Trp Gly Pro Leu Ala Arg Asp Thr
65                  70                  75                  80

Leu Val Trp Asp Thr Pro Tyr His Thr Val Trp Asp Cys Asp Phe Ser
                85                  90                  95

Thr Gly Lys Ile Gly Trp Phe Leu Gly Gly Gln Leu Asn Val Ser Val
            100                 105                 110

Asn Cys Leu Asp Gln His Val Arg Lys Ser Pro Glu Ser Val Ala Leu
        115                 120                 125

Ile Trp Glu Arg Asp Glu Pro Gly Thr Glu Val Arg Ile Thr Tyr Arg
    130                 135                 140

Glu Leu Leu Glu Thr Thr Cys Arg Leu Ala Asn Thr Leu Lys Arg His
145                 150                 155                 160

Gly Val His Arg Gly Asp Arg Val Ala Ile Tyr Met Pro Val Ser Pro
                165                 170                 175

Leu Ala Val Ala Ala Met Leu Ala Cys Ala Arg Ile Gly Ala Val His
            180                 185                 190

Thr Val Ile Phe Ala Gly Phe Ser Ala Glu Ser Leu Ala Gly Arg Ile
        195                 200                 205

Asn Asp Ala Lys Cys Lys Val Val Ile Thr Phe Asn Gln Gly Leu Arg
    210                 215                 220

Gly Gly Arg Val Val Glu Leu Lys Lys Ile Val Asp Glu Ala Val Lys
225                 230                 235                 240
```

```
His Cys Pro Thr Val Gln His Val Leu Val Ala His Arg Thr Asp Asn
                245                 250                 255

Lys Val His Met Gly Asp Leu Asp Val Pro Leu Glu Gln Glu Met Ala
            260                 265                 270

Lys Glu Asp Pro Val Cys Ala Pro Glu Ser Met Gly Ser Glu Asp Met
        275                 280                 285

Leu Phe Met Leu Tyr Thr Ser Gly Ser Thr Gly Met Pro Lys Gly Ile
    290                 295                 300

Val His Thr Gln Ala Gly Tyr Leu Leu Tyr Ala Ala Leu Thr His Lys
305                 310                 315                 320

Leu Val Phe Asp His Gln Pro Gly Asp Ile Phe Gly Cys Val Ala Asp
                325                 330                 335

Ile Gly Trp Ile Thr Gly His Ser Tyr Val Val Tyr Gly Pro Leu Cys
            340                 345                 350

Asn Gly Ala Thr Ser Val Leu Phe Glu Ser Thr Pro Val Tyr Pro Asn
        355                 360                 365

Ala Gly Arg Tyr Trp Glu Thr Val Glu Arg Leu Lys Ile Asn Gln Phe
    370                 375                 380

Tyr Gly Ala Pro Thr Ala Val Arg Leu Leu Leu Lys Tyr Gly Asp Ala
385                 390                 395                 400

Trp Val Lys Lys Tyr Asp Arg Ser Ser Leu Arg Thr Leu Gly Ser Val
                405                 410                 415

Gly Glu Pro Ile Asn Cys Glu Ala Trp Glu Trp Leu His Arg Val Val
            420                 425                 430

Gly Asp Ser Arg Cys Thr Leu Val Asp Thr Trp Trp Gln Thr Glu Thr
        435                 440                 445

Gly Gly Ile Cys Ile Ala Pro Arg Pro Ser Glu Glu Gly Ala Glu Ile
    450                 455                 460
```

```
Leu Pro Ala Met Ala Met Arg Pro Phe Phe Gly Ile Val Pro Val Leu
465                 470                 475                 480

Met Asp Glu Lys Gly Ser Val Val Glu Gly Ser Asn Val Ser Gly Ala
                485                 490                 495

Leu Cys Ile Ser Gln Ala Trp Pro Gly Met Ala Arg Thr Ile Tyr Gly
            500                 505                 510

Asp His Gln Arg Phe Val Asp Ala Tyr Phe Lys Ala Tyr Pro Gly Tyr
        515                 520                 525

Tyr Phe Thr Gly Asp Gly Ala Tyr Arg Thr Glu Gly Gly Tyr Tyr Gln
    530                 535                 540

Ile Thr Gly Arg Met Asp Asp Val Ile Asn Ile Ser Gly His Arg Leu
545                 550                 555                 560

Gly Thr Ala Glu Ile Glu Asp Ala Ile Ala Asp His Pro Ala Val Pro
                565                 570                 575

Glu Ser Ala Val Ile Gly Tyr Pro His Asp Ile Lys Gly Glu Ala Ala
            580                 585                 590

Phe Ala Phe Ile Val Val Lys Asp Ser Ala Gly Asp Ser Asp Val Val
        595                 600                 605

Val Gln Glu Leu Lys Ser Met Val Ala Thr Lys Ile Ala Lys Tyr Ala
    610                 615                 620

Val Pro Asp Glu Ile Leu Val Val Lys Arg Leu Pro Lys Thr Arg Ser
625                 630                 635                 640

Gly Lys Val Met Arg Arg Leu Leu Arg Lys Ile Ile Thr Ser Glu Ala
                645                 650                 655

Gln Glu Leu Gly Asp Thr Thr Thr Leu Glu Asp Pro Ser Ile Ile Ala
            660                 665                 670

Glu Ile Leu Ser Val Tyr Gln Lys Cys Lys Asp Lys Gln Ala Ala Ala
        675                 680                 685

Lys
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<210> 2040
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 516; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000365916"

<400> 2040
Met Ala Ala Arg Thr Leu Gly Arg Gly Val Gly Arg Leu Leu Gly Ser
1 5 10 15

Leu Arg Gly Leu Ser Gly Gln Pro Ala Arg Pro Pro Cys Gly Val Ser
20 25 30

Ala Pro Arg Arg Ala Ala Ser Gly Pro Ser Gly Ser Ala Pro Ala Val
35 40 45

Ala Ala Ala Ala Ala Gln Pro Gly Ser Tyr Pro Ala Leu Ser Ala Gln
50 55 60

Ala Ala Arg Glu Pro Ala Ala Phe Trp Gly Pro Leu Ala Arg Asp Thr
65 70 75 80

Leu Val Trp Asp Thr Pro Tyr His Thr Val Trp Asp Cys Asp Phe Ser
85 90 95

Thr Gly Lys Ile Gly Trp Phe Leu Gly Gly Gln Leu Asn Val Ser Val
100 105 110

Asn Cys Leu Asp Gln His Val Arg Lys Ser Pro Glu Ser Val Ala Leu
115 120 125

Ile Trp Glu Arg Asp Glu Pro Gly Thr Glu Val Arg Ile Thr Tyr Ser
130 135 140

Pro Trp Leu Gln Met Pro Cys Gly Pro
145 150

<210> 2041
<211> 575
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 516; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9NUB1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000388793"

<400> 2041
Met Ala Ala Arg Thr Leu Gly Arg Gly Val Gly Arg Leu Leu Gly Ser
1 5 10 15

Leu Arg Gly Leu Ser Gly Gln Pro Ala Arg Pro Pro Cys Gly Val Ser
20 25 30

Ala Pro Arg Arg Ala Ala Ser Gly Pro Ser Gly Ser Ala Pro Ala Val
35 40 45

Ala Ala Ala Ala Ala Gln Pro Gly Ser Tyr Pro Ala Leu Ser Ala Gln
50 55 60

Ala Ala Arg Glu Pro Ala Ala Phe Trp Gly Pro Leu Ala Arg Asp Thr
65 70 75 80

```
Leu Val Trp Asp Thr Pro Tyr His Thr Val Trp Asp Cys Asp Phe Ser
                85                  90                  95

Thr Gly Lys Ile Gly Trp Phe Leu Gly Gly Gln Leu Asn Val Ser Val
            100                 105                 110

Asn Cys Leu Asp Gln His Val Arg Lys Ser Pro Glu Ser Val Ala Leu
        115                 120                 125

Ile Trp Glu Arg Asp Glu Pro Gly Thr Glu Val Arg Ile Thr Tyr Arg
    130                 135                 140

Glu Leu Leu Glu Thr Thr Cys Arg Leu Ala Asn Thr Leu Lys Arg His
145                 150                 155                 160

Gly Val His Arg Gly Asp Arg Val Ala Ile Tyr Met Pro Val Ser Pro
                165                 170                 175

Leu Ala Val Ala Ala Met Leu Ala Cys Ala Arg Ile Gly Ala Val His
            180                 185                 190

Thr Val Ile Phe Ala Gly Phe Ser Ala Glu Ser Leu Ala Gly Arg Ile
        195                 200                 205

Asn Asp Ala Lys Cys Lys Val Val Ile Thr Phe Asn Gln Gly Leu Arg
    210                 215                 220

Gly Gly Arg Val Val Glu Leu Lys Lys Ile Val Asp Glu Ala Val Lys
225                 230                 235                 240

His Cys Pro Thr Val Gln His Val Leu Val Ala His Arg Thr Asp Asn
                245                 250                 255

Lys Val His Met Gly Asp Leu Asp Val Pro Leu Glu Gln Glu Met Ala
            260                 265                 270

Lys Glu Asp Pro Val Cys Ala Pro Glu Ser Met Gly Ser Glu Asp Met
        275                 280                 285

Leu Phe Met Leu Tyr Thr Ser Gly Ser Thr Gly Met Pro Lys Gly Ile
    290                 295                 300
```

```
Val His Thr Gln Ala Gly Tyr Leu Leu Tyr Ala Ala Leu Thr His Lys
305                 310                 315                 320

Leu Val Phe Asp His Gln Pro Gly Asp Ile Phe Gly Cys Val Ala Asp
                325                 330                 335

Ile Gly Trp Ile Thr Gly His Ser Tyr Val Val Tyr Gly Pro Leu Cys
            340                 345                 350

Asn Gly Ala Thr Ser Val Leu Phe Glu Ser Thr Pro Val Tyr Pro Asn
        355                 360                 365

Ala Gly Arg Tyr Trp Glu Thr Val Glu Arg Leu Lys Ile Asn Gln Phe
    370                 375                 380

Tyr Gly Ala Pro Thr Ala Val Arg Leu Leu Leu Lys Tyr Gly Asp Ala
385                 390                 395                 400

Trp Val Lys Lys Tyr Asp Arg Ser Ser Leu Arg Thr Leu Gly Ser Val
                405                 410                 415

Gly Glu Pro Ile Asn Cys Glu Ala Trp Glu Trp Leu His Arg Val Val
            420                 425                 430

Gly Asp Ser Arg Cys Thr Leu Val Asp Thr Trp Trp Gln Thr Glu Thr
        435                 440                 445

Gly Gly Ile Cys Ile Ala Pro Arg Pro Ser Glu Glu Gly Ala Glu Ile
    450                 455                 460

Leu Pro Ala Met Ala Met Arg Pro Phe Phe Gly Ile Val Pro Val Leu
465                 470                 475                 480

Met Asp Glu Lys Gly Ser Val Val Glu Gly Ser Asn Val Ser Gly Ala
                485                 490                 495

Leu Cys Ile Ser Gln Ala Trp Pro Gly Met Ala Arg Thr Ile Tyr Gly
            500                 505                 510

Asp His Gln Arg Phe Val Asp Ala Tyr Phe Lys Ala Tyr Pro Gly Tyr
        515                 520                 525

Tyr Phe Thr Gly Asp Gly Ala Tyr Arg Thr Glu Gly Gly Tyr Tyr Gln
```

```
    530                 535                 540

Ile Thr Gly Arg Met Asp Asp Val Ile Asn Ile Leu Gln Ile Val Gly
545                 550                 555                 560

Phe Phe Arg Glu Ala Ile Arg Asn Ser Gly Asp Leu Leu Glu His
                565                 570                 575

<210> 2042
<211> 568
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 516; "

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<223> /note="Gene Symbol: ACSS1; "

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<223> /note="Gene Name:
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      member 1; "

<220>
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<223> /note="Uniprot ID:  Q9NUB1; "

<220>
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<223> /note="ENSP ID: ENSP00000439304"

<400> 2042
Met Arg Arg Arg Lys Glu Arg Gln Pro Trp Asp Arg Phe His Phe Leu
1               5                   10                  15

His Phe Ala Pro His Gly Arg Glu Leu Leu Glu Thr Thr Cys Arg Leu
            20                  25                  30

Ala Asn Thr Leu Lys Arg His Gly Val His Arg Gly Asp Arg Val Ala
        35                  40                  45

Ile Tyr Met Pro Val Ser Pro Leu Ala Val Ala Ala Met Leu Ala Cys
    50                  55                  60

Ala Arg Ile Gly Ala Val His Thr Val Ile Phe Ala Gly Phe Ser Ala
65                  70                  75                  80
```

```
Glu Ser Leu Ala Gly Arg Ile Asn Asp Ala Lys Cys Lys Val Val Ile
                85                  90                  95

Thr Phe Asn Gln Gly Leu Arg Gly Gly Arg Val Val Glu Leu Lys Lys
            100                 105                 110

Ile Val Asp Glu Ala Val Lys His Cys Pro Thr Val Gln His Val Leu
        115                 120                 125

Val Ala His Arg Thr Asp Asn Lys Val His Met Gly Asp Leu Asp Val
    130                 135                 140

Pro Leu Glu Gln Glu Met Ala Lys Glu Asp Pro Val Cys Ala Pro Glu
145                 150                 155                 160

Ser Met Gly Ser Glu Asp Met Leu Phe Met Leu Tyr Thr Ser Gly Ser
                165                 170                 175

Thr Gly Met Pro Lys Gly Ile Val His Thr Gln Ala Gly Tyr Leu Leu
            180                 185                 190

Tyr Ala Ala Leu Thr His Lys Leu Val Phe Asp His Gln Pro Gly Asp
        195                 200                 205

Ile Phe Gly Cys Val Ala Asp Ile Gly Trp Ile Thr Gly His Ser Tyr
    210                 215                 220

Val Val Tyr Gly Pro Leu Cys Asn Gly Ala Thr Ser Val Leu Phe Glu
225                 230                 235                 240

Ser Thr Pro Val Tyr Pro Asn Ala Gly Arg Tyr Trp Glu Thr Val Glu
                245                 250                 255

Arg Leu Lys Ile Asn Gln Phe Tyr Gly Ala Pro Thr Ala Val Arg Leu
            260                 265                 270

Leu Leu Lys Tyr Gly Asp Ala Trp Val Lys Lys Tyr Asp Arg Ser Ser
        275                 280                 285

Leu Arg Thr Leu Gly Ser Val Gly Glu Pro Ile Asn Cys Glu Ala Trp
    290                 295                 300
```

```
Glu Trp Leu His Arg Val Val Gly Asp Ser Arg Cys Thr Leu Val Asp
305                 310                 315                 320

Thr Trp Trp Gln Thr Glu Thr Gly Gly Ile Cys Ile Ala Pro Arg Pro
                325                 330                 335

Ser Glu Glu Gly Ala Glu Ile Leu Pro Ala Met Ala Met Arg Pro Phe
            340                 345                 350

Phe Gly Ile Val Pro Val Leu Met Asp Glu Lys Gly Ser Val Val Glu
        355                 360                 365

Gly Ser Asn Val Ser Gly Ala Leu Cys Ile Ser Gln Ala Trp Pro Gly
    370                 375                 380

Met Ala Arg Thr Ile Tyr Gly Asp His Gln Arg Phe Val Asp Ala Tyr
385                 390                 395                 400

Phe Lys Ala Tyr Pro Gly Tyr Tyr Phe Thr Gly Asp Gly Ala Tyr Arg
                405                 410                 415

Thr Glu Gly Gly Tyr Tyr Gln Ile Thr Gly Arg Met Asp Asp Val Ile
            420                 425                 430

Asn Ile Ser Gly His Arg Leu Gly Thr Ala Glu Ile Glu Asp Ala Ile
        435                 440                 445

Ala Asp His Pro Ala Val Pro Glu Ser Ala Val Ile Gly Tyr Pro His
    450                 455                 460

Asp Ile Lys Gly Glu Ala Ala Phe Ala Phe Ile Val Val Lys Asp Ser
465                 470                 475                 480

Ala Gly Asp Ser Asp Val Val Val Gln Glu Leu Lys Ser Met Val Ala
                485                 490                 495

Thr Lys Ile Ala Lys Tyr Ala Val Pro Asp Glu Ile Leu Val Val Lys
            500                 505                 510

Arg Leu Pro Lys Thr Arg Ser Gly Lys Val Met Arg Arg Leu Leu Arg
        515                 520                 525
```

Lys Ile Ile Thr Ser Glu Ala Gln Glu Leu Gly Asp Thr Thr Thr Leu
530 535 540

Glu Asp Pro Ser Ile Ile Ala Glu Ile Leu Ser Val Tyr Gln Lys Cys
545 550 555 560

Lys Asp Lys Gln Ala Ala Ala Lys
565

<210> 2043
<211> 714
<212> PRT
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<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<223> /note="Uniprot ID: Q9NR19; "

<220>
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<400> 2043
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1 5 10 15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
20 25 30

Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
35 40 45

Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Trp Gly Asp
50 55 60

Ile Ala Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu

65 70 75 80

Arg Tyr Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met
85 90 95

Lys Gly Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val
100 105 110

His Glu Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr Trp Glu Gly Asn
115 120 125

Glu Pro Gly Glu Thr Thr Gln Ile Thr Tyr His Gln Leu Leu Val Gln
130 135 140

Val Cys Gln Phe Ser Asn Val Leu Arg Lys Gln Gly Ile Gln Lys Gly
145 150 155 160

Asp Arg Val Ala Ile Tyr Met Pro Met Ile Pro Glu Leu Val Val Ala
165 170 175

Met Leu Ala Cys Ala Arg Ile Gly Ala Leu His Ser Ile Val Phe Ala
180 185 190

Gly Phe Ser Ser Glu Ser Leu Cys Glu Arg Ile Leu Asp Ser Ser Cys
195 200 205

Ser Leu Leu Ile Thr Thr Asp Ala Phe Tyr Arg Gly Glu Lys Leu Val
210 215 220

Asn Leu Lys Glu Leu Ala Asp Glu Ala Leu Gln Lys Cys Gln Glu Lys
225 230 235 240

Gly Phe Pro Val Arg Cys Cys Ile Val Val Lys His Leu Gly Arg Ala
245 250 255

Glu Leu Gly Met Gly Asp Ser Thr Ser Gln Ser Pro Pro Ile Lys Arg
260 265 270

Ser Cys Pro Asp Val Gln Gly Lys Leu Lys Glu Lys Ser Lys Arg Val
275 280 285

Gln Pro Gln Ile Ser Trp Asn Gln Gly Ile Asp Leu Trp Trp His Glu
290 295 300

```
Leu Met Gln Glu Ala Gly Asp Glu Cys Glu Pro Glu Trp Cys Asp Ala
305                 310                 315                 320

Glu Asp Pro Leu Phe Ile Leu Tyr Thr Ser Gly Ser Thr Gly Lys Pro
                325                 330                 335

Lys Gly Val Val His Thr Val Gly Gly Tyr Met Leu Tyr Val Ala Thr
            340                 345                 350

Thr Phe Lys Tyr Val Phe Asp Phe His Ala Glu Asp Val Phe Trp Cys
        355                 360                 365

Thr Ala Asp Ile Gly Trp Ile Thr Gly His Ser Tyr Val Thr Tyr Gly
    370                 375                 380

Pro Leu Ala Asn Gly Ala Thr Ser Val Leu Phe Glu Gly Ile Pro Thr
385                 390                 395                 400

Tyr Pro Asp Val Asn Arg Leu Trp Ser Ile Val Asp Lys Tyr Lys Val
                405                 410                 415

Thr Lys Phe Tyr Thr Ala Pro Thr Ala Ile Arg Leu Leu Met Lys Phe
            420                 425                 430

Gly Asp Glu Pro Val Thr Lys His Ser Arg Ala Ser Leu Gln Val Leu
        435                 440                 445

Gly Thr Val Gly Glu Pro Ile Asn Pro Glu Ala Trp Leu Trp Tyr His
    450                 455                 460

Arg Val Val Gly Ala Gln Arg Cys Pro Ile Val Asp Thr Phe Trp Gln
465                 470                 475                 480

Thr Glu Thr Gly Gly His Met Leu Thr Pro Leu Pro Gly Ala Thr Pro
                485                 490                 495

Met Lys Pro Gly Ser Ala Thr Phe Pro Phe Phe Gly Val Ala Pro Ala
            500                 505                 510

Ile Leu Asn Glu Ser Gly Glu Glu Leu Glu Gly Glu Ala Glu Gly Tyr
        515                 520                 525
```

```
Leu Val Phe Lys Gln Pro Trp Pro Gly Ile Met Arg Thr Val Tyr Gly
    530                 535                 540

Asn His Glu Arg Phe Glu Thr Thr Tyr Phe Lys Lys Phe Pro Gly Tyr
545                 550                 555                 560

Tyr Val Thr Gly Asp Gly Cys Gln Arg Asp Gln Asp Gly Tyr Tyr Trp
                565                 570                 575

Ile Thr Gly Arg Ile Asp Asp Met Leu Asn Val Ser Gly His Leu Leu
            580                 585                 590

Ser Thr Ala Glu Val Glu Ser Ala Leu Val Glu His Glu Ala Val Ala
        595                 600                 605

Glu Ala Ala Val Val Gly His Pro His Pro Val Lys Gly Glu Cys Leu
    610                 615                 620

Tyr Cys Phe Val Thr Leu Cys Asp Gly His Thr Phe Ser Pro Lys Leu
625                 630                 635                 640

Thr Glu Glu Leu Lys Lys Gln Ile Arg Glu Lys Ile Gly Pro Ile Ala
                645                 650                 655

Thr Pro Asp Tyr Ile Gln Asn Ala Pro Gly Leu Pro Lys Thr Arg Ser
            660                 665                 670

Gly Lys Ile Met Arg Arg Val Leu Arg Lys Ile Ala Gln Asn Asp His
        675                 680                 685

Asp Leu Gly Asp Met Ser Thr Val Ala Asp Pro Ser Val Ile Ser His
    690                 695                 700

Leu Phe Ser His Arg Cys Leu Thr Ile Gln
705                 710


<210> 2044
<211> 701
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "
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<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
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acyl-CoA synthetase short-chain family
member 2; "

<220>
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<223> /note="Uniprot ID: Q9NR19; "

<220>
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<400> 2044
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1   5   10   15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
            20   25   30

Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
        35   40   45

Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Trp Gly Asp
    50   55   60

Ile Ala Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu
65   70   75   80

Arg Tyr Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met
                85   90   95

Lys Gly Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val
            100   105   110

His Glu Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr Trp Glu Gly Asn
        115   120   125

Glu Pro Gly Glu Thr Thr Gln Ile Thr Tyr His Gln Leu Leu Val Gln
    130   135   140

Val Cys Gln Phe Ser Asn Val Leu Arg Lys Gln Gly Ile Gln Lys Gly

145 150 155 160

Asp Arg Val Ala Ile Tyr Met Pro Met Ile Pro Glu Leu Val Val Ala
165 170 175

Met Leu Ala Cys Ala Arg Ile Gly Ala Leu His Ser Ile Val Phe Ala
180 185 190

Gly Phe Ser Ser Glu Ser Leu Cys Glu Arg Ile Leu Asp Ser Ser Cys
195 200 205

Ser Leu Leu Ile Thr Thr Asp Ala Phe Tyr Arg Gly Glu Lys Leu Val
210 215 220

Asn Leu Lys Glu Leu Ala Asp Glu Ala Leu Gln Lys Cys Gln Glu Lys
225 230 235 240

Gly Phe Pro Val Arg Cys Cys Ile Val Val Lys His Leu Gly Arg Ala
245 250 255

Glu Leu Gly Met Gly Asp Ser Thr Ser Gln Ser Pro Pro Ile Lys Arg
260 265 270

Ser Cys Pro Asp Val Gln Ile Ser Trp Asn Gln Gly Ile Asp Leu Trp
275 280 285

Trp His Glu Leu Met Gln Glu Ala Gly Asp Glu Cys Glu Pro Glu Trp
290 295 300

Cys Asp Ala Glu Asp Pro Leu Phe Ile Leu Tyr Thr Ser Gly Ser Thr
305 310 315 320

Gly Lys Pro Lys Gly Val Val His Thr Val Gly Gly Tyr Met Leu Tyr
325 330 335

Val Ala Thr Thr Phe Lys Tyr Val Phe Asp Phe His Ala Glu Asp Val
340 345 350

Phe Trp Cys Thr Ala Asp Ile Gly Trp Ile Thr Gly His Ser Tyr Val
355 360 365

Thr Tyr Gly Pro Leu Ala Asn Gly Ala Thr Ser Val Leu Phe Glu Gly
370 375 380

```
Ile Pro Thr Tyr Pro Asp Val Asn Arg Leu Trp Ser Ile Val Asp Lys
385                 390                 395                 400

Tyr Lys Val Thr Lys Phe Tyr Thr Ala Pro Thr Ala Ile Arg Leu Leu
                405                 410                 415

Met Lys Phe Gly Asp Glu Pro Val Thr Lys His Ser Arg Ala Ser Leu
            420                 425                 430

Gln Val Leu Gly Thr Val Gly Glu Pro Ile Asn Pro Glu Ala Trp Leu
        435                 440                 445

Trp Tyr His Arg Val Val Gly Ala Gln Arg Cys Pro Ile Val Asp Thr
    450                 455                 460

Phe Trp Gln Thr Glu Thr Gly Gly His Met Leu Thr Pro Leu Pro Gly
465                 470                 475                 480

Ala Thr Pro Met Lys Pro Gly Ser Ala Thr Phe Pro Phe Phe Gly Val
                485                 490                 495

Ala Pro Ala Ile Leu Asn Glu Ser Gly Glu Glu Leu Glu Gly Glu Ala
            500                 505                 510

Glu Gly Tyr Leu Val Phe Lys Gln Pro Trp Pro Gly Ile Met Arg Thr
        515                 520                 525

Val Tyr Gly Asn His Glu Arg Phe Glu Thr Thr Tyr Phe Lys Lys Phe
    530                 535                 540

Pro Gly Tyr Tyr Val Thr Gly Asp Gly Cys Gln Arg Asp Gln Asp Gly
545                 550                 555                 560

Tyr Tyr Trp Ile Thr Gly Arg Ile Asp Asp Met Leu Asn Val Ser Gly
                565                 570                 575

His Leu Leu Ser Thr Ala Glu Val Glu Ser Ala Leu Val Glu His Glu
            580                 585                 590

Ala Val Ala Glu Ala Ala Val Val Gly His Pro His Pro Val Lys Gly
        595                 600                 605
```

```
Glu Cys Leu Tyr Cys Phe Val Thr Leu Cys Asp Gly His Thr Phe Ser
    610                 615                 620

Pro Lys Leu Thr Glu Glu Leu Lys Lys Gln Ile Arg Glu Lys Ile Gly
625                 630                 635                 640

Pro Ile Ala Thr Pro Asp Tyr Ile Gln Asn Ala Pro Gly Leu Pro Lys
                645                 650                 655

Thr Arg Ser Gly Lys Ile Met Arg Arg Val Leu Arg Lys Ile Ala Gln
            660                 665                 670

Asn Asp His Asp Leu Gly Asp Met Ser Thr Val Ala Asp Pro Ser Val
        675                 680                 685

Ile Ser His Leu Phe Ser His Arg Cys Leu Thr Ile Gln
    690                 695                 700


<210> 2045
<211> 163
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase short-chain family
      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417783"

<400> 2045
Met Met Val Arg Trp Ala Leu Leu Cys Glu Phe Trp Gly Asp Ile Ala
1               5                   10                  15

Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu Arg Tyr
            20                  25                  30
```

```
Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met Lys Gly
        35                  40                  45

Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val His Glu
    50                  55                  60

Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr Trp Glu Gly Asn Glu Pro
65                  70                  75                  80

Gly Glu Thr Thr Gln Ile Thr Tyr His Gln Leu Leu Val Gln Val Cys
                85                  90                  95

Gln Phe Ser Asn Val Leu Arg Lys Gln Gly Ile Gln Lys Gly Asp Arg
            100                 105                 110

Val Ala Ile Tyr Met Pro Met Ile Pro Glu Leu Val Val Ala Met Leu
        115                 120                 125

Ala Cys Ala Arg Ile Gly Ala Leu His Ser Ile Val Phe Ala Gly Phe
    130                 135                 140

Ser Ser Glu Ser Leu Cys Glu Arg Ile Leu Asp Ser Ser Cys Ser Leu
145                 150                 155                 160

Leu Ile Thr
```

<210> 2046
<211> 37
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 517; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 2; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000418152"

<400> 2046
Met Met Val Arg Trp Ala Leu Leu Cys Gly Glu Cys Arg Ile Leu Gly
1   5   10   15

Arg His Cys Gln Gly Ile Leu Leu Glu Asp Ser Met Pro Trp Pro Ile
            20   25   30

Pro Ser Val Gln Leu
        35

<210> 2047
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase short-chain family
      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418362"

<400> 2047
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1   5   10   15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
            20   25   30

Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
        35   40   45

Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Trp Gly Asp
    50   55   60

Ile Ala Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu
65   70   75   80

```
Arg Tyr Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met
                85                  90                  95

Lys Gly Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val
            100                 105                 110

His Glu Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr
        115                 120
```

<210> 2048
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
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<223> /note="Gene Symbol: ACSS2; "

<220>
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<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418608"

<400> 2048

```
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1               5                  10                  15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
            20                  25                  30

Pro Glu Asn Ser Gly Glu Thr Leu Pro Arg Asn Phe Thr Gly Arg Leu
        35                  40                  45

His Ala Leu Ala His Ser Phe Gly Thr Thr Leu Met
    50                  55                  60
```

<210> 2049
<211> 182
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
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<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418812"

<400> 2049
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1 5 10 15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
20 25 30

Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
35 40 45

Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Trp Gly Asp
50 55 60

Ile Ala Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu
65 70 75 80

Arg Tyr Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met
85 90 95

Lys Gly Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val
100 105 110

His Glu Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr Cys Gly Asp Val
115 120 125

Val Leu Pro Cys Trp Pro Gly Trp Ser Gln Leu Pro Asp Leu Arg Glu
130 135 140

```
Gly Asn Glu Pro Gly Glu Thr Thr Gln Ile Thr Tyr His Gln Leu Leu
145                 150                 155                 160


Val Gln Val Cys Gln Phe Ser Asn Val Leu Arg Lys Gln Gly Ile Gln
                165                 170                 175


Lys Gly Asp Arg Val Ala
            180


<210> 2050
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
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<223> /note="Gene Name:
      acyl-CoA synthetase short-chain family
      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419167"

<400> 2050
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1               5                   10                  15


Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
            20                  25                  30


Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
        35                  40                  45


Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Tyr Trp Lys
    50                  55                  60


Thr Pro Cys Pro Gly Pro Phe Leu Arg Tyr Asn Phe Asp Val Thr Lys
65                  70                  75                  80


Gly Lys Ile Phe Ile Glu Trp Met Lys Gly Ala Thr Thr Asn Ile Cys
```

85 90 95

Tyr Asn Val Leu Asp Arg Asn Val His Glu Lys Lys Leu Gly Asp Lys
100 105 110

Val Ala Phe Tyr Trp Glu Gly Asn Glu Pro Gly Glu Thr Thr Gln Ile
115 120 125

Thr Tyr His Gln Leu Leu Val Gln Val Cys Gln Phe Ser Asn Val Leu
130 135 140

Arg Lys Gln
145

<210> 2051
<211> 203
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419925"

<400> 2051
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1 5 10 15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
20 25 30

Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
35 40 45

Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Trp Gly Asp
50 55 60

```
Ile Ala Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu
65                  70                  75                  80

Arg Tyr Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met
                85                  90                  95

Lys Gly Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val
            100                 105                 110

His Glu Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr Trp Ser Thr Ser
        115                 120                 125

Gly Asn Ser Ser Tyr Arg Tyr Thr Cys Arg Glu Gly Asn Glu Pro Gly
    130                 135                 140

Glu Thr Thr Gln Ile Thr Tyr His Gln Leu Leu Val Gln Val Cys Gln
145                 150                 155                 160

Phe Ser Asn Val Leu Arg Lys Gln Gly Ile Gln Lys Gly Asp Arg Val
                165                 170                 175

Ala Ile Tyr Met Pro Met Ile Pro Glu Leu Val Val Ala Met Leu Ala
            180                 185                 190

Cys Ala Arg Ile Gly Ala Leu His Ser Ile Val
        195                 200


<210> 2052
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
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      member 2; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000420105"

<400> 2052
Met Met Val Arg Trp Ala Leu Leu Cys Glu Phe Trp Gly Asp Ile Ala
1   5   10   15

Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu Arg Tyr
            20   25   30

Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met Lys Gly
        35   40   45

Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val His Glu
    50   55   60

Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr
65   70

<210> 2053
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 517; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS2; "

<220>
<221> source
<223> /note="Gene Name:
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      member 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420351"

<400> 2053
Met Gly Leu Pro Glu Glu Arg Val Arg Ser Gly Ser Gly Ser Arg Gly
1   5   10   15

Gln Glu Glu Ala Gly Ala Gly Gly Arg Ala Arg Ser Trp Ser Pro Pro
            20   25   30

```
Pro Glu Val Ser Arg Ser Ala His Val Pro Ser Leu Gln Arg Tyr Arg
        35                  40                  45

Glu Leu His Arg Arg Ser Val Glu Glu Pro Arg Glu Phe Trp Gly Asp
    50                  55                  60

Ile Ala Lys Glu Phe Tyr Trp Lys Thr Pro Cys Pro Gly Pro Phe Leu
65                  70                  75                  80

Arg Tyr Asn Phe Asp Val Thr Lys Gly Lys Ile Phe Ile Glu Trp Met
                85                  90                  95

Lys Gly Ala Thr Thr Asn Ile Cys Tyr Asn Val Leu Asp Arg Asn Val
            100                 105                 110

His Glu Lys Lys Leu Gly Asp Lys Val Ala Phe Tyr Trp Cys Ser Ser
        115                 120                 125

Ser Pro Gly Gln Gly Ser Cys Ala Gln Ser Met Gly Thr Thr Asn Ala
    130                 135                 140

Leu Arg Gln Pro Thr Leu Arg Ser Phe Leu Asp Thr Met Leu Gln Glu
145                 150                 155                 160

Met Ala Ala Ser Gly Thr Arg Met Ala Ile Thr Gly Ser Leu Ala Gly
                165                 170                 175

Leu Met Thr Cys Ser Met Tyr Leu Asp Thr Cys
            180                 185


<210> 2054
<211> 685
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 518; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase short-chain family
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member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000261206"

<400> 2054

```
Met Lys Pro Ser Trp Leu Gln Cys Arg Lys Val Thr Ser Ala Gly Gly
1               5                  10                  15

Leu Gly Gly Pro Leu Pro Gly Ser Ser Pro Ala Arg Gly Ala Gly Ala
            20                  25                  30

Ala Leu Arg Ala Leu Val Val Pro Gly Pro Arg Gly Gly Leu Gly Gly
        35                  40                  45

Arg Gly Cys Arg Ala Leu Ser Ser Gly Ser Gly Ser Glu Tyr Lys Thr
    50                  55                  60

His Phe Ala Ala Ser Val Thr Asp Pro Glu Arg Phe Trp Gly Lys Ala
65                  70                  75                  80

Ala Glu Gln Ile Ser Trp Tyr Lys Pro Trp Thr Lys Thr Leu Glu Asn
                85                  90                  95

Lys His Ser Pro Ser Thr Arg Phe Val Glu Gly Met Leu Asn Ile Cys
            100                 105                 110

Tyr Asn Ala Val Asp Arg His Ile Glu Asn Gly Lys Gly Asp Lys Ile
        115                 120                 125

Ala Ile Ile Tyr Asp Ser Pro Val Thr Asn Thr Lys Ala Thr Phe Thr
    130                 135                 140

Tyr Lys Glu Val Leu Glu Gln Val Ser Lys Leu Ala Gly Val Leu Val
145                 150                 155                 160

Lys His Gly Ile Lys Lys Gly Asp Thr Val Val Ile Tyr Met Pro Met
                165                 170                 175

Ile Pro Gln Ala Met Tyr Thr Met Leu Ala Cys Ala Arg Ile Gly Ala
            180                 185                 190

Ile His Ser Leu Ile Phe Gly Gly Phe Ala Ser Lys Glu Leu Ser Ser
        195                 200                 205
```

```
Arg Ile Asp His Val Lys Pro Lys Val Val Val Thr Ala Ser Phe Gly
    210                 215                 220

Ile Glu Pro Gly Arg Arg Val Glu Tyr Val Pro Leu Val Glu Glu Ala
225                 230                 235                 240

Leu Lys Ile Gly Gln His Lys Pro Asp Lys Ile Leu Ile Tyr Asn Arg
                245                 250                 255

Pro Asn Met Glu Ala Val Pro Leu Ala Pro Gly Arg Asp Leu Asp Trp
            260                 265                 270

Asp Glu Glu Met Ala Lys Ala Gln Ser His Asp Cys Val Pro Val Leu
        275                 280                 285

Ser Glu His Pro Leu Tyr Ile Leu Tyr Thr Ser Gly Thr Thr Gly Leu
    290                 295                 300

Pro Lys Gly Val Ile Arg Pro Thr Gly Gly Tyr Ala Val Met Leu His
305                 310                 315                 320

Trp Ser Met Ser Ser Ile Tyr Gly Leu Gln Pro Gly Glu Val Trp Trp
                325                 330                 335

Ala Ala Ser Asp Leu Gly Trp Val Val Gly His Ser Tyr Ile Cys Tyr
            340                 345                 350

Gly Pro Leu Leu His Gly Asn Thr Thr Val Leu Tyr Glu Gly Lys Pro
        355                 360                 365

Val Gly Thr Pro Asp Ala Gly Ala Tyr Phe Arg Val Leu Ala Glu His
    370                 375                 380

Gly Val Ala Ala Leu Phe Thr Ala Pro Thr Ala Ile Arg Ala Ile Arg
385                 390                 395                 400

Gln Gln Asp Pro Gly Ala Ala Leu Gly Lys Gln Tyr Ser Leu Thr Arg
                405                 410                 415

Phe Lys Thr Leu Phe Val Ala Gly Glu Arg Cys Asp Val Glu Thr Leu
            420                 425                 430
```

```
Glu Trp Ser Lys Asn Val Phe Arg Val Pro Val Leu Asp His Trp Trp
        435                 440                 445

Gln Thr Glu Thr Gly Ser Pro Ile Thr Ala Ser Cys Val Gly Leu Gly
    450                 455                 460

Asn Ser Lys Thr Pro Pro Pro Gly Gln Ala Gly Lys Ser Val Pro Gly
465                 470                 475                 480

Tyr Asn Val Met Ile Leu Asp Asp Asn Met Gln Lys Leu Lys Ala Arg
                485                 490                 495

Cys Leu Gly Asn Ile Val Val Lys Leu Pro Leu Pro Pro Gly Ala Phe
            500                 505                 510

Ser Gly Leu Trp Lys Asn Gln Glu Ala Phe Lys His Leu Tyr Phe Glu
        515                 520                 525

Lys Phe Pro Gly Tyr Tyr Asp Thr Met Asp Ala Gly Tyr Met Asp Glu
    530                 535                 540

Glu Gly Tyr Leu Tyr Val Met Ser Arg Val Asp Asp Val Ile Asn Val
545                 550                 555                 560

Ala Gly His Arg Ile Ser Ala Gly Ala Ile Glu Glu Ser Ile Leu Ser
                565                 570                 575

His Gly Thr Val Ala Asp Cys Ala Val Val Gly Lys Glu Asp Pro Leu
            580                 585                 590

Lys Gly His Val Pro Leu Ala Leu Cys Val Leu Arg Lys Asp Ile Asn
        595                 600                 605

Ala Thr Glu Glu Gln Val Leu Glu Glu Ile Val Lys His Val Arg Gln
    610                 615                 620

Asn Ile Gly Pro Val Ala Ala Phe Arg Asn Ala Val Phe Val Lys Gln
625                 630                 635                 640

Leu Pro Lys Thr Arg Ser Gly Lys Ile Pro Arg Ser Ala Leu Ser Ala
                645                 650                 655
```

```
Ile Val Asn Gly Lys Pro Tyr Lys Ile Thr Ser Thr Ile Glu Asp Pro
            660                 665                 670

Ser Ile Phe Gly His Val Glu Glu Met Leu Lys Gln Ala
        675                 680                 685


<210> 2055
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 518; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS3; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA synthetase short-chain family
      member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000447748"

<400> 2055
Met Leu Asn Ile Cys Tyr Asn Ala Val Asp Arg His Ile Glu Asn Gly
1               5                   10                  15

Lys Gly Asp Lys Ile Ala Ile Ile Tyr Asp Ser Pro Val Thr Asn Thr
            20                  25                  30

Lys Ala Thr Phe Thr Tyr Lys Glu Val Leu Glu Gln Val Ser Lys Leu
        35                  40                  45

Ala Gly Val Leu Val Lys His Gly Ile Lys Lys Gly Asp Thr Val Val
    50                  55                  60

Ile Tyr Met Pro Met Ile Pro Gln Ala Met Tyr Thr Met Leu Ala Cys
65                  70                  75                  80

Ala Arg Ile Gly Ala Ile His Ser Leu Ile Phe Gly Gly
                85                  90


<210> 2056
```

<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 518; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000449507"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2056
Xaa Leu Ala Glu His Gly Val Ala Ala Leu Phe Thr Ala Pro Thr Ala
1 5 10 15

Ile Arg Ala Ile Arg Gln Gln Asp Pro Gly Ala Ala Leu Gly Lys Gln
20 25 30

Tyr Ser Leu Thr Arg Phe Lys Thr Leu Phe Val Ala Gly Glu Arg Cys
35 40 45

Asp Val Glu Thr Leu Glu Trp Ser Lys Asn Val Phe Arg Val Pro Val
50 55 60

Leu Asp His Trp Trp Gln Thr Gly Ile Lys His
65 70 75

<210> 2057
<211> 686
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 518; "

<220>
<221> source
<223> /note="Gene Symbol: ACSS3; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA synthetase short-chain family
member 3; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H6R3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000449535"

<400> 2057
Met Lys Pro Ser Trp Leu Gln Cys Arg Lys Val Thr Ser Ala Gly Gly
1   5   10   15

Leu Gly Gly Pro Leu Pro Gly Ser Ser Pro Ala Arg Gly Ala Gly Ala
            20   25   30

Ala Leu Arg Ala Leu Val Val Pro Gly Pro Arg Gly Gly Leu Gly Gly
        35   40   45

Arg Gly Cys Arg Ala Leu Ser Ser Gly Ser Gly Ser Glu Tyr Lys Thr
    50   55   60

His Phe Ala Ala Ser Val Thr Asp Pro Glu Arg Phe Trp Gly Lys Ala
65   70   75   80

Ala Glu Gln Ile Ser Trp Tyr Lys Pro Trp Thr Lys Thr Leu Glu Asn
                85   90   95

Lys His Ser Pro Ser Thr Arg Trp Phe Val Glu Gly Met Leu Asn Ile
            100   105   110

Cys Tyr Asn Ala Val Asp Arg His Ile Glu Asn Gly Lys Gly Asp Lys
        115   120   125

Ile Ala Ile Ile Tyr Asp Ser Pro Val Thr Asn Thr Lys Ala Thr Phe
    130   135   140

Thr Tyr Lys Glu Val Leu Glu Gln Val Ser Lys Leu Ala Gly Val Leu

145 150 155 160

Val Lys His Gly Ile Lys Lys Gly Asp Thr Val Val Ile Tyr Met Pro
165 170 175

Met Ile Pro Gln Ala Met Tyr Thr Met Leu Ala Cys Ala Arg Ile Gly
180 185 190

Ala Ile His Ser Leu Ile Phe Gly Gly Phe Ala Ser Lys Glu Leu Ser
195 200 205

Ser Arg Ile Asp His Val Lys Pro Lys Val Val Val Thr Ala Ser Phe
210 215 220

Gly Ile Glu Pro Gly Arg Arg Val Glu Tyr Val Pro Leu Val Glu Glu
225 230 235 240

Ala Leu Lys Ile Gly Gln His Lys Pro Asp Lys Ile Leu Ile Tyr Asn
245 250 255

Arg Pro Asn Met Glu Ala Val Pro Leu Ala Pro Gly Arg Asp Leu Asp
260 265 270

Trp Asp Glu Glu Met Ala Lys Ala Gln Ser His Asp Cys Val Pro Val
275 280 285

Leu Ser Glu His Pro Leu Tyr Ile Leu Tyr Thr Ser Gly Thr Thr Gly
290 295 300

Leu Pro Lys Gly Val Ile Arg Pro Thr Gly Gly Tyr Ala Val Met Leu
305 310 315 320

His Trp Ser Met Ser Ser Ile Tyr Gly Leu Gln Pro Gly Glu Val Trp
325 330 335

Trp Ala Ala Ser Asp Leu Gly Trp Val Val Gly His Ser Tyr Ile Cys
340 345 350

Tyr Gly Pro Leu Leu His Gly Asn Thr Thr Val Leu Tyr Glu Gly Lys
355 360 365

Pro Val Gly Thr Pro Asp Ala Gly Ala Tyr Phe Arg Val Leu Ala Glu
370 375 380

```
His Gly Val Ala Ala Leu Phe Thr Ala Pro Thr Ala Ile Arg Ala Ile
385                 390                 395                 400

Arg Gln Gln Asp Pro Gly Ala Ala Leu Gly Lys Gln Tyr Ser Leu Thr
                405                 410                 415

Arg Phe Lys Thr Leu Phe Val Ala Gly Glu Arg Cys Asp Val Glu Thr
            420                 425                 430

Leu Glu Trp Ser Lys Asn Val Phe Arg Val Pro Val Leu Asp His Trp
        435                 440                 445

Trp Gln Thr Glu Thr Gly Ser Pro Ile Thr Ala Ser Cys Val Gly Leu
    450                 455                 460

Gly Asn Ser Lys Thr Pro Pro Pro Gly Gln Ala Gly Lys Ser Val Pro
465                 470                 475                 480

Gly Tyr Asn Val Met Ile Leu Asp Asp Asn Met Gln Lys Leu Lys Ala
                485                 490                 495

Arg Cys Leu Gly Asn Ile Val Val Lys Leu Pro Leu Pro Pro Gly Ala
            500                 505                 510

Phe Ser Gly Leu Trp Lys Asn Gln Glu Ala Phe Lys His Leu Tyr Phe
        515                 520                 525

Glu Lys Phe Pro Gly Tyr Tyr Asp Thr Met Asp Ala Gly Tyr Met Asp
    530                 535                 540

Glu Glu Gly Tyr Leu Tyr Val Met Ser Arg Val Asp Asp Val Ile Asn
545                 550                 555                 560

Val Ala Gly His Arg Ile Ser Ala Gly Ala Ile Glu Glu Ser Ile Leu
                565                 570                 575

Ser His Gly Thr Val Ala Asp Cys Ala Val Val Gly Lys Glu Asp Pro
            580                 585                 590

Leu Lys Gly His Val Pro Leu Ala Leu Cys Val Leu Arg Lys Asp Ile
        595                 600                 605
```

```
Asn Ala Thr Glu Glu Gln Val Leu Glu Glu Ile Val Lys His Val Arg
    610                 615                 620

Gln Asn Ile Gly Pro Val Ala Ala Phe Arg Asn Ala Val Phe Val Lys
625                 630                 635                 640

Gln Leu Pro Lys Thr Arg Ser Gly Lys Ile Pro Arg Ser Ala Leu Ser
                645                 650                 655

Ala Ile Val Asn Gly Lys Pro Tyr Lys Ile Thr Ser Thr Ile Glu Asp
            660                 665                 670

Pro Ser Ile Phe Gly His Val Glu Glu Met Leu Lys Gln Ala
        675                 680                 685
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<210> 2058
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 519; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT1; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q86TX2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000311224"

<400> 2058

```
Met Ala Ala Thr Leu Ile Leu Glu Pro Ala Gly Arg Cys Cys Trp Asp
1               5                   10                  15

Glu Pro Val Arg Ile Ala Val Arg Gly Leu Ala Pro Glu Gln Pro Val
            20                  25                  30

Thr Leu Arg Ala Ser Leu Arg Asp Glu Lys Gly Ala Leu Phe Gln Ala
```

```
        35                  40                  45

His Ala Arg Tyr Arg Ala Asp Thr Leu Gly Glu Leu Asp Leu Glu Arg
    50                  55                  60

Ala Pro Ala Leu Gly Gly Ser Phe Ala Gly Leu Glu Pro Met Gly Leu
65                  70                  75                  80

Leu Trp Ala Leu Glu Pro Glu Lys Pro Leu Val Arg Leu Val Lys Arg
                85                  90                  95

Asp Val Arg Thr Pro Leu Ala Val Glu Leu Glu Val Leu Asp Gly His
            100                 105                 110

Asp Pro Asp Pro Gly Arg Leu Leu Cys Arg Val Arg His Glu Arg Tyr
        115                 120                 125

Phe Leu Pro Pro Gly Val Arg Arg Glu Pro Val Arg Ala Gly Arg Val
    130                 135                 140

Arg Gly Thr Leu Phe Leu Pro Pro Glu Pro Gly Pro Phe Pro Gly Ile
145                 150                 155                 160

Val Asp Met Phe Gly Thr Gly Gly Gly Leu Leu Glu Tyr Arg Ala Ser
                165                 170                 175

Leu Leu Ala Gly Lys Gly Phe Ala Val Met Ala Leu Ala Tyr Tyr Asn
            180                 185                 190

Tyr Glu Asp Leu Pro Lys Thr Met Glu Thr Leu His Leu Glu Tyr Phe
        195                 200                 205

Glu Glu Ala Val Asn Tyr Leu Leu Ser His Pro Glu Val Lys Gly Pro
    210                 215                 220

Gly Val Gly Leu Leu Gly Ile Ser Lys Gly Gly Glu Leu Cys Leu Ser
225                 230                 235                 240

Met Ala Ser Phe Leu Lys Gly Ile Thr Ala Ala Val Val Ile Asn Gly
                245                 250                 255

Ser Val Ala Asn Val Gly Gly Thr Leu Arg Tyr Lys Gly Glu Thr Leu
            260                 265                 270
```

```
Pro Pro Val Gly Val Asn Arg Asn Arg Ile Lys Val Thr Lys Asp Gly
        275                 280                 285

Tyr Ala Asp Ile Val Asp Val Leu Asn Ser Pro Leu Glu Gly Pro Asp
    290                 295                 300

Gln Lys Ser Phe Ile Pro Val Glu Arg Ala Glu Ser Thr Phe Leu Phe
305                 310                 315                 320

Leu Val Gly Gln Asp Asp His Asn Trp Lys Ser Glu Phe Tyr Ala Asn
                325                 330                 335

Glu Ala Cys Lys Arg Leu Gln Ala His Gly Arg Arg Lys Pro Gln Ile
            340                 345                 350

Ile Cys Tyr Pro Glu Thr Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro
        355                 360                 365

Leu Cys Arg Ala Ser Leu His Ala Leu Val Gly Ser Pro Ile Ile Trp
    370                 375                 380

Gly Gly Glu Pro Arg Ala His Ala Met Ala Gln Val Asp Ala Trp Lys
385                 390                 395                 400

Gln Leu Gln Thr Phe Phe His Lys His Leu Gly Gly His Glu Gly Thr
                405                 410                 415

Ile Pro Ser Lys Val
            420


<210> 2059
<211> 395
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 519; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT1; "

<220>
<221> source
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<223> /note="Gene Name:
acyl-CoA thioesterase 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451764"

<400> 2059

```
Met Ala Ala Thr Leu Ile Leu Glu Pro Ala Gly Arg Cys Cys Trp Asp
1               5                  10                  15

Glu Pro Val Arg Ile Ala Val Arg Gly Leu Ala Pro Glu Gln Pro Val
            20                  25                  30

Thr Leu Arg Ala Ser Leu Arg Asp Glu Lys Gly Ala Leu Phe Gln Ala
        35                  40                  45

His Ala Arg Tyr Arg Ala Asp Thr Leu Gly Glu Leu Asp Leu Glu Arg
    50                  55                  60

Ala Pro Ala Leu Gly Gly Ser Phe Ala Gly Leu Glu Pro Met Gly Leu
65                  70                  75                  80

Leu Trp Ala Leu Glu Pro Glu Lys Pro Leu Val Arg Leu Val Lys Arg
                85                  90                  95

Asp Val Arg Thr Pro Leu Ala Val Glu Leu Glu Val Leu Asp Gly His
            100                 105                 110

Asp Pro Asp Pro Gly Arg Leu Leu Cys Arg Val Arg His Glu Arg Tyr
        115                 120                 125

Phe Leu Pro Pro Gly Val Arg Arg Glu Pro Val Arg Ala Gly Arg Val
    130                 135                 140

Arg Gly Thr Leu Phe Leu Pro Pro Glu Pro Gly Pro Phe Pro Gly Ile
145                 150                 155                 160

Val Asp Met Phe Gly Thr Gly Gly Gly Leu Leu Glu Tyr Arg Ala Ser
                165                 170                 175

Leu Leu Ala Gly Lys Gly Phe Ala Val Met Ala Leu Ala Tyr Tyr Asn
            180                 185                 190

Tyr Glu Asp Leu Pro Lys Thr Met Glu Thr Leu His Leu Glu Tyr Phe
```

195 200 205

Glu Glu Ala Val Asn Tyr Leu Leu Ser His Pro Glu Gly Ile Thr Ala
210 215 220

Ala Val Val Ile Asn Gly Ser Val Ala Asn Val Gly Gly Thr Leu Arg
225 230 235 240

Tyr Lys Gly Glu Thr Leu Pro Pro Val Gly Val Asn Arg Asn Arg Ile
245 250 255

Lys Val Thr Lys Asp Gly Tyr Ala Asp Ile Val Asp Val Leu Asn Ser
260 265 270

Pro Leu Glu Gly Pro Asp Gln Lys Ser Phe Ile Pro Val Glu Arg Ala
275 280 285

Glu Ser Thr Phe Leu Phe Leu Val Gly Gln Asp Asp His Asn Trp Lys
290 295 300

Ser Glu Phe Tyr Ala Asn Glu Ala Cys Lys Arg Leu Gln Ala His Gly
305 310 315 320

Arg Arg Lys Pro Gln Ile Ile Cys Tyr Pro Glu Thr Gly His Tyr Ile
325 330 335

Glu Pro Pro Tyr Phe Pro Leu Cys Arg Ala Ser Leu His Ala Leu Val
340 345 350

Gly Ser Pro Ile Ile Trp Gly Gly Glu Pro Arg Ala His Ala Met Ala
355 360 365

Gln Val Asp Ala Trp Lys Gln Leu Gln Thr Phe Phe His Lys His Leu
370 375 380

Gly Gly His Glu Gly Thr Ile Pro Ser Lys Val
385 390 395

<210> 2060
<211> 594
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 520; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT11; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 11; "

<220>
<221> source
<223> /note="Uniprot ID: Q8WXI4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000340260"

<400> 2060
Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Leu Ala Ser Val
1   5   10   15

Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp
            20   25   30

Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
        35   40   45

Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
    50   55   60

Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
65   70   75   80

Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
                85   90   95

Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
            100   105   110

Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
        115   120   125

Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
    130   135   140

```
Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
145                 150                 155                 160

Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val
                165                 170                 175

Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
            180                 185                 190

Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
        195                 200                 205

Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu
    210                 215                 220

Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly
225                 230                 235                 240

Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg
                245                 250                 255

Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe
            260                 265                 270

Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val
        275                 280                 285

Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala
    290                 295                 300

Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe
305                 310                 315                 320

Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro
                325                 330                 335

Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala
            340                 345                 350

Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys
        355                 360                 365

Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
```

370 375 380

Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
385 390 395 400

Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
405 410 415

Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
420 425 430

His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
435 440 445

Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
450 455 460

Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
465 470 475 480

Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
485 490 495

Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
500 505 510

Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
515 520 525

Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Val
530 535 540

Ser Tyr Tyr Asn Gln Ala Thr Pro Gly Val Leu Asn Tyr Val Thr Thr
545 550 555 560

Asn Val Ala Gly Leu Ser Ser Glu Phe Tyr Thr Thr Phe Lys Ala Cys
565 570 575

Glu Gln Phe Leu Leu Asp Asn Arg Asn Asp Leu Ala Pro Ser Leu Gln
580 585 590

Thr Leu

<210> 2061
<211> 607
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 520; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT11; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 11; "

<220>
<221> source
<223> /note="Uniprot ID: Q8WXI4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000360366"

<400> 2061
Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Leu Ala Ser Val
1   5   10   15

Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp
            20   25   30

Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
        35   40   45

Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
    50   55   60

Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
65   70   75   80

Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
                85   90   95

Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
            100   105   110

```
Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
        115                 120                 125

Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
    130                 135                 140

Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
145                 150                 155                 160

Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val
                165                 170                 175

Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
            180                 185                 190

Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
        195                 200                 205

Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu
    210                 215                 220

Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly
225                 230                 235                 240

Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg
                245                 250                 255

Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe
            260                 265                 270

Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val
        275                 280                 285

Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala
    290                 295                 300

Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe
305                 310                 315                 320

Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro
                325                 330                 335

Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala
```

```
            340                 345                 350

Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys
        355                 360                 365

Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
    370                 375                 380

Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
385                 390                 395                 400

Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
                405                 410                 415

Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
            420                 425                 430

His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
        435                 440                 445

Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
    450                 455                 460

Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
465                 470                 475                 480

Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
                485                 490                 495

Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
            500                 505                 510

Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
        515                 520                 525

Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Cys
    530                 535                 540

Cys Trp Val Arg Val Ser Leu Thr Glu Leu Val Ser Ala Ser Gly Phe
545                 550                 555                 560

Tyr Ser Trp Gly Leu Glu Ser Arg Ser Lys Gly Arg Arg Ser Asp Gly
                565                 570                 575
```

```
Trp Asn Gly Lys Leu Ala Gly Gly His Leu Ser Thr Leu Lys Ala Ile
            580                 585                 590

Pro Val Ala Lys Ile Asn Ser Arg Phe Gly Tyr Leu Gln Asp Thr
        595                 600                 605


<210> 2062
<211> 555
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 521; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT12; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 12; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8WYK0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000303246"

<400> 2062
Met Glu Arg Pro Ala Pro Gly Glu Val Val Met Ser Gln Ala Ile Gln
1               5                   10                  15

Pro Ala His Ala Thr Ala Arg Gly Glu Leu Ser Ala Gly Gln Leu Leu
            20                  25                  30

Lys Trp Ile Asp Thr Thr Ala Cys Leu Ala Ala Glu Lys His Ala Gly
        35                  40                  45

Val Ser Cys Val Thr Ala Ser Val Asp Asp Ile Gln Phe Glu Glu Thr
    50                  55                  60

Ala Arg Val Gly Gln Val Ile Thr Ile Lys Ala Lys Val Thr Arg Ala
65                  70                  75                  80
```

```
Phe Ser Thr Ser Met Glu Ile Ser Ile Lys Val Met Val Gln Asp Met
                85                  90                  95

Leu Thr Gly Ile Glu Lys Leu Val Ser Val Ala Phe Ser Thr Phe Val
            100                 105                 110

Ala Lys Pro Val Gly Lys Glu Lys Ile His Leu Lys Pro Val Thr Leu
        115                 120                 125

Leu Thr Glu Gln Asp His Val Glu His Asn Leu Ala Ala Glu Arg Arg
    130                 135                 140

Lys Val Arg Leu Gln His Glu Asp Thr Phe Asn Asn Leu Met Lys Glu
145                 150                 155                 160

Ser Ser Lys Phe Asp Asp Leu Ile Phe Asp Glu Glu Glu Gly Ala Val
                165                 170                 175

Ser Thr Arg Gly Thr Ser Val Gln Ser Ile Glu Leu Val Leu Pro Pro
            180                 185                 190

His Ala Asn His His Gly Asn Thr Phe Gly Gly Gln Ile Met Ala Trp
        195                 200                 205

Met Glu Thr Val Ala Thr Ile Ser Ala Ser Arg Leu Cys Trp Ala His
    210                 215                 220

Pro Phe Leu Lys Ser Val Asp Met Phe Lys Phe Arg Gly Pro Ser Thr
225                 230                 235                 240

Val Gly Asp Arg Leu Val Phe Thr Ala Ile Val Asn Asn Thr Phe Gln
                245                 250                 255

Thr Cys Val Glu Val Gly Val Arg Val Glu Ala Phe Asp Cys Gln Glu
            260                 265                 270

Trp Ala Glu Gly Arg Gly Arg His Ile Asn Ser Ala Phe Leu Ile Tyr
        275                 280                 285

Asn Ala Ala Asp Asp Lys Glu Asn Leu Ile Thr Phe Pro Arg Ile Gln
    290                 295                 300

Pro Ile Ser Lys Asp Asp Phe Arg Arg Tyr Arg Gly Ala Ile Ala Arg
```

305 310 315 320

Lys Arg Ile Arg Leu Gly Arg Lys Tyr Val Ile Ser His Lys Glu Glu
325 330 335

Val Pro Leu Cys Ile His Trp Asp Ile Ser Lys Gln Ala Ser Leu Ser
340 345 350

Asp Ser Asn Val Glu Ala Leu Lys Lys Leu Ala Ala Lys Arg Gly Trp
355 360 365

Glu Val Thr Ser Thr Val Glu Lys Ile Lys Ile Tyr Thr Leu Glu Glu
370 375 380

His Asp Val Leu Ser Val Trp Val Glu Lys His Val Gly Ser Pro Ala
385 390 395 400

His Leu Ala Tyr Arg Leu Leu Ser Asp Phe Thr Lys Arg Pro Leu Trp
405 410 415

Asp Pro His Phe Val Ser Cys Glu Val Ile Asp Trp Val Ser Glu Asp
420 425 430

Asp Gln Leu Tyr His Ile Thr Cys Pro Ile Leu Asn Asp Asp Lys Pro
435 440 445

Lys Asp Leu Val Val Leu Val Ser Arg Arg Lys Pro Leu Lys Asp Gly
450 455 460

Asn Thr Tyr Thr Val Ala Val Lys Ser Val Ile Leu Pro Ser Val Pro
465 470 475 480

Pro Ser Pro Gln Tyr Ile Arg Ser Glu Ile Ile Cys Ala Gly Phe Leu
485 490 495

Ile His Ala Ile Asp Ser Asn Ser Cys Ile Val Ser Tyr Phe Asn His
500 505 510

Met Ser Ala Ser Ile Leu Pro Tyr Phe Ala Gly Asn Leu Gly Gly Trp
515 520 525

Ser Lys Ser Ile Glu Glu Thr Ala Ala Ser Cys Ile Gln Phe Leu Glu
530 535 540

Asn Pro Pro Asp Asp Gly Phe Val Ser Thr Phe
545 550 555

<210> 2063
<211> 167
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 521; "

<220>
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<223> /note="Gene Symbol: ACOT12; "

<220>
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<223> /note="Gene Name:
acyl-CoA thioesterase 12; "

<220>
<221> source
<223> /note="Uniprot ID: Q8WYK0; "

<220>
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<223> /note="ENSP ID: ENSP00000421628"

<400> 2063
Met Glu Arg Pro Ala Pro Gly Glu Val Val Met Ser Gln Ala Ile Gln
1 5 10 15

Pro Ala His Ala Thr Ala Arg Gly Glu Leu Ser Ala Gly Gln Leu Leu
20 25 30

Lys Trp Ile Asp Thr Thr Ala Cys Leu Ala Ala Glu Lys His Ala Gly
35 40 45

Val Ser Cys Val Thr Ala Ser Val Asp Asp Ile Gln Phe Glu Glu Thr
50 55 60

Ala Arg Val Gly Gln Val Ile Thr Ile Lys Ala Lys Val Thr Arg Ala
65 70 75 80

Phe Ser Thr Ser Met Glu Ile Ser Ile Lys Val Met Val Gln Asp Met
85 90 95

```
Leu Thr Gly Ile Glu Lys Leu Val Ser Val Ala Phe Ser Thr Phe Val
            100                 105                 110

Ala Lys Pro Val Gly Lys Glu Lys Ile His Leu Lys Pro Val Thr Leu
        115                 120                 125

Leu Thr Glu Gln Asp His Val Glu His Asn Leu Ala Ala Glu Arg Arg
    130                 135                 140

Lys Val Arg Leu Gln His Glu Asp Thr Phe Asn Asn Leu Met Lys Glu
145                 150                 155                 160

Ser Ser Lys Phe Asp Gly Gln
                165


<210> 2064
<211> 140
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 522; "

<220>
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<223> /note="Gene Symbol: ACOT13; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 13; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NPJ3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000230048"

<400> 2064
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
1               5                   10                  15

Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
            20                  25                  30

Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
        35                  40                  45
```

```
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
    50                  55                  60

Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
65                  70                  75                  80

Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
                85                  90                  95

Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
            100                 105                 110

Leu Ala Phe Thr Ser Val Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu
        115                 120                 125

Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
    130                 135                 140


<210> 2065
<211> 117
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 522; "

<220>
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<223> /note="Gene Symbol: ACOT13; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 13; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9NPJ3; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000445552"

<400> 2065
Met Val Arg Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val Ile
1               5                   10                  15
```

Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr Leu
            20   25   30

His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met Ala
        35   40   45

Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met Asn
    50   55   60

Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr
65   70   75   80

Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Asp
                85   90   95

Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr
            100   105   110

Lys His Leu Gly Asn
        115

<210> 2066
<211> 483
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 523; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 2; "

<220>
<221> source
<223> /note="Uniprot ID: P49753; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000238651"

<400> 2066
Met Ser Asn Lys Leu Leu Ser Pro His Pro His Ser Val Val Leu Arg
1   5   10   15

```
Ser Glu Phe Lys Met Ala Ser Ser Pro Ala Val Leu Arg Ala Ser Arg
            20                  25                  30

Leu Tyr Gln Trp Ser Leu Lys Ser Ser Ala Gln Phe Leu Gly Ser Pro
        35                  40                  45

Gln Leu Arg Gln Val Gly Gln Ile Ile Arg Val Pro Ala Arg Met Ala
    50                  55                  60

Ala Thr Leu Ile Leu Glu Pro Ala Gly Arg Cys Cys Trp Asp Glu Pro
65                  70                  75                  80

Val Arg Ile Ala Val Arg Gly Leu Ala Pro Glu Gln Pro Val Thr Leu
                85                  90                  95

Arg Ala Ser Leu Arg Asp Glu Lys Gly Ala Leu Phe Gln Ala His Ala
            100                 105                 110

Arg Tyr Arg Ala Asp Thr Leu Gly Glu Leu Asp Leu Glu Arg Ala Pro
        115                 120                 125

Ala Leu Gly Gly Ser Phe Ala Gly Leu Glu Pro Met Gly Leu Leu Trp
    130                 135                 140

Ala Leu Glu Pro Glu Lys Pro Leu Val Arg Leu Val Lys Arg Asp Val
145                 150                 155                 160

Arg Thr Pro Leu Ala Val Glu Leu Glu Val Leu Asp Gly His Asp Pro
                165                 170                 175

Asp Pro Gly Arg Leu Leu Cys Gln Thr Arg His Glu Arg Tyr Phe Leu
            180                 185                 190

Pro Pro Gly Val Arg Arg Glu Pro Val Arg Val Gly Arg Val Arg Gly
        195                 200                 205

Thr Leu Phe Leu Pro Pro Glu Pro Gly Pro Phe Pro Gly Ile Val Asp
    210                 215                 220

Met Phe Gly Thr Gly Gly Gly Leu Leu Glu Tyr Arg Ala Ser Leu Leu
225                 230                 235                 240
```

```
Ala Gly Lys Gly Phe Ala Val Met Ala Leu Ala Tyr Tyr Asn Tyr Glu
                245                 250                 255

Asp Leu Pro Lys Thr Met Glu Thr Leu His Leu Glu Tyr Phe Glu Glu
            260                 265                 270

Ala Met Asn Tyr Leu Leu Ser His Pro Glu Val Lys Gly Pro Gly Val
        275                 280                 285

Gly Leu Leu Gly Ile Ser Lys Gly Gly Glu Leu Cys Leu Ser Met Ala
    290                 295                 300

Ser Phe Leu Lys Gly Ile Thr Ala Ala Val Val Ile Asn Gly Ser Val
305                 310                 315                 320

Ala Asn Val Gly Gly Thr Leu His Tyr Lys Gly Glu Thr Leu Pro Pro
                325                 330                 335

Val Gly Val Asn Arg Asn Arg Ile Lys Val Thr Lys Asp Gly Tyr Ala
            340                 345                 350

Asp Ile Val Asp Val Leu Asn Ser Pro Leu Glu Gly Pro Asp Gln Lys
        355                 360                 365

Ser Phe Ile Pro Val Glu Arg Ala Glu Ser Thr Phe Leu Phe Leu Val
    370                 375                 380

Gly Gln Asp Asp His Asn Trp Lys Ser Glu Phe Tyr Ala Asn Glu Ala
385                 390                 395                 400

Cys Lys Arg Leu Gln Ala His Gly Arg Arg Lys Pro Gln Ile Ile Cys
                405                 410                 415

Tyr Pro Glu Thr Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro Leu Cys
            420                 425                 430

Arg Ala Ser Leu His Ala Leu Val Gly Ser Pro Ile Ile Trp Gly Gly
        435                 440                 445

Glu Pro Arg Ala His Ala Met Ala Gln Val Asp Ala Trp Lys Gln Leu
    450                 455                 460
```

Gln Thr Phe Phe His Lys His Leu Gly Gly His Glu Gly Thr Ile Pro
465 470 475 480

Ser Lys Val

<210> 2067
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 523; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000440961"

<400> 2067
Met Ala Ser Ser Pro Ala Val Leu Arg Ala Ser Arg Leu Tyr Gln Trp
1 5 10 15

Ser Leu Lys Ser Ser Ala Gln Phe Leu Gly Ser Pro Gln Leu Arg Gln
20 25 30

Asn Leu Gly Pro Phe Leu Gly Leu Trp Thr Cys Ser Glu Leu Glu Val
35 40 45

Ala Cys Trp Ser Ile Gly Leu Val Cys Trp Leu Gly Arg Val Leu Leu
50 55 60

<210> 2068
<211> 463
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 523; "

<220>

<221> source
<223> /note="Gene Symbol: ACOT2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000477685"

<400> 2068

```
Met Ala Ser Ser Pro Ala Val Leu Arg Ala Ser Arg Leu Tyr Gln Trp
1               5                  10                  15

Ser Leu Lys Ser Ser Ala Gln Phe Leu Gly Ser Pro Gln Leu Arg Gln
            20                  25                  30

Val Gly Gln Ile Ile Arg Val Pro Ala Arg Met Ala Ala Thr Leu Ile
        35                  40                  45

Leu Glu Pro Ala Gly Arg Cys Cys Trp Asp Glu Pro Val Arg Ile Ala
    50                  55                  60

Val Arg Gly Leu Ala Pro Glu Gln Pro Val Thr Leu Arg Ala Ser Leu
65                  70                  75                  80

Arg Asp Glu Lys Gly Ala Leu Phe Gln Ala His Ala Arg Tyr Arg Ala
                85                  90                  95

Asp Thr Leu Gly Glu Leu Asp Leu Glu Arg Ala Pro Ala Leu Gly Gly
            100                 105                 110

Ser Phe Ala Gly Leu Glu Pro Met Gly Leu Leu Trp Ala Leu Glu Pro
        115                 120                 125

Glu Lys Pro Leu Val Arg Leu Val Lys Arg Asp Val Arg Thr Pro Leu
    130                 135                 140

Ala Val Glu Leu Glu Val Leu Asp Gly His Asp Pro Asp Pro Gly Arg
145                 150                 155                 160

Leu Leu Cys Gln Thr Arg His Glu Arg Tyr Phe Leu Pro Pro Gly Val
                165                 170                 175
```

```
Arg Arg Glu Pro Val Arg Val Gly Arg Val Arg Gly Thr Leu Phe Leu
            180                 185                 190

Pro Pro Glu Pro Gly Pro Phe Pro Gly Ile Val Asp Met Phe Gly Thr
        195                 200                 205

Gly Gly Gly Leu Leu Glu Tyr Arg Ala Ser Leu Leu Ala Gly Lys Gly
    210                 215                 220

Phe Ala Val Met Ala Leu Ala Tyr Tyr Asn Tyr Glu Asp Leu Pro Lys
225                 230                 235                 240

Thr Met Glu Thr Leu His Leu Glu Tyr Phe Glu Glu Ala Met Asn Tyr
                245                 250                 255

Leu Leu Ser His Pro Glu Val Lys Gly Pro Gly Val Gly Leu Leu Gly
            260                 265                 270

Ile Ser Lys Gly Gly Glu Leu Cys Leu Ser Met Ala Ser Phe Leu Lys
        275                 280                 285

Gly Ile Thr Ala Ala Val Val Ile Asn Gly Ser Val Ala Asn Val Gly
    290                 295                 300

Gly Thr Leu His Tyr Lys Gly Glu Thr Leu Pro Pro Val Gly Val Asn
305                 310                 315                 320

Arg Asn Arg Ile Lys Val Thr Lys Asp Gly Tyr Ala Asp Ile Val Asp
                325                 330                 335

Val Leu Asn Ser Pro Leu Glu Gly Pro Asp Gln Lys Ser Phe Ile Pro
            340                 345                 350

Val Glu Arg Ala Glu Ser Thr Phe Leu Phe Leu Val Gly Gln Asp Asp
        355                 360                 365

His Asn Trp Lys Ser Glu Phe Tyr Ala Asn Glu Ala Cys Lys Arg Leu
    370                 375                 380

Gln Ala His Gly Arg Arg Lys Pro Gln Ile Ile Cys Tyr Pro Glu Thr
385                 390                 395                 400

Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro Leu Cys Arg Ala Ser Leu
```

405 410 415

His Ala Leu Val Gly Ser Pro Ile Ile Trp Gly Gly Glu Pro Arg Ala
420 425 430

His Ala Met Ala Gln Val Asp Ala Trp Lys Gln Leu Gln Thr Phe Phe
435 440 445

His Lys His Leu Gly Gly His Glu Gly Thr Ile Pro Ser Lys Val
450 455 460

<210> 2069
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 523; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT2; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483704"

<400> 2069
Met Ala Ala Thr Leu Ile Leu Glu Pro Ala Gly Arg Cys Cys Trp Asp
1 5 10 15

Glu Pro Val Arg Ile Ala Val Arg Gly Leu Ala Pro Glu Gln Pro Val
20 25 30

Thr Leu Arg Ala Ser Leu Arg Asp Glu Lys Gly Ala Leu Phe Gln Ala
35 40 45

His Ala Arg Tyr Arg Ala Asp Thr Leu Gly Glu Leu Asp Leu Glu Arg
50 55 60

Ala Pro Ala Leu Gly Gly Ser Phe Ala Gly Leu Glu Pro Met Gly Leu
65 70 75 80

```
Leu Trp Ala Leu Glu Pro Glu Lys Pro Leu Val Arg Leu Val Lys Arg
                85                  90                  95

Asp Val Arg Thr Pro Leu Ala Val Glu Leu Glu Val Leu Asp Gly His
            100                 105                 110

Asp Pro Asp Pro Gly Arg Leu Leu Cys Gln Thr Arg His Glu Arg Tyr
        115                 120                 125

Phe Leu Pro Pro Gly Val Arg Arg Glu Pro Val Arg Val Gly Arg Val
    130                 135                 140

Arg Gly Thr Leu Phe Leu Pro Pro Glu Pro Gly Pro Phe Pro Gly Ile
145                 150                 155                 160

Val Asp Met Phe Gly Thr Gly Gly Gly Leu Leu Glu Tyr Arg Ala Ser
                165                 170                 175

Leu Leu Ala Gly Lys Gly Phe Ala Val Met Ala Leu Ala Tyr Tyr Asn
            180                 185                 190

Tyr Glu Asp Leu Pro Lys Thr Met Glu Thr Leu His Leu Glu Tyr Phe
        195                 200                 205

Glu Glu Ala Met Asn Tyr Leu Leu Ser His Pro Glu Val Lys Gly Pro
    210                 215                 220

Gly Val Gly Leu Leu Gly Ile Ser Lys Gly Gly Glu Leu Cys Leu Ser
225                 230                 235                 240

Met Ala Ser Phe Leu Lys Gly Ile Thr Ala Ala Val Val Ile Asn Gly
                245                 250                 255

Ser Val Ala Asn Val Gly Gly Thr Leu His Tyr Lys Gly Glu Thr Leu
            260                 265                 270

Pro Pro Val Gly Val Asn Arg Asn Arg Ile Lys Val Thr Lys Asp Gly
        275                 280                 285

Tyr Ala Asp Ile Val Asp Val Leu Asn Ser Pro Leu Glu Gly Pro Asp
    290                 295                 300
```

```
Gln Lys Ser Phe Ile Pro Val Glu Arg Ala Glu Ser Thr Phe Leu Phe
305                 310                 315                 320

Leu Val Gly Gln Asp Asp His Asn Trp Lys Ser Glu Phe Tyr Ala Asn
                325                 330                 335

Glu Ala Cys Lys Arg Leu Gln Ala His Gly Arg Arg Lys Pro Gln Ile
            340                 345                 350

Ile Cys Tyr Pro Glu Thr Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro
        355                 360                 365

Leu Cys Arg Ala Ser Leu His Ala Leu Val Gly Ser Pro Ile Ile Trp
    370                 375                 380

Gly Gly Glu Pro Arg Ala His Ala Met Ala Gln Val Asp Ala Trp Lys
385                 390                 395                 400

Gln Leu Gln Thr Phe Phe His Lys His Leu Gly Gly His Glu Gly Thr
                405                 410                 415

Ile Pro Ser Lys Val
            420


<210> 2070
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 524; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT4; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 4; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8N9L9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000323071"
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<400> 2070
Met Ser Ala Thr Leu Ile Leu Glu Pro Pro Gly Arg Cys Cys Trp Asn
1 5 10 15

Glu Pro Val Arg Ile Ala Val Arg Gly Leu Ala Pro Glu Gln Arg Val
20 25 30

Thr Leu Arg Ala Ser Leu Arg Asp Glu Lys Gly Ala Leu Phe Arg Ala
35 40 45

His Ala Arg Tyr Cys Ala Asp Ala Arg Gly Glu Leu Asp Leu Glu Arg
50 55 60

Ala Pro Ala Leu Gly Gly Ser Phe Ala Gly Leu Glu Pro Met Gly Leu
65 70 75 80

Leu Trp Ala Leu Glu Pro Glu Lys Pro Phe Trp Arg Phe Leu Lys Arg
85 90 95

Asp Val Gln Ile Pro Phe Val Val Glu Leu Glu Val Leu Asp Gly His
100 105 110

Asp Pro Glu Pro Gly Arg Leu Leu Cys Gln Ala Gln His Glu Arg His
115 120 125

Phe Leu Pro Pro Gly Val Arg Arg Gln Ser Val Arg Ala Gly Arg Val
130 135 140

Arg Ala Thr Leu Phe Leu Pro Pro Gly Pro Gly Pro Phe Pro Gly Ile
145 150 155 160

Ile Asp Ile Phe Gly Ile Gly Gly Gly Leu Leu Glu Tyr Arg Ala Ser
165 170 175

Leu Leu Ala Gly His Gly Phe Ala Thr Leu Ala Leu Ala Tyr Tyr Asn
180 185 190

Phe Glu Asp Leu Pro Asn Asn Met Asp Asn Ile Ser Leu Glu Tyr Phe
195 200 205

Glu Glu Ala Val Cys Tyr Met Leu Gln His Pro Gln Val Lys Gly Pro
210 215 220

```
Gly Ile Gly Leu Leu Gly Ile Ser Leu Gly Ala Asp Ile Cys Leu Ser
225                 230                 235                 240

Met Ala Ser Phe Leu Lys Asn Val Ser Ala Thr Val Ser Ile Asn Gly
                245                 250                 255

Ser Gly Ile Ser Gly Asn Thr Ala Ile Asn Tyr Lys His Ser Ser Ile
            260                 265                 270

Pro Pro Leu Gly Tyr Asp Leu Arg Arg Ile Lys Val Ala Phe Ser Gly
        275                 280                 285

Leu Val Asp Ile Val Asp Ile Arg Asn Ala Leu Val Gly Gly Tyr Lys
    290                 295                 300

Asn Pro Ser Met Ile Pro Ile Glu Lys Ala Gln Gly Pro Ile Leu Leu
305                 310                 315                 320

Ile Val Gly Gln Asp Asp His Asn Trp Arg Ser Glu Leu Tyr Ala Gln
                325                 330                 335

Thr Val Ser Glu Arg Leu Gln Ala His Gly Lys Glu Lys Pro Gln Ile
            340                 345                 350

Ile Cys Tyr Pro Gly Thr Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro
        355                 360                 365

Leu Cys Pro Ala Ser Leu His Arg Leu Leu Asn Lys His Val Ile Trp
    370                 375                 380

Gly Gly Glu Pro Arg Ala His Ser Lys Ala Gln Glu Asp Ala Trp Lys
385                 390                 395                 400

Gln Ile Leu Ala Phe Phe Cys Lys His Leu Gly Gly Thr Gln Lys Thr
                405                 410                 415

Ala Val Pro Lys Leu
            420
```

<210> 2071
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 525; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT6; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q3I5F7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370531"

<400> 2071
Met Leu Gln His Pro Lys Val Lys Gly Pro Ser Ile Ala Leu Leu Gly
1   5   10   15

Phe Ser Lys Gly Gly Asp Leu Cys Leu Ser Met Ala Ser Phe Leu Lys
            20   25   30

Gly Ile Thr Ala Thr Val Leu Ile Asn Ala Cys Val Ala Asn Thr Val
        35   40   45

Ala Pro Leu His Tyr Lys Asp Met Ile Ile Pro Lys Leu Val Asp Asp
    50   55   60

Leu Gly Lys Val Lys Ile Thr Lys Ser Gly Phe Leu Thr Phe Met Asp
65   70   75   80

Thr Trp Ser Asn Pro Leu Glu Glu His Asn His Gln Ser Leu Val Pro
                85   90   95

Leu Glu Lys Ala Gln Val Pro Phe Leu Phe Ile Val Gly Met Asp Asp
            100   105   110

Gln Ser Trp Lys Ser Glu Phe Tyr Ala Gln Ile Ala Ser Glu Arg Leu
        115   120   125

Gln Ala His Gly Lys Glu Arg Pro Gln Ile Ile Cys Tyr Pro Glu Thr
    130   135   140

```
Gly His Cys Ile Asp Pro Pro Tyr Phe Pro Pro Ser Arg Ala Ser Val
145                 150                 155                 160


His Ala Val Leu Gly Glu Ala Ile Phe Tyr Gly Gly Glu Pro Lys Ala
                165                 170                 175


His Ser Lys Ala Gln Val Asp Ala Trp Gln Gln Ile Gln Thr Phe Phe
            180                 185                 190


His Lys His Leu Asn Gly Lys Lys Ser Val Lys His Ser Lys Ile
        195                 200                 205


<210> 2072
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 525; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT6; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451464"

<400> 2072
Met Leu Gln His Pro Lys Val Lys Gly Pro Ser Ile Ala Leu Leu Gly
1               5                   10                  15


Phe Ser Lys Gly Gly Asp Leu Cys Leu Ser Met Ala Ser Phe Leu Lys
            20                  25                  30


Gly Ile Thr Ala Thr Val Leu Ile Asn Ala Cys Val Ala Asn Thr Val
        35                  40                  45


Ala Pro Leu His Tyr Lys Asp Met Ile Ile Pro Lys Leu Val Asp Asp
    50                  55                  60
```

```
Leu Gly Lys Val Lys Ile Thr Lys Ser Gly Phe Leu Thr Phe Met Asp
65                  70                  75                  80

Thr Trp Ser Asn Pro Leu Glu Glu His Asn His Gln Ser Leu Val Pro
                85                  90                  95

Leu Glu Lys Ala Gln Val Pro Phe Leu Phe Ile Val Gly Met Asp Asp
            100                 105                 110

Gln Ser Trp Lys Ser Glu Phe Tyr Ala Gln Ile Ala Ser Glu Arg Leu
        115                 120                 125

Gln Ala His Gly Lys Glu Arg Pro Gln Ile Ile Cys Tyr Pro Glu Thr
    130                 135                 140

Gly His Cys Ile Asp Pro Pro Tyr Phe Pro Pro Ser Arg Ala Ser Val
145                 150                 155                 160

His Ala Val Leu Gly Glu Ala Ile
                165


<210> 2073
<211> 370
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 526; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT7; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 7; "

<220>
<221> source
<223> /note="Uniprot ID:  O00154; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000354615"

<400> 2073
Met Ala Arg Pro Gly Leu Ile His Ser Ala Pro Gly Leu Pro Asp Thr
1               5                   10                  15
```

```
Cys Ala Leu Leu Gln Pro Pro Ala Ala Ser Ala Ala Ala Ala Pro Ser
            20                  25                  30

Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
        35                  40                  45

Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
    50                  55                  60

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
65                  70                  75                  80

His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
                85                  90                  95

Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
            100                 105                 110

His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
        115                 120                 125

Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
    130                 135                 140

Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
145                 150                 155                 160

Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln
                165                 170                 175

Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
            180                 185                 190

Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
        195                 200                 205

Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
    210                 215                 220

Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
225                 230                 235                 240
```

```
Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
                245                 250                 255

Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
            260                 265                 270

Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
        275                 280                 285

Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
    290                 295                 300

Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
305                 310                 315                 320

Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
                325                 330                 335

Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
            340                 345                 350

Gly Arg Tyr Leu Gln Met Lys Ala Lys Arg Gln Gly His Ala Glu Pro
        355                 360                 365

Gln Pro
    370
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<210> 2074
<211> 329
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA thioesterase 7; "

<220>
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<223> /note="Uniprot ID: O00154; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000367073"

<400> 2074

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Met Ala Phe Gln Leu Ser Arg Ile Met Arg Pro Asp Asp Ala Asn Val
1               5                  10                  15

Ala Gly Asn Val His Gly Gly Thr Ile Leu Lys Met Ile Glu Glu Ala
            20                  25                  30

Gly Ala Ile Ile Ser Thr Arg His Cys Asn Ser Gln Asn Gly Glu Arg
        35                  40                  45

Cys Val Ala Ala Leu Ala Arg Val Glu Arg Thr Asp Phe Leu Ser Pro
    50                  55                  60

Met Cys Ile Gly Glu Val Ala His Val Ser Ala Glu Ile Thr Tyr Thr
65                  70                  75                  80

Ser Lys His Ser Val Glu Val Gln Val Asn Val Met Ser Glu Asn Ile
                85                  90                  95

Leu Thr Gly Ala Lys Lys Leu Thr Asn Lys Ala Thr Leu Trp Tyr Val
            100                 105                 110

Pro Leu Ser Leu Lys Asn Val Asp Lys Val Leu Glu Val Pro Pro Val
        115                 120                 125

Val Tyr Ser Arg Gln Glu Gln Glu Glu Glu Gly Arg Lys Arg Tyr Glu
    130                 135                 140

Ala Gln Lys Leu Glu Arg Met Glu Thr Lys Trp Arg Asn Gly Asp Ile
145                 150                 155                 160

Val Gln Pro Val Leu Asn Pro Glu Pro Asn Thr Val Ser Tyr Ser Gln
                165                 170                 175

Ser Ser Leu Ile His Leu Val Gly Pro Ser Asp Cys Thr Leu His Gly
            180                 185                 190

Phe Val His Gly Gly Val Thr Met Lys Leu Met Asp Glu Val Ala Gly
        195                 200                 205
```

```
Ile Val Ala Ala Arg His Cys Lys Thr Asn Ile Val Thr Ala Ser Val
    210                 215                 220

Asp Ala Ile Asn Phe His Asp Lys Ile Arg Lys Gly Cys Val Ile Thr
225                 230                 235                 240

Ile Ser Gly Arg Met Thr Phe Thr Ser Asn Lys Ser Met Glu Ile Glu
                245                 250                 255

Val Leu Val Asp Ala Asp Pro Val Val Asp Ser Ser Gln Lys Arg Tyr
            260                 265                 270

Arg Ala Ala Ser Ala Phe Phe Thr Tyr Val Ser Leu Ser Gln Glu Gly
        275                 280                 285

Arg Ser Leu Pro Val Pro Gln Leu Val Pro Glu Thr Glu Asp Glu Lys
    290                 295                 300

Lys Arg Phe Glu Glu Gly Lys Gly Arg Tyr Leu Gln Met Lys Ala Lys
305                 310                 315                 320

Arg Gln Gly His Ala Glu Pro Gln Pro
                325
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<210> 2075
<211> 350
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<400> 2075
Met Leu Leu Leu Arg Arg Ser Leu Ser Leu Asn Val Leu Arg Lys Glu
1 5 10 15

Val Asp Arg Ala Cys Phe Gly Glu Lys Ala Lys Gln Ile Met Arg Pro
20 25 30

Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly Thr Ile Leu Lys
35 40 45

Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg His Cys Asn Ser
50 55 60

Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg Val Glu Arg Thr
65 70 75 80

Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala His Val Ser Ala
85 90 95

Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val Gln Val Asn Val
100 105 110

Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu Thr Asn Lys Ala
115 120 125

Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val Asp Lys Val Leu
130 135 140

Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln Glu Glu Glu Gly
145 150 155 160

Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met Glu Thr Lys Trp
165 170 175

Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro Glu Pro Asn Thr
180 185 190

Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val Gly Pro Ser Asp
195 200 205

Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr Met Lys Leu Met

```
    210                 215                 220

Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys Lys Thr Asn Ile
225                 230                 235                 240

Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp Lys Ile Arg Lys
                245                 250                 255

Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe Thr Ser Asn Lys
            260                 265                 270

Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro Val Val Asp Ser
        275                 280                 285

Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe Thr Tyr Val Ser
    290                 295                 300

Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln Leu Val Pro Glu
305                 310                 315                 320

Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys Gly Arg Tyr Leu
                325                 330                 335

Gln Met Lys Ala Lys Arg Gln Gly His Ala Glu Pro Gln Pro
            340                 345                 350


<210> 2076
<211> 380
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O00154; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000367086"

<400> 2076
Met Lys Leu Leu Ala Arg Ala Leu Arg Leu Cys Glu Phe Gly Arg Gln
1   5   10   15

Ala Ser Ser Arg Arg Leu Val Ala Gly Gln Gly Cys Val Gly Pro Arg
            20   25   30

Arg Gly Cys Cys Ala Pro Val Gln Val Val Gly Pro Arg Ala Asp Leu
        35   40   45

Pro Pro Cys Gly Ala Cys Ile Thr Gly Arg Ile Met Arg Pro Asp Asp
    50   55   60

Ala Asn Val Ala Gly Asn Val His Gly Gly Thr Ile Leu Lys Met Ile
65   70   75   80

Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg His Cys Asn Ser Gln Asn
                85   90   95

Gly Glu Arg Cys Val Ala Ala Leu Ala Arg Val Glu Arg Thr Asp Phe
            100   105   110

Leu Ser Pro Met Cys Ile Gly Glu Val Ala His Val Ser Ala Glu Ile
        115   120   125

Thr Tyr Thr Ser Lys His Ser Val Glu Val Gln Val Asn Val Met Ser
    130   135   140

Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu Thr Asn Lys Ala Thr Leu
145   150   155   160

Trp Tyr Val Pro Leu Ser Leu Lys Asn Val Asp Lys Val Leu Glu Val
                165   170   175

Pro Pro Val Val Tyr Ser Arg Gln Glu Gln Glu Glu Glu Gly Arg Lys
            180   185   190

Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met Glu Thr Lys Trp Arg Asn
        195   200   205

```
Gly Asp Ile Val Gln Pro Val Leu Asn Pro Glu Pro Asn Thr Val Ser
    210                 215                 220

Tyr Ser Gln Ser Ser Leu Ile His Leu Val Gly Pro Ser Asp Cys Thr
225                 230                 235                 240

Leu His Gly Phe Val His Gly Gly Val Thr Met Lys Leu Met Asp Glu
                245                 250                 255

Val Ala Gly Ile Val Ala Ala Arg His Cys Lys Thr Asn Ile Val Thr
            260                 265                 270

Ala Ser Val Asp Ala Ile Asn Phe His Asp Lys Ile Arg Lys Gly Cys
        275                 280                 285

Val Ile Thr Ile Ser Gly Arg Met Thr Phe Thr Ser Asn Lys Ser Met
    290                 295                 300

Glu Ile Glu Val Leu Val Asp Ala Asp Pro Val Val Asp Ser Ser Gln
305                 310                 315                 320

Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe Thr Tyr Val Ser Leu Ser
                325                 330                 335

Gln Glu Gly Arg Ser Leu Pro Val Pro Gln Leu Val Pro Glu Thr Glu
            340                 345                 350

Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys Gly Arg Tyr Leu Gln Met
        355                 360                 365

Lys Ala Lys Arg Gln Gly His Ala Glu Pro Gln Pro
    370                 375                 380


<210> 2077
<211> 283
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 526; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT7; "
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID: O00154; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000367091"

<400> 2077
Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
1   5   10   15

Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
            20   25   30

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
        35   40   45

His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
    50   55   60

Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
65   70   75   80

His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
                85   90   95

Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
            100   105   110

Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
        115   120   125

Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln
    130   135   140

Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
145   150   155   160

Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
                165   170   175

```
Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
            180                 185                 190

Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
        195                 200                 205

Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
    210                 215                 220

Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
225                 230                 235                 240

Lys Ile Arg Lys Ala His Val Met Pro Ala Gly Ala Asp His Thr Ala
                245                 250                 255

Pro Ser Ser Ser Pro Ser Thr Gly Thr Lys Cys Ser Leu Leu Arg His
            260                 265                 270

His His Leu Gly Thr His Asp Leu His Glu Gln
        275                 280


<210> 2078
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 526; "

<220>
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<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O00154; "

<220>
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<223> /note="ENSP ID: ENSP00000402532"

<400> 2078
Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
```

```
1               5                   10                  15

Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
            20                  25                  30

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
        35                  40                  45

His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
    50                  55                  60

Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
65                  70                  75                  80

His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
                85                  90                  95

Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
            100                 105                 110

Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
        115                 120                 125

Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln
    130                 135                 140

Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
145                 150                 155                 160

Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
                165                 170                 175

Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
            180                 185                 190

Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
        195                 200                 205

Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
    210                 215                 220

Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
225                 230                 235                 240
```

Lys Ile Arg Lys Ala Pro
245

<210> 2079
<211> 370
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 526; "

<220>
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<220>
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<220>
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<223> /note="Uniprot ID: O00154; "

<220>
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<400> 2079
Met Ala Arg Pro Gly Leu Ile His Ser Ala Pro Gly Leu Pro Asp Thr
1 5 10 15

Cys Ala Leu Leu Gln Pro Pro Ala Ala Ser Ala Ala Ala Ala Pro Ser
20 25 30

Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
35 40 45

Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
50 55 60

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
65 70 75 80

His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
85 90 95

```
Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
            100                 105                 110

His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
        115                 120                 125

Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
    130                 135                 140

Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
145                 150                 155                 160

Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln
                165                 170                 175

Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
            180                 185                 190

Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
        195                 200                 205

Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
    210                 215                 220

Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
225                 230                 235                 240

Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
                245                 250                 255

Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
            260                 265                 270

Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
        275                 280                 285

Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
    290                 295                 300

Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
305                 310                 315                 320

Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
```

325 330 335

Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
340 345 350

Gly Arg Tyr Leu Gln Met Lys Ala Lys Arg Gln Gly His Ala Glu Pro
355 360 365

Gln Pro
370

<210> 2080
<211> 279
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 526; "

<220>
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<220>
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<223> /note="Gene Name:
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000465719"

<400> 2080
Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly Thr
1 5 10 15

Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg His
20 25 30

Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg Val
35 40 45

Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala His
50 55 60

Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val Gln
65 70 75 80

```
Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu Thr
                85                  90                  95

Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val Asp
            100                 105                 110

Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln Glu
        115                 120                 125

Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met Glu
    130                 135                 140

Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro Glu
145                 150                 155                 160

Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val Gly
                165                 170                 175

Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr Met
            180                 185                 190

Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys Lys
        195                 200                 205

Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp Lys
    210                 215                 220

Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe Thr
225                 230                 235                 240

Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro Val
                245                 250                 255

Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe Thr
            260                 265                 270

Tyr Val Ser Leu Ser Gln Glu
        275
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<210> 2081
<211> 338
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
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<223> /note="Uniprot ID: O00154; "

<220>
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<400> 2081
Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
1   5   10   15

Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
            20   25   30

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
        35   40   45

His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
    50   55   60

Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
65   70   75   80

His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
                85   90   95

Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
            100   105   110

Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
        115   120   125

Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Gln Glu Gln
    130   135   140

Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
145 150 155 160

Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
165 170 175

Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
180 185 190

Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
195 200 205

Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
210 215 220

Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
225 230 235 240

Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
245 250 255

Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
260 265 270

Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
275 280 285

Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
290 295 300

Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
305 310 315 320

Gly Arg Tyr Leu Gln Met Lys Ala Lys Arg Gln Gly His Ala Glu Pro
325 330 335

Gln Pro

<210> 2082
<211> 319
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 527; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT8; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
<221> source
<223> /note="Uniprot ID: O14734; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000217455"

<400> 2082

Met	Ser	Ser	Pro	Gln	Ala	Pro	Glu	Asp	Gly	Gln	Gly	Cys	Gly	Asp	Arg
1				5				10						15	

Gly	Asp	Pro	Pro	Gly	Asp	Leu	Arg	Ser	Val	Leu	Val	Thr	Thr	Val	Leu
			20					25					30		

Asn	Leu	Glu	Pro	Leu	Asp	Glu	Asp	Leu	Phe	Arg	Gly	Arg	His	Tyr	Trp
		35					40					45			

Val	Pro	Ala	Lys	Arg	Leu	Phe	Gly	Gly	Gln	Ile	Val	Gly	Gln	Ala	Leu
	50					55					60				

Val	Ala	Ala	Ala	Lys	Ser	Val	Ser	Glu	Asp	Val	His	Val	His	Ser	Leu
65					70					75					80

His	Cys	Tyr	Phe	Val	Arg	Ala	Gly	Asp	Pro	Lys	Leu	Pro	Val	Leu	Tyr
				85					90					95	

Gln	Val	Glu	Arg	Thr	Arg	Thr	Gly	Ser	Ser	Phe	Ser	Val	Arg	Ser	Val
			100					105					110		

Lys	Ala	Val	Gln	His	Gly	Lys	Pro	Ile	Phe	Ile	Cys	Gln	Ala	Ser	Phe
		115					120					125			

Gln	Gln	Ala	Gln	Pro	Ser	Pro	Met	Gln	His	Gln	Phe	Ser	Met	Pro	Thr

```
    130                 135                 140

Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu Ile Asp Gln
145                 150                 155                 160

Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu Ala Leu Asn
                165                 170                 175

Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro Val Asn Pro
            180                 185                 190

Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln Met Phe Trp
        195                 200                 205

Val Arg Ala Arg Gly Tyr Ile Gly Glu Gly Asp Met Lys Met His Cys
    210                 215                 220

Cys Val Ala Ala Tyr Ile Ser Asp Tyr Ala Phe Leu Gly Thr Ala Leu
225                 230                 235                 240

Leu Pro His Gln Trp Gln His Lys Val His Phe Met Val Ser Leu Asp
                245                 250                 255

His Ser Met Trp Phe His Ala Pro Phe Arg Ala Asp His Trp Met Leu
            260                 265                 270

Tyr Glu Cys Glu Ser Pro Trp Ala Gly Gly Ser Arg Gly Leu Val His
        275                 280                 285

Gly Arg Leu Trp Arg Gln Asp Gly Val Leu Ala Val Thr Cys Ala Gln
    290                 295                 300

Glu Gly Val Ile Arg Val Lys Pro Gln Val Ser Glu Ser Lys Leu
305                 310                 315


<210> 2083
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 527; "

<220>
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<221> source
<223> /note="Gene Symbol: ACOT8; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403862"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2083
Xaa Leu Phe Arg Gly Arg His Tyr Trp Val Pro Ala Lys Arg Leu Phe
1 5 10 15

Gly Gly Gln Ile Val Gly Gln Ala Leu Val Ala Ala Ala Lys Ser Val
20 25 30

Ser Glu Asp Val His Val His Ser Leu His Cys Tyr Phe Val Arg Ala
35 40 45

Glu Gln Met Pro Ser Cys Val Leu Arg Arg Ser Pro Ala Glu Lys Ser
50 55 60

Leu Trp Thr Phe Thr Val Cys Asp Leu Tyr
65 70

<210> 2084
<211> 92
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000416217"

<400> 2084
Ser Pro Gln Ala Pro Glu Asp Gly Gln Gly Cys Gly Asp Arg Gly Asp
1   5   10   15

Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu Asn Leu
            20   25   30

Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp Val Pro
        35   40   45

Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu Val Ala
    50   55   60

Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu His Cys
65   70   75   80

Tyr Phe Val Arg Ala Asp Ala Leu Met Cys Ser Ala
                85   90

<210> 2085
<211> 209
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 527; "

<220>
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<220>
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<223> /note="Gene Name:
      acyl-CoA thioesterase 8; "

<220>
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<223> /note="ENSP ID: ENSP00000419403"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2085
Xaa Tyr Trp Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly
1 5 10 15

Gln Ala Leu Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val
20 25 30

His Ser Leu His Cys Tyr Phe Val Arg Ala Gly Asp Pro Lys Leu Pro
35 40 45

Val Leu Tyr Gln Val Glu Arg Thr Arg Thr Gly Ser Ser Phe Ser Val
50 55 60

Arg Ser Val Lys Ala Val Gln His Gly Lys Pro Ile Phe Ile Cys Gln
65 70 75 80

Ala Ser Phe Gln Gln Ala Gln Pro Ser Pro Met Gln His Gln Phe Ser
85 90 95

Met Pro Thr Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu
100 105 110

Ile Asp Gln Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu
115 120 125

Ala Leu Asn Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro
130 135 140

Val Asn Pro Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln
145 150 155 160

Met Phe Trp Val Arg Ala Arg Gly Tyr Ile Gly Gly Ser Arg Gly Leu
165 170 175

Val His Gly Arg Leu Trp Arg Gln Asp Gly Val Leu Ala Val Thr Cys
180 185 190

Ala Gln Glu Gly Val Ile Arg Val Lys Pro Gln Val Ser Glu Ser Lys
195 200 205

Leu

<210> 2086
<211> 94
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
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<400> 2086
Met Ser Ser Pro Gln Ala Pro Glu Asp Gly Gln Gly Cys Gly Asp Arg
1 5 10 15

Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
20 25 30

Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp
35 40 45

Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu
50 55 60

Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu
65 70 75 80

His Cys Tyr Phe Val Arg Ala Asp Ala Leu Met Cys Ser Ala
85 90

<210> 2087
<211> 132
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
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<223> /note="ENSP ID: ENSP00000433923"

<400> 2087
Met Ser Ser Pro Gln Ala Pro Glu Asp Gly Gln Gly Cys Gly Asp Arg
1 5 10 15

Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
20 25 30

Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp
35 40 45

Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu
50 55 60

Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu
65 70 75 80

His Cys Tyr Phe Val Arg Ala Glu Gln Met Pro Ser Cys Val Leu Arg
85 90 95

Arg Ser Pro Ala Glu Lys Ser Leu Trp Thr Phe Thr Gly Thr Arg Ser
100 105 110

Cys Gln Tyr Cys Thr Lys Trp Ser Gly His Glu Gln Gly Arg Ala Ser
115 120 125

Arg Cys Ala Leu
130

<210> 2088
<211> 171
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434216"

<400> 2088
Met Ser Ser Pro Gln Ala Pro Glu Asp Gly Gln Gly Cys Gly Asp Arg
1 5 10 15

Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
20 25 30

Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Asp Pro Asn Leu Gln
35 40 45

Lys Arg Tyr Pro Leu Ala Leu Asn Arg Ile Ala Ala Gln Glu Val Pro
50 55 60

Ile Glu Ile Lys Pro Val Asn Pro Ser Pro Leu Ser Gln Leu Gln Arg
65 70 75 80

Met Glu Pro Lys Gln Met Phe Trp Val Arg Ala Arg Gly Tyr Ile Gly
85 90 95

Glu Gly Asp Met Lys Met His Cys Cys Val Ala Ala Tyr Ile Ser Asp
100 105 110

Tyr Ala Phe Leu Gly Thr Ala Leu Leu Pro His Gln Trp Gln His Lys
115 120 125

Val His Phe Met Val Ser Leu Asp His Ser Met Trp Phe His Ala Pro
130 135 140

Phe Arg Ala Asp His Trp Met Leu Tyr Glu Cys Glu Ser Pro Trp Ala
145 150 155 160

Gly Phe Gly Ile Phe Ile Phe Lys Met Arg Gly
165 170

<210> 2089
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 527; "

<220>
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<223> /note="Gene Symbol: ACOT8; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435115"

<400> 2089
Met Ser Ser Pro Gln Ala Pro Glu Asp Gly Gln Gly Cys Gly Asp Arg
1 5 10 15

Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
20 25 30

Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Pro Glu Ala Ala
35 40 45

Ser Thr Val Pro Ser Gly Ala Asp Thr Asn Arg Val Glu Leu Leu Gly
50 55 60

Ala Leu Cys Glu Gly Arg Ala Thr Trp Glu Ala His Leu His Leu Pro
65 70 75 80

Gly Leu Leu Pro Ala Gly Pro Ala Gln Pro His Ala Ala Pro Val Leu
85 90 95

His Ala His Cys Ala Thr Thr Arg Arg Ala Ala
100 105

<210> 2090
<211> 226
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 527; "

<220>
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<223> /note="Gene Symbol: ACOT8; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435581"

<400> 2090
Met Ser Ser Pro Gln Ala Pro Glu Asp Gly Gln Gly Cys Gly Asp Arg
1 5 10 15

Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
20 25 30

Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp
35 40 45

Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu
50 55 60

Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu
65 70 75 80

His Cys Tyr Phe Val Arg Ala Gly Asp Pro Lys Leu Pro Val Leu Tyr
85 90 95

Gln Val Glu Arg Thr Arg Thr Gly Ser Ser Phe Ser Val Arg Ser Val
100 105 110

Lys Ala Val Gln His Gly Lys Pro Ile Phe Ile Cys Gln Ala Ser Phe
115 120 125

Gln Gln Ala Gln Pro Ser Pro Met Gln His Gln Phe Ser Met Pro Thr
130 135 140

Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu Ile Asp Gln
145 150 155 160

```
Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu Ala Leu Asn
                165                 170                 175

Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro Val Asn Pro
            180                 185                 190

Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln Met Phe Trp
        195                 200                 205

Val Arg Ala Arg Gly Tyr Ile Gly Pro Glu Leu Glu Ser Pro Gly Ala
    210                 215                 220

Gln Gly
225
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<210> 2091
<211> 439
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 528; "

<220>
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<223> /note="Gene Symbol: ACOT9; "

<220>
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<223> /note="Gene Name:
acyl-CoA thioesterase 9; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y305; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000336580"

<400> 2091

```
Met Arg Arg Ala Ala Leu Arg Leu Cys Ala Leu Gly Lys Gly Gln Leu
1               5                  10                  15

Thr Pro Gly Arg Gly Leu Thr Gln Gly Pro Gln Asn Pro Lys Lys Gln
            20                  25                  30
```

```
Gly Ile Phe His Ile His Glu Val Arg Asp Lys Leu Arg Glu Ile Val
        35                  40                  45

Gly Ala Ser Thr Asn Trp Arg Asp His Val Lys Ala Met Glu Glu Arg
    50                  55                  60

Lys Leu Leu His Ser Phe Leu Ala Lys Ser Gln Asp Gly Leu Pro Pro
65                  70                  75                  80

Arg Arg Met Lys Asp Ser Tyr Ile Glu Val Leu Leu Pro Leu Gly Ser
                85                  90                  95

Glu Pro Glu Leu Arg Glu Lys Tyr Leu Thr Val Gln Asn Thr Val Arg
            100                 105                 110

Phe Gly Arg Ile Leu Glu Asp Leu Asp Ser Leu Gly Val Leu Ile Cys
        115                 120                 125

Tyr Met His Asn Lys Ile His Ser Ala Lys Met Ser Pro Leu Ser Ile
    130                 135                 140

Val Thr Ala Leu Val Asp Lys Ile Asp Met Cys Lys Lys Ser Leu Ser
145                 150                 155                 160

Pro Glu Gln Asp Ile Lys Phe Ser Gly His Val Ser Trp Val Gly Lys
                165                 170                 175

Thr Ser Met Glu Val Lys Met Gln Met Phe Gln Leu His Gly Asp Glu
            180                 185                 190

Phe Cys Pro Val Leu Asp Ala Thr Phe Val Met Val Ala Arg Asp Ser
        195                 200                 205

Glu Asn Lys Gly Pro Ala Phe Val Asn Pro Leu Ile Pro Glu Ser Pro
    210                 215                 220

Glu Glu Glu Glu Leu Phe Arg Gln Gly Glu Leu Asn Lys Gly Arg Arg
225                 230                 235                 240

Ile Ala Phe Ser Ser Thr Ser Leu Leu Lys Met Ala Pro Ser Ala Glu
                245                 250                 255

Glu Arg Thr Thr Ile His Glu Met Phe Leu Ser Thr Leu Asp Pro Lys
```

```
            260                 265                 270

Thr Ile Ser Phe Arg Ser Arg Val Leu Pro Ser Asn Ala Val Trp Met
        275                 280                 285

Glu Asn Ser Lys Leu Lys Ser Leu Glu Ile Cys His Pro Gln Glu Arg
    290                 295                 300

Asn Ile Phe Asn Arg Ile Phe Gly Gly Phe Leu Met Arg Lys Ala Tyr
305                 310                 315                 320

Glu Leu Ala Trp Ala Thr Ala Cys Ser Phe Gly Gly Ser Arg Pro Phe
                325                 330                 335

Val Val Ala Val Asp Asp Ile Met Phe Gln Lys Pro Val Glu Val Gly
            340                 345                 350

Ser Leu Leu Phe Leu Ser Ser Gln Val Cys Phe Thr Gln Asn Asn Tyr
        355                 360                 365

Ile Gln Val Arg Val His Ser Glu Val Ala Ser Leu Gln Glu Lys Gln
    370                 375                 380

His Thr Thr Thr Asn Val Phe His Phe Thr Phe Met Ser Glu Lys Glu
385                 390                 395                 400

Val Pro Leu Val Phe Pro Lys Thr Tyr Gly Glu Ser Met Leu Tyr Leu
                405                 410                 415

Asp Gly Gln Arg His Phe Asn Ser Met Ser Gly Pro Ala Thr Leu Arg
            420                 425                 430

Lys Asp Tyr Leu Val Glu Pro
        435


<210> 2092
<211> 379
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 528; "

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<221> source
<223> /note="Gene Symbol: ACOT9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 9; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y305; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000368597"

<400> 2092

Met	Glu	Glu	Arg	Lys	Leu	Leu	His	Ser	Phe	Leu	Ala	Lys	Ser	Gln	Asp
1				5					10						15
Gly	Leu	Pro	Pro	Arg	Arg	Met	Lys	Asp	Ser	Tyr	Ile	Glu	Val	Leu	Leu
			20					25					30		
Pro	Leu	Gly	Ser	Glu	Pro	Glu	Leu	Arg	Glu	Lys	Tyr	Leu	Thr	Val	Gln
		35					40					45			
Asn	Thr	Val	Arg	Phe	Gly	Arg	Ile	Leu	Glu	Asp	Leu	Asp	Ser	Leu	Gly
	50					55					60				
Val	Leu	Ile	Cys	Tyr	Met	His	Asn	Lys	Ile	His	Ser	Ala	Lys	Met	Ser
65					70					75					80
Pro	Leu	Ser	Ile	Val	Thr	Ala	Leu	Val	Asp	Lys	Ile	Asp	Met	Cys	Lys
				85					90					95	
Lys	Ser	Leu	Ser	Pro	Glu	Gln	Asp	Ile	Lys	Phe	Ser	Gly	His	Val	Ser
			100					105					110		
Trp	Val	Gly	Lys	Thr	Ser	Met	Glu	Val	Lys	Met	Gln	Met	Phe	Gln	Leu
		115					120					125			
His	Gly	Asp	Glu	Phe	Cys	Pro	Val	Leu	Asp	Ala	Thr	Phe	Val	Met	Val
	130					135					140				
Ala	Arg	Asp	Ser	Glu	Asn	Lys	Gly	Pro	Ala	Phe	Val	Asn	Pro	Leu	Ile
145					150					155					160

```
Pro Glu Ser Pro Glu Glu Glu Glu Leu Phe Arg Gln Gly Glu Leu Asn
                165                 170                 175

Lys Gly Arg Arg Ile Ala Phe Ser Ser Thr Ser Leu Leu Lys Met Ala
            180                 185                 190

Pro Ser Ala Glu Glu Arg Thr Thr Ile His Glu Met Phe Leu Ser Thr
        195                 200                 205

Leu Asp Pro Lys Thr Ile Ser Phe Arg Ser Arg Val Leu Pro Ser Asn
    210                 215                 220

Ala Val Trp Met Glu Asn Ser Lys Leu Lys Ser Leu Glu Ile Cys His
225                 230                 235                 240

Pro Gln Glu Arg Asn Ile Phe Asn Arg Ile Phe Gly Gly Phe Leu Met
                245                 250                 255

Arg Lys Ala Tyr Glu Leu Ala Trp Ala Thr Ala Cys Ser Phe Gly Gly
            260                 265                 270

Ser Arg Pro Phe Val Val Ala Val Asp Asp Ile Met Phe Gln Lys Pro
        275                 280                 285

Val Glu Val Gly Ser Leu Leu Phe Leu Ser Ser Gln Val Cys Phe Thr
    290                 295                 300

Gln Asn Asn Tyr Ile Gln Val Arg Val His Ser Glu Val Ala Ser Leu
305                 310                 315                 320

Gln Glu Lys Gln His Thr Thr Thr Asn Val Phe His Phe Thr Phe Met
                325                 330                 335

Ser Glu Lys Glu Val Pro Leu Val Phe Pro Lys Thr Tyr Gly Glu Ser
            340                 345                 350

Met Leu Tyr Leu Asp Gly Gln Arg His Phe Asn Ser Met Ser Gly Pro
        355                 360                 365

Ala Thr Leu Arg Lys Asp Tyr Leu Val Glu Pro
    370                 375
```

<210> 2093

<211> 448
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 528; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 9; "

<220>
<221> source
<223> /note="Uniprot ID: Q9Y305; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000368605"

<400> 2093

Met	Arg	Arg	Ala	Ala	Leu	Arg	Leu	Cys	Ala	Leu	Gly	Lys	Gly	Gln	Leu
1				5				10					15		
Thr	Pro	Gly	Arg	Gly	Leu	Thr	Gln	Gly	Pro	Gln	Asn	Pro	Lys	Lys	Gln
			20					25					30		
Gly	Ile	Phe	His	Ile	His	Glu	Ala	Cys	Ser	Ser	Ile	His	Val	Asn	His
		35					40					45			
Val	Arg	Asp	Lys	Leu	Arg	Glu	Ile	Val	Gly	Ala	Ser	Thr	Asn	Trp	Arg
	50					55					60				
Asp	His	Val	Lys	Ala	Met	Glu	Glu	Arg	Lys	Leu	Leu	His	Ser	Phe	Leu
65					70					75					80
Ala	Lys	Ser	Gln	Asp	Gly	Leu	Pro	Pro	Arg	Arg	Met	Lys	Asp	Ser	Tyr
				85					90					95	
Ile	Glu	Val	Leu	Leu	Pro	Leu	Gly	Ser	Glu	Pro	Glu	Leu	Arg	Glu	Lys
			100					105					110		
Tyr	Leu	Thr	Val	Gln	Asn	Thr	Val	Arg	Phe	Gly	Arg	Ile	Leu	Glu	Asp
		115					120					125			

```
Leu Asp Ser Leu Gly Val Leu Ile Cys Tyr Met His Asn Lys Ile His
    130                 135                 140

Ser Ala Lys Met Ser Pro Leu Ser Ile Val Thr Ala Leu Val Asp Lys
145                 150                 155                 160

Ile Asp Met Cys Lys Lys Ser Leu Ser Pro Glu Gln Asp Ile Lys Phe
                165                 170                 175

Ser Gly His Val Ser Trp Val Gly Lys Thr Ser Met Glu Val Lys Met
            180                 185                 190

Gln Met Phe Gln Leu His Gly Asp Glu Phe Cys Pro Val Leu Asp Ala
        195                 200                 205

Thr Phe Val Met Val Ala Arg Asp Ser Glu Asn Lys Gly Pro Ala Phe
    210                 215                 220

Val Asn Pro Leu Ile Pro Glu Ser Pro Glu Glu Glu Glu Leu Phe Arg
225                 230                 235                 240

Gln Gly Glu Leu Asn Lys Gly Arg Arg Ile Ala Phe Ser Ser Thr Ser
                245                 250                 255

Leu Leu Lys Met Ala Pro Ser Ala Glu Glu Arg Thr Thr Ile His Glu
            260                 265                 270

Met Phe Leu Ser Thr Leu Asp Pro Lys Thr Ile Ser Phe Arg Ser Arg
        275                 280                 285

Val Leu Pro Ser Asn Ala Val Trp Met Glu Asn Ser Lys Leu Lys Ser
    290                 295                 300

Leu Glu Ile Cys His Pro Gln Glu Arg Asn Ile Phe Asn Arg Ile Phe
305                 310                 315                 320

Gly Gly Phe Leu Met Arg Lys Ala Tyr Glu Leu Ala Trp Ala Thr Ala
                325                 330                 335

Cys Ser Phe Gly Gly Ser Arg Pro Phe Val Val Ala Val Asp Asp Ile
            340                 345                 350
```

```
Met Phe Gln Lys Pro Val Glu Val Gly Ser Leu Leu Phe Leu Ser Ser
        355                 360                 365

Gln Val Cys Phe Thr Gln Asn Asn Tyr Ile Gln Val Arg Val His Ser
    370                 375                 380

Glu Val Ala Ser Leu Gln Glu Lys Gln His Thr Thr Thr Asn Val Phe
385                 390                 395                 400

His Phe Thr Phe Met Ser Glu Lys Glu Val Pro Leu Val Phe Pro Lys
                405                 410                 415

Thr Tyr Gly Glu Ser Met Leu Tyr Leu Asp Gly Gln Arg His Phe Asn
            420                 425                 430

Ser Met Ser Gly Pro Ala Thr Leu Arg Lys Asp Tyr Leu Val Glu Pro
        435                 440                 445


<210> 2094
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 528; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417778"

<400> 2094
Met Glu Glu Arg Lys Leu Leu His Ser Phe Leu Ala Lys Ser Gln Asp
1               5                   10                  15

Gly Leu Pro Pro Arg Arg Met Lys Asp Ser Tyr Ile Glu Val Leu Leu
            20                  25                  30

Pro Leu Gly Ser Glu Pro Glu Leu Arg Glu Lys Tyr Leu Thr Val Gln
        35                  40                  45
```

```
Asn Thr Val Arg Phe Gly Arg Ile Leu Glu Asp Leu Asp Ser Leu Gly
    50                  55                  60

Val Leu Ile Cys Tyr Met His Asn Lys Ile His Ser Ala Lys Met Ser
65                  70                  75                  80

Pro Leu Ser Ile Val Thr Ala Leu Val Asp Lys Ile Asp Met Cys Lys
                85                  90                  95

Lys Ser Leu Ser Pro Glu Gln Asp Ile Lys Phe Ser Gly His Val Ser
            100                 105                 110

Trp Val Gly Lys Thr Ser Met Glu Val Lys Met Gln Met Phe Gln Ala
        115                 120                 125

Gly Ile Cys Lys Ser Thr His Pro
    130                 135


<210> 2095
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 528; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT9; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA thioesterase 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420238"

<400> 2095
Met Arg Arg Ala Ala Leu Arg Leu Cys Ala Leu Gly Lys Gly Gln Leu
1               5                   10                  15

Thr Pro Gly Arg Gly Leu Thr Gln Gly Pro Gln Asn Pro Lys Lys Gln
            20                  25                  30
```

Gly Ile Phe His Ile His Glu Gly Lys His Gly Val Ser Val
35 40 45

<210> 2096
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 528; "

<220>
<221> source
<223> /note="Gene Symbol: ACOT9; "

<220>
<221> source
<223> /note="Gene Name:
acyl-CoA thioesterase 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420490"

<400> 2096
Ile Val Gly Ala Ser Thr Asn Trp Arg Asp His Val Lys Ala Met Glu
1 5 10 15

Glu Arg Lys Leu Leu His Ser Phe Leu Ala Lys Ser Gln Asp Gly Leu
20 25 30

Pro Pro Arg Arg Met Lys Asp Ser Tyr Ile Glu Val Leu Leu Pro Leu
35 40 45

Gly Ser Glu Pro Glu Leu Arg Glu Lys Tyr Leu Thr Val Gln Asn Thr
50 55 60

Val Arg Phe Gly Arg Ile Leu Glu Asp Leu Asp Ser Leu Gly Asp Met
65 70 75 80

Cys Lys Lys Ser Leu Ser Pro Glu Gln Asp Ile Lys Phe Ser Gly His
85 90 95

Val Ser Trp Val Gly Lys Thr Ser Met Glu Val Lys Met Gln Met Phe
100 105 110

Gln Leu His Gly Asp Glu Phe Cys Pro Val Leu Asp Ala Thr Phe Val
115 120 125

```
Met Val Ala Arg Asp Ser Glu Asn Lys Gly Pro Ala Phe Val Asn Pro
    130                 135                 140

Leu Ile Pro Glu Ser Pro Glu Glu Glu Glu Leu Phe Arg Gln Gly Glu
145                 150                 155                 160

Leu Asn Lys Gly Arg Arg Ile Ala Phe Ser Ser Thr Ser Leu Leu Lys
                165                 170                 175

Met Ala Pro Ser Ala Glu Glu Arg Thr Thr Ile His Glu Met Phe Leu
            180                 185                 190

Ser Thr Leu Asp Pro Lys Thr Ile Ser Phe Arg Ser Arg Val Leu Pro
        195                 200                 205

Ser Asn Ala Val Trp Met Glu Asn Ser Lys Leu Lys Ser Leu Glu Ile
    210                 215                 220

Cys His Pro Gln Glu Arg Asn Ile Phe Asn Arg Ile Phe Gly Gly Phe
225                 230                 235                 240

Leu Met Arg Lys Ala Tyr Glu Leu Ala Trp Ala Thr Ala Cys Ser Phe
                245                 250                 255

Gly Gly Ser Arg Pro Phe Val Val
            260


<210> 2097
<211> 328
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 529; "

<220>
<221> source
<223> /note="Gene Symbol: AWAT1; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA wax alcohol acyltransferase 1; "

<220>
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<221> source
<223> /note="Uniprot ID: Q58HT5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000363645"

<400> 2097
Met Ala His Ser Lys Gln Pro Ser His Phe Gln Ser Leu Met Leu Leu
1   5   10   15

Gln Trp Pro Leu Ser Tyr Leu Ala Ile Phe Trp Ile Leu Gln Pro Leu
            20   25   30

Phe Val Tyr Leu Leu Phe Thr Ser Leu Trp Pro Leu Pro Val Leu Tyr
        35   40   45

Phe Ala Trp Leu Phe Leu Asp Trp Lys Thr Pro Glu Arg Gly Gly Arg
    50   55   60

Arg Ser Ala Trp Val Arg Asn Trp Cys Val Trp Thr His Ile Arg Asp
65   70   75   80

Tyr Phe Pro Ile Thr Ile Leu Lys Thr Lys Asp Leu Ser Pro Glu His
                85   90   95

Asn Tyr Leu Met Gly Val His Pro His Gly Leu Leu Thr Phe Gly Ala
            100   105   110

Phe Cys Asn Phe Cys Thr Glu Ala Thr Gly Phe Ser Lys Thr Phe Pro
        115   120   125

Gly Ile Thr Pro His Leu Ala Thr Leu Ser Trp Phe Phe Lys Ile Pro
    130   135   140

Phe Val Arg Glu Tyr Leu Met Ala Lys Gly Val Cys Ser Val Ser Gln
145   150   155   160

Pro Ala Ile Asn Tyr Leu Leu Ser His Gly Thr Gly Asn Leu Val Gly
                165   170   175

Ile Val Val Gly Gly Val Gly Glu Ala Leu Gln Ser Val Pro Asn Thr
            180   185   190

Thr Thr Leu Ile Leu Gln Lys Arg Lys Gly Phe Val Arg Thr Ala Leu

```
        195                 200                 205

Gln His Gly Ala His Leu Val Pro Thr Phe Thr Phe Gly Glu Thr Glu
    210                 215                 220

Val Tyr Asp Gln Val Leu Phe His Lys Asp Ser Arg Met Tyr Lys Phe
225                 230                 235                 240

Gln Ser Cys Phe Arg Arg Ile Phe Gly Phe Tyr Cys Cys Val Phe Tyr
                245                 250                 255

Gly Gln Ser Phe Cys Gln Gly Ser Thr Gly Leu Leu Pro Tyr Ser Arg
            260                 265                 270

Pro Ile Val Thr Val Val Gly Glu Pro Leu Pro Leu Pro Gln Ile Glu
        275                 280                 285

Lys Pro Ser Gln Glu Met Val Asp Lys Tyr His Ala Leu Tyr Met Asp
    290                 295                 300

Ala Leu His Lys Leu Phe Asp Gln His Lys Thr His Tyr Gly Cys Ser
305                 310                 315                 320

Glu Thr Gln Lys Leu Phe Phe Leu
                325


<210> 2098
<211> 333
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 530; "

<220>
<221> source
<223> /note="Gene Symbol: AWAT2; "

<220>
<221> source
<223> /note="Gene Name:
      acyl-CoA wax alcohol acyltransferase 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q6E213; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000421172"

<400> 2098
Met Leu Leu Pro Ser Lys Lys Asp Leu Lys Thr Ala Leu Asp Val Phe
1   5   10   15

Ala Val Phe Gln Trp Ser Phe Ser Ala Leu Leu Ile Thr Thr Thr Val
            20   25   30

Ile Ala Val Asn Leu Tyr Leu Val Val Phe Thr Pro Tyr Trp Pro Val
        35   40   45

Thr Val Leu Ile Leu Thr Trp Leu Ala Phe Asp Trp Lys Thr Pro Gln
    50   55   60

Arg Gly Gly Arg Arg Phe Thr Cys Val Arg His Trp Arg Leu Trp Lys
65   70   75   80

His Tyr Ser Asp Tyr Phe Pro Leu Lys Leu Leu Lys Thr His Asp Ile
                85   90   95

Cys Pro Ser Arg Asn Tyr Ile Leu Val Cys His Pro His Gly Leu Phe
            100   105   110

Ala His Gly Trp Phe Gly His Phe Ala Thr Glu Ala Ser Gly Phe Ser
        115   120   125

Lys Ile Phe Pro Gly Ile Thr Pro Tyr Ile Leu Thr Leu Gly Ala Phe
    130   135   140

Phe Trp Met Pro Phe Leu Arg Glu Tyr Val Met Ser Thr Gly Ala Cys
145   150   155   160

Ser Val Ser Arg Ser Ser Ile Asp Phe Leu Leu Thr His Lys Gly Thr
                165   170   175

Gly Asn Met Val Ile Val Val Ile Gly Gly Leu Ala Glu Cys Arg Tyr
            180   185   190

Ser Leu Pro Gly Ser Ser Thr Leu Val Leu Lys Asn Arg Ser Gly Phe
        195   200   205

```
Val Arg Met Ala Leu Gln His Gly Val Pro Leu Ile Pro Ala Tyr Ala
    210                 215                 220

Phe Gly Glu Thr Asp Leu Tyr Asp Gln His Ile Phe Thr Pro Gly Gly
225                 230                 235                 240

Phe Val Asn Arg Phe Gln Lys Trp Phe Gln Ser Met Val His Ile Tyr
                245                 250                 255

Pro Cys Ala Phe Tyr Gly Arg Gly Phe Thr Lys Asn Ser Trp Gly Leu
            260                 265                 270

Leu Pro Tyr Ser Arg Pro Val Thr Thr Ile Val Gly Glu Pro Leu Pro
        275                 280                 285

Met Pro Lys Ile Glu Asn Pro Ser Gln Glu Ile Val Ala Lys Tyr His
    290                 295                 300

Thr Leu Tyr Ile Asp Ala Leu Arg Lys Leu Phe Asp Gln His Lys Thr
305                 310                 315                 320

Lys Phe Gly Ile Ser Glu Thr Gln Glu Leu Glu Ile Ile
                325                 330


<210> 2099
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 530; "

<220>
<221> source
<223> /note="Gene Symbol: AWAT2; "

<220>
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<223> /note="Gene Name:
      acyl-CoA wax alcohol acyltransferase 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000427523"

<400> 2099
Glu Ala Ser Gly Phe Ser Lys Ile Phe Pro Gly Ile Thr Pro Tyr Ile
1               5                   10                  15
```

```
Leu Thr Leu Gly Ala Phe Phe Trp Met Pro Phe Leu Arg Glu Tyr Val
            20                  25                  30

Met Ser Thr Gly Ala Cys Ser Val Ser Arg Ser Ser Ile Asp Phe Leu
        35                  40                  45

Leu Thr His Lys Gly Thr Gly Asn Met Val Ile Val Val Ile Gly Gly
    50                  55                  60

Leu Ala Glu Cys Arg Tyr Ser Leu Pro Gly Ser Ser Thr Leu Val Leu
65                  70                  75                  80

Lys Asn Arg Ser Gly Phe Val Arg Met Ala Leu Gln His Gly Gln Pro
                85                  90                  95

Gly Val Gly His Gly Ala Pro Thr Leu Asn Leu Asp Leu Gly Thr Ala
            100                 105                 110

Gly Leu Gly Ser Glu Lys Pro Val Gly Arg Pro Arg Asp His Ala Pro
        115                 120                 125

Ser Ala Cys Leu Ala Phe Asp Lys Val Pro Thr Phe Leu Gly Phe Arg
    130                 135                 140

Arg Tyr Ala Phe Ala Leu Gln Gly Ala Ser Asn Thr Cys Leu Cys Leu
145                 150                 155                 160

Trp Gly Asp Gly Pro Leu
                165


<210> 2100
<211> 422
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
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<223> /note="Gene Name:
acylglycerol kinase; "

<220>
<221> source
<223> /note="Uniprot ID: Q53H12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000347581"

<400> 2100

```
Met Thr Val Phe Phe Lys Thr Leu Arg Asn His Trp Lys Lys Thr Thr
1               5                  10                  15

Ala Gly Leu Cys Leu Leu Thr Trp Gly Gly His Trp Leu Tyr Gly Lys
            20                  25                  30

His Cys Asp Asn Leu Leu Arg Arg Ala Ala Cys Gln Glu Ala Gln Val
        35                  40                  45

Phe Gly Asn Gln Leu Ile Pro Pro Asn Ala Gln Val Lys Lys Ala Thr
    50                  55                  60

Val Phe Leu Asn Pro Ala Ala Cys Lys Gly Lys Ala Arg Thr Leu Phe
65                  70                  75                  80

Glu Lys Asn Ala Ala Pro Ile Leu His Leu Ser Gly Met Asp Val Thr
                85                  90                  95

Ile Val Lys Thr Asp Tyr Glu Gly Gln Ala Lys Lys Leu Leu Glu Leu
            100                 105                 110

Met Glu Asn Thr Asp Val Ile Ile Val Ala Gly Gly Asp Gly Thr Leu
        115                 120                 125

Gln Glu Val Val Thr Gly Val Leu Arg Arg Thr Asp Glu Ala Thr Phe
    130                 135                 140

Ser Lys Ile Pro Ile Gly Phe Ile Pro Leu Gly Glu Thr Ser Ser Leu
145                 150                 155                 160

Ser His Thr Leu Phe Ala Glu Ser Gly Asn Lys Val Gln His Ile Thr
                165                 170                 175

Asp Ala Thr Leu Ala Ile Val Lys Gly Glu Thr Val Pro Leu Asp Val
```

```
            180                 185                 190

Leu Gln Ile Lys Gly Glu Lys Glu Gln Pro Val Phe Ala Met Thr Gly
        195                 200                 205

Leu Arg Trp Gly Ser Phe Arg Asp Ala Gly Val Lys Val Ser Lys Tyr
    210                 215                 220

Trp Tyr Leu Gly Pro Leu Lys Ile Lys Ala Ala His Phe Phe Ser Thr
225                 230                 235                 240

Leu Lys Glu Trp Pro Gln Thr His Gln Ala Ser Ile Ser Tyr Thr Gly
                245                 250                 255

Pro Thr Glu Arg Pro Pro Asn Glu Pro Glu Glu Thr Pro Val Gln Arg
            260                 265                 270

Pro Ser Leu Tyr Arg Arg Ile Leu Arg Arg Leu Ala Ser Tyr Trp Ala
        275                 280                 285

Gln Pro Gln Asp Ala Leu Ser Gln Glu Val Ser Pro Glu Val Trp Lys
    290                 295                 300

Asp Val Gln Leu Ser Thr Ile Glu Leu Ser Ile Thr Thr Arg Asn Asn
305                 310                 315                 320

Gln Leu Asp Pro Thr Ser Lys Glu Asp Phe Leu Asn Ile Cys Ile Glu
                325                 330                 335

Pro Asp Thr Ile Ser Lys Gly Asp Phe Ile Thr Ile Gly Ser Arg Lys
            340                 345                 350

Val Arg Asn Pro Lys Leu His Val Glu Gly Thr Glu Cys Leu Gln Ala
        355                 360                 365

Ser Gln Cys Thr Leu Leu Ile Pro Glu Gly Ala Gly Gly Ser Phe Ser
    370                 375                 380

Ile Asp Ser Glu Glu Tyr Glu Ala Met Pro Val Glu Val Lys Leu Leu
385                 390                 395                 400

Pro Arg Lys Leu Gln Phe Phe Cys Asp Pro Arg Lys Arg Glu Gln Met
                405                 410                 415
```

Leu Thr Ser Pro Thr Gln
420

<210> 2101
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
acylglycerol kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418101"

<400> 2101
Met Thr Val Phe Phe Lys Thr Leu Arg Asn His Trp Lys Lys Thr Thr
1 5 10 15

Ala Gly Leu Cys Leu Leu Thr Trp Gly Gly His Trp Leu Tyr Gly Lys
20 25 30

His Cys Asp Asn Leu Leu Arg Arg Ala Ala Cys Gln Glu Ala Gln Val
35 40 45

Phe Gly Asn Gln Leu Ile Pro Pro Asn Ala Gln Val Lys Lys Ala Thr
50 55 60

Val Phe Leu Asn Pro Ala Ala Cys Lys Gly Thr Leu Phe Glu Lys Asn
65 70 75 80

Ala Ala Pro Ile Leu His Leu Ser Gly Met Asp Val Thr Ile Val Lys
85 90 95

Thr Asp Tyr Glu Gly Gln Ala Lys Lys Leu Leu Glu Leu Met Glu Asn
100 105 110

```
Thr Asp Val Ile Ile Val Ala Gly Gly Asp Gly Thr Leu Gln Glu Val
        115                 120                 125

Val Thr Gly Val Leu Arg Arg Thr Asp Glu Ala Thr Phe Ser Lys Ile
    130                 135                 140

Pro Ile Gly Phe Ile Pro Leu Gly Glu Thr Ser Ser Leu Ser His Thr
145                 150                 155                 160

Leu Phe Ala Glu Ser Gly Asn Lys Val Gln His Ile Thr Asp Ala Thr
                165                 170                 175

Leu Ala Ile Val Lys Gly Glu Thr Val Pro Leu Asp Val Leu Gln Ile
            180                 185                 190

Lys Gly Glu Lys Glu Gln Pro Val Phe Ala Met Thr Gly Leu Arg Trp
        195                 200                 205

Gly Ser Phe Arg Asp Ala Gly Val Lys Val Ser Lys Tyr Trp Tyr Leu
    210                 215                 220

Gly Pro Leu Lys Ile Lys Ala Ala His Phe Phe Ser Thr Leu Lys Pro
225                 230                 235                 240

Phe Pro Lys Arg
```

<210> 2102
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
acylglycerol kinase; "

<220>
<221> source
<223> /note="Uniprot ID: Q53H12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418789"

<400> 2102
Met Thr Val Phe Phe Lys Thr Leu Arg Asn His Trp Lys Lys Thr Thr
1   5   10   15

Ala Gly Leu Cys Leu Leu Thr Trp Gly Gly His Trp Leu Tyr Gly Lys
            20   25   30

His Cys Asp Asn Leu Leu Arg Arg Ala Ala Cys Gln Glu Ala Gln His
        35   40   45

Tyr Gln Asp Glu Ser Arg Trp Glu Pro Thr Leu Ser Arg Thr Pro Gly
    50   55   60

Ser
65

<210> 2103
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
      acylglycerol kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420540"

<400> 2103
Met Thr Val Phe Phe Lys Thr Leu Arg Asn His Trp Lys Lys Thr Thr
1   5   10   15

Ala Gly Leu Cys Leu Leu Thr Trp Gly Gly His Trp Leu Tyr Gly Lys
            20   25   30

```
His Trp Cys Leu Ala Ile Asn Ser Phe Leu Pro Met His Lys
        35                  40                  45


<210> 2104
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
      acylglycerol kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420776"

<400> 2104
Met Glu Asn Thr Asp Ser Asp Asn Leu Leu Arg Arg Ala Ala Cys Gln
1               5                   10                  15


Glu Ala Gln Val Phe Gly Asn Gln Leu Ile Pro Pro Asn Ala Gln Val
            20                  25                  30


Lys Lys Ala Thr Val Phe Leu Asn Pro Ala Ala Cys Lys Gly Lys Ala
        35                  40                  45


Arg Thr Leu Phe Glu Lys Asn Ala Ala Pro Ile Leu His Leu Ser Gly
    50                  55                  60


Met Asp Val Thr Ile Val Lys Thr Asp Tyr Glu Gly Gln Ala Lys Lys
65                  70                  75                  80


Leu Leu Glu Leu Met Glu Asn Thr Asp Val Ile Ile Val Ala Gly Gly
                85                  90                  95


Asp Gly Thr Leu Gln Glu Val Val Thr Gly Val Leu Arg Arg Thr Asp
            100                 105                 110


Glu Ala Thr Phe Ser Lys Ile Pro Ile Gly Phe Ile Pro Leu Gly Glu
        115                 120                 125
```

```
Thr Ser Ser Leu Ser His Thr Leu Phe Ala Glu Ser Gly Asn Lys Val
    130                 135                 140

Gln His Ile Thr Asp Ala Thr Leu Ala Ile Val Lys Gly Glu Thr Val
145                 150                 155                 160

Pro Leu Asp Val Leu Gln Ile Lys Gly Glu Lys Glu Gln Pro Val Phe
                165                 170                 175

Ala Met Thr Gly Leu Arg Trp Gly Ser Phe Arg Asp Ala Gly Val Lys
            180                 185                 190

Val Ser Lys Tyr Trp Tyr Leu Gly Pro Leu Lys Ile Lys Ala Ala His
        195                 200                 205

Phe Phe Ser Thr Leu Lys Glu Trp Pro Gln Thr His Gln Ala Ser Ile
    210                 215                 220

Ser Tyr Thr Gly Pro Thr Glu Arg Pro Pro Asn Glu Pro Glu Glu Thr
225                 230                 235                 240

Pro Val Gln Arg Pro Ser Leu Tyr Arg Arg Ile Leu Arg Arg Leu Ala
                245                 250                 255

Ser Tyr Trp Ala Gln Pro Gln Asp Ala Leu Ser Gln Glu Val Ser Pro
            260                 265                 270

Glu Val Trp Lys Asp Val Gln Leu Ser Thr Ile Glu Leu Ser Ile Thr
        275                 280                 285

Thr Arg Asn Asn Gln Leu Asp Pro Thr Ser Lys Glu Asp Phe Leu Asn
    290                 295                 300

Ile Cys Ile Glu Pro Asp Thr Ile Ser Lys Gly Asp Phe Ile Thr Ile
305                 310                 315                 320

Gly Ser Arg Lys Val Arg Asn Pro Lys Leu His Val Glu Gly Thr Glu
                325                 330                 335

Cys Leu Gln Ala Ser Gln Cys Thr Leu Leu Ile Pro Glu Gly Ala Gly
            340                 345                 350
```

Gly Ser Phe Ser Ile Asp Ser Glu Glu Tyr Glu Ala Met Pro Val Glu
        355   360   365

Val Lys Leu Leu Pro Arg Lys Leu Gln Phe Phe Cys Asp Pro Arg Lys
    370   375   380

Arg Glu Gln Met Leu Thr Ser Pro Thr Gln
385   390

<210> 2105
<211> 226
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
      acylglycerol kinase; "

<220>
<221> source
<223> /note="Uniprot ID: Q53H12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458417"

<400> 2105
Gly Glu Lys Glu Gln Pro Val Phe Ala Met Thr Gly Leu Arg Trp Gly
1   5   10   15

Ser Phe Arg Asp Ala Gly Val Lys Val Ser Lys Tyr Trp Tyr Leu Gly
            20   25   30

Pro Leu Lys Ile Lys Ala Ala His Phe Phe Ser Thr Leu Lys Glu Trp
        35   40   45

Pro Gln Thr His Gln Ala Ser Ile Ser Tyr Thr Gly Pro Thr Glu Arg
    50   55   60

Pro Pro Asn Glu Pro Glu Glu Thr Pro Val Gln Arg Pro Ser Leu Tyr

65 70 75 80

Arg Arg Ile Leu Arg Arg Leu Ala Ser Tyr Trp Ala Gln Pro Gln Asp
85 90 95

Ala Leu Ser Gln Glu Val Ser Pro Glu Val Trp Lys Asp Val Gln Leu
100 105 110

Ser Thr Ile Glu Leu Ser Ile Thr Thr Arg Asn Asn Gln Leu Asp Pro
115 120 125

Thr Ser Lys Glu Asp Phe Leu Asn Ile Cys Ile Glu Pro Asp Thr Ile
130 135 140

Ser Lys Gly Asp Phe Ile Thr Ile Gly Ser Arg Lys Val Arg Asn Pro
145 150 155 160

Lys Leu His Val Glu Gly Thr Glu Cys Leu Gln Ala Ser Gln Cys Thr
165 170 175

Leu Leu Ile Pro Glu Gly Ala Gly Gly Ser Phe Ser Ile Asp Ser Glu
180 185 190

Glu Tyr Glu Ala Met Pro Val Glu Val Lys Leu Leu Pro Arg Lys Leu
195 200 205

Gln Phe Phe Cys Asp Pro Arg Lys Arg Glu Gln Met Leu Thr Ser Pro
210 215 220

Thr Gln
225

<210> 2106
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>

<221> source
<223> /note="Gene Name:
acylglycerol kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000459752"

<400> 2106
Gly Glu Lys Glu Gln Pro Val Phe Ala Met Thr Gly Leu Arg Trp Gly
1 5 10 15

Ser Phe Arg Asp Ala Gly Val Lys Val Ser Lys Tyr Trp Tyr Leu Gly
20 25 30

Pro Leu Lys Ile Lys Ala Ala His Phe Phe Ser Thr Leu Lys Pro Phe
35 40 45

Pro Lys Arg
50

<210> 2107
<211> 226
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
acylglycerol kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000461611"

<400> 2107
Gly Glu Lys Glu Gln Pro Val Phe Ala Met Thr Gly Leu Arg Trp Gly
1 5 10 15

Ser Phe Arg Asp Ala Gly Val Lys Val Ser Lys Tyr Trp Tyr Leu Gly
20 25 30

Pro Leu Lys Ile Lys Ala Ala His Phe Phe Ser Thr Leu Lys Glu Trp

```
        35                  40                  45

Pro Gln Thr His Gln Ala Ser Ile Ser Tyr Thr Gly Pro Thr Glu Arg
    50                  55                  60

Pro Pro Asn Glu Pro Glu Glu Thr Pro Val Gln Arg Pro Ser Leu Tyr
65                  70                  75                  80

Arg Arg Ile Leu Arg Arg Leu Ala Ser Tyr Trp Ala Gln Pro Gln Asp
                85                  90                  95

Ala Leu Ser Gln Glu Val Ser Pro Glu Val Trp Lys Asp Val Gln Leu
            100                 105                 110

Ser Thr Ile Glu Leu Ser Ile Thr Thr Arg Asn Asn Gln Leu Asp Pro
        115                 120                 125

Thr Ser Lys Glu Asp Phe Leu Asn Ile Cys Ile Glu Pro Asp Thr Ile
    130                 135                 140

Ser Lys Gly Asp Phe Ile Thr Ile Gly Ser Arg Lys Val Arg Asn Pro
145                 150                 155                 160

Lys Leu His Val Glu Gly Thr Glu Cys Leu Gln Ala Ser Gln Cys Thr
                165                 170                 175

Leu Leu Ile Pro Glu Gly Ala Gly Gly Ser Phe Ser Ile Asp Ser Glu
            180                 185                 190

Glu Tyr Glu Ala Met Pro Val Glu Val Lys Leu Leu Pro Arg Lys Leu
        195                 200                 205

Gln Phe Phe Cys Asp Pro Arg Lys Arg Glu Gln Met Leu Thr Ser Pro
    210                 215                 220

Thr Gln
225


<210> 2108
<211> 244
<212> PRT
<213> Homo sapiens

<220>
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<221> source
<223> /note="Payload ID: 531; "

<220>
<221> source
<223> /note="Gene Symbol: AGK; "

<220>
<221> source
<223> /note="Gene Name:
acylglycerol kinase; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487274"

<400> 2108

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Met Thr Val Phe Phe Lys Thr Leu Arg Asn His Trp Lys Lys Thr Thr
1               5                  10                  15

Ala Gly Leu Cys Leu Leu Thr Trp Gly Gly His Trp Leu Tyr Gly Lys
            20                  25                  30

His Cys Asp Asn Leu Leu Arg Arg Ala Ala Cys Gln Glu Ala Gln Val
        35                  40                  45

Phe Gly Asn Gln Leu Ile Pro Pro Asn Ala Gln Val Lys Lys Ala Thr
    50                  55                  60

Val Phe Leu Asn Pro Ala Ala Cys Lys Gly Thr Leu Phe Glu Lys Asn
65                  70                  75                  80

Ala Ala Pro Ile Leu His Leu Ser Gly Met Asp Val Thr Ile Val Lys
                85                  90                  95

Thr Asp Tyr Glu Gly Gln Ala Lys Lys Leu Leu Glu Leu Met Glu Asn
            100                 105                 110

Thr Asp Val Ile Ile Val Ala Gly Gly Asp Gly Thr Leu Gln Glu Val
        115                 120                 125

Val Thr Gly Val Leu Arg Arg Thr Asp Glu Ala Thr Phe Ser Lys Ile
    130                 135                 140

Pro Ile Gly Phe Ile Pro Leu Gly Glu Thr Ser Ser Leu Ser His Thr
145                 150                 155                 160
```

```
Leu Phe Ala Glu Ser Gly Asn Lys Val Gln His Ile Thr Asp Ala Thr
                165                 170                 175

Leu Ala Ile Val Lys Gly Glu Thr Val Pro Leu Asp Val Leu Gln Ile
            180                 185                 190

Lys Gly Glu Lys Glu Gln Pro Val Phe Ala Met Thr Gly Leu Arg Trp
        195                 200                 205

Gly Ser Phe Arg Asp Ala Gly Val Lys Val Ser Lys Tyr Trp Tyr Leu
    210                 215                 220

Gly Pro Leu Lys Ile Lys Ala Ala His Phe Phe Ser Thr Leu Lys Pro
225                 230                 235                 240

Phe Pro Lys Arg
```

<210> 2109
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 532; "

<220>
<221> source
<223> /note="Gene Symbol: AOAH; "

<220>
<221> source
<223> /note="Gene Name:
acyloxyacyl hydrolase (neutrophil); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416051"

<400> 2109

```
Met Gln Ser Pro Trp Lys Ile Leu Thr Val Ala Pro Leu Phe Leu Leu
1               5                   10                  15

Leu Ser Leu Gln Ser Ser Ala Ser Pro Ala Asn Asp Asp Gln Ser Arg
            20                  25                  30

Pro Ser Leu Ser Asn Gly His Thr Cys Val Glu Lys Leu Phe Leu Lys
        35                  40                  45
```

```
Thr Thr Cys Tyr Leu Val Ile Asp Lys Phe Gly Ser Asp Ile Ile Lys
    50                  55                  60

Leu Leu Ser Ala Asp Met Asn Ala Asp Val Val Cys His Thr Leu Glu
65                  70                  75                  80

Phe Cys Lys Gln Asn Thr Gly Gln Pro Leu Cys His Leu Tyr Pro Leu
                85                  90                  95

Pro Lys Glu Thr Trp Lys Phe Thr Leu Gln Lys Ala
            100                 105


<210> 2110
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 532; "

<220>
<221> source
<223> /note="Gene Symbol: AOAH; "

<220>
<221> source
<223> /note="Gene Name:
      acyloxyacyl hydrolase (neutrophil); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000416472"

<400> 2110
Met Gln Ser Pro Trp Lys Ile Leu Thr Val Ala Pro Leu Phe Leu Leu
1               5                   10                  15

Leu Ser Leu Gln Ser Ser Ala Ser Pro Ala Asn Asp Asp Gln Ser Arg
            20                  25                  30

Pro Ser Leu Ser Asn Gly His Thr Cys Val Ala Ser Ser Ala Glu Lys
        35                  40                  45

Pro Gln Leu Ser
    50
```

<210> 2111
<211> 688
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 532; "

<220>
<221> source
<223> /note="Gene Symbol: AOAH; "

<220>
<221> source
<223> /note="Gene Name:
acyloxyacyl hydrolase (neutrophil); "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479664"

<400> 2111
Met Gln Ser Pro Trp Lys Ile Leu Thr Val Ala Pro Leu Phe Leu Leu
1 5 10 15

Leu Ser Leu Gln Ser Ser Ala Ser Pro Ala Asn Asp Asp Gln Ser Arg
20 25 30

Pro Ser Leu Ser Asn Gly His Thr Cys Val Gly Cys Val Leu Val Val
35 40 45

Ser Val Ile Glu Gln Leu Ala Gln Val His Asn Ser Thr Val Gln Ala
50 55 60

Ser Met Glu Arg Leu Cys Ser Tyr Leu Pro Glu Lys Leu Phe Leu Lys
65 70 75 80

Thr Thr Cys Tyr Leu Val Ile Asp Lys Phe Gly Ser Asp Ile Ile Lys
85 90 95

Leu Leu Ser Ala Asp Met Asn Ala Asp Val Val Cys His Thr Leu Glu
100 105 110

Phe Cys Lys Gln Asn Thr Gly Gln Pro Leu Cys His Leu Tyr Pro Leu
115 120 125

Pro Lys Glu Thr Trp Lys Phe Thr Leu Gln Lys Ala Arg Gln Ile Val
130 135 140

Lys Lys Ser Pro Ile Leu Lys Tyr Ser Arg Ser Gly Ser Asp Ile Cys
145 150 155 160

Ser Leu Pro Val Leu Ala Lys Ile Cys Gln Lys Ile Lys Leu Ala Met
165 170 175

Glu Gln Ser Val Pro Phe Lys Asp Val Asp Ser Asp Lys Tyr Ser Val
180 185 190

Phe Pro Thr Leu Arg Gly Tyr His Trp Arg Gly Arg Asp Cys Asn Asp
195 200 205

Ser Asp Glu Ser Val Tyr Pro Gly Arg Arg Pro Asn Asn Trp Asp Val
210 215 220

His Gln Asp Ser Asn Cys Asn Gly Ile Trp Gly Val Asp Pro Lys Asp
225 230 235 240

Gly Val Pro Tyr Glu Lys Lys Phe Cys Glu Gly Ser Gln Pro Arg Gly
245 250 255

Ile Ile Leu Leu Gly Asp Ser Ala Gly Ala His Phe His Ile Ser Pro
260 265 270

Glu Trp Ile Thr Ala Ser Gln Met Ser Leu Asn Ser Phe Ile Asn Leu
275 280 285

Pro Thr Ala Leu Thr Asn Glu Leu Asp Trp Pro Gln Leu Ser Gly Ala
290 295 300

Thr Gly Phe Leu Asp Ser Thr Val Gly Ile Lys Glu Lys Ser Ile Tyr
305 310 315 320

Leu Arg Leu Trp Lys Arg Asn His Cys Asn His Arg Asp Tyr Gln Asn
325 330 335

Ile Ser Arg Asn Gly Ala Ser Ser Arg Asn Leu Lys Lys Phe Ile Glu
340 345 350

Ser Leu Ser Arg Asn Lys Val Leu Asp Tyr Pro Ala Ile Val Ile Tyr
355 360 365

```
Ala Met Ile Gly Asn Asp Val Cys Ser Gly Lys Ser Asp Pro Val Pro
    370                 375                 380

Ala Met Thr Thr Pro Glu Lys Leu Tyr Ser Asn Val Met Gln Thr Leu
385                 390                 395                 400

Lys His Leu Asn Ser His Leu Pro Asn Gly Ser His Val Ile Leu Tyr
                405                 410                 415

Gly Leu Pro Asp Gly Thr Phe Leu Trp Asp Asn Leu His Asn Arg Tyr
            420                 425                 430

His Pro Leu Gly Gln Leu Asn Lys Asp Met Thr Tyr Ala Gln Leu Tyr
        435                 440                 445

Ser Phe Leu Asn Cys Leu Gln Val Ser Pro Cys His Gly Trp Met Ser
    450                 455                 460

Ser Asn Lys Thr Leu Arg Thr Leu Thr Ser Glu Arg Ala Glu Gln Leu
465                 470                 475                 480

Ser Asn Thr Leu Lys Lys Ile Ala Ala Ser Glu Lys Phe Thr Asn Phe
                485                 490                 495

Asn Leu Phe Tyr Met Asp Phe Ala Phe His Glu Ile Ile Gln Glu Trp
            500                 505                 510

Gln Lys Arg Gly Gly Gln Pro Trp Gln Leu Ile Glu Pro Val Asp Gly
        515                 520                 525

Phe His Pro Asn Glu Arg Lys Ser Ile Leu Leu Lys Gly Ile Leu Met
    530                 535                 540

Thr Ser Gln Thr Leu Asp Asn Gln Glu Trp Thr Gln Leu Thr Ser Trp
545                 550                 555                 560

Ile Lys Gly Asn Leu Thr Cys Asp Ser Arg Thr Arg Glu Trp Leu Cys
                565                 570                 575

Cys Cys Trp Arg Ile Ile Ser Gly Lys Arg Cys Ser Ser Ser Gly Pro
            580                 585                 590
```

```
Lys Ser Trp Glu Arg Arg Ile Arg Ser Thr Pro Arg Leu Asn Arg Cys
        595                 600                 605

Leu Glu Thr Lys Ala Gly Thr Glu Pro Leu Arg Ser Met His Pro Trp
    610                 615                 620

Gly Ala Gln Gly Gly Arg Gly Leu Gly Lys Leu Ile Pro Gln Thr Leu
625                 630                 635                 640

Trp Gly Leu Pro Arg His Arg Pro Lys Gly Leu Phe Phe Ser Ser Ile
                645                 650                 655

Phe Ala Lys Cys Leu Ser Leu Asn Glu Glu His Ile Trp Thr Thr Val
            660                 665                 670

Gln Cys Cys Val Leu Pro Gly Ser Val Thr Leu Pro Leu Phe Leu Lys
        675                 680                 685


<210> 2112
<211> 575
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 532; "

<220>
<221> source
<223> /note="Gene Symbol: AOAH; "

<220>
<221> source
<223> /note="Gene Name:
      acyloxyacyl hydrolase (neutrophil); "

<220>
<221> source
<223> /note="Uniprot ID:  P28039; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483783"

<400> 2112
Met Gln Ser Pro Trp Lys Ile Leu Thr Val Ala Pro Leu Phe Leu Leu
1               5                   10                  15

Leu Ser Leu Gln Ser Ser Ala Ser Pro Ala Asn Asp Asp Gln Ser Arg
            20                  25                  30
```

```
Pro Ser Leu Ser Asn Gly His Thr Cys Val Gly Cys Val Leu Val Val
        35                  40                  45

Ser Val Ile Glu Gln Leu Ala Gln Val His Asn Ser Thr Val Gln Ala
    50                  55                  60

Ser Met Glu Arg Leu Cys Ser Tyr Leu Pro Glu Lys Leu Phe Leu Lys
65                  70                  75                  80

Thr Thr Cys Tyr Leu Val Ile Asp Lys Phe Gly Ser Asp Ile Ile Lys
                85                  90                  95

Leu Leu Ser Ala Asp Met Asn Ala Asp Val Val Cys His Thr Leu Glu
            100                 105                 110

Phe Cys Lys Gln Asn Thr Gly Gln Pro Leu Cys His Leu Tyr Pro Leu
        115                 120                 125

Pro Lys Glu Thr Trp Lys Phe Thr Leu Gln Lys Ala Arg Gln Ile Val
    130                 135                 140

Lys Lys Ser Pro Ile Leu Lys Tyr Ser Arg Ser Gly Ser Asp Ile Cys
145                 150                 155                 160

Ser Leu Pro Val Leu Ala Lys Ile Cys Gln Lys Ile Lys Leu Ala Met
                165                 170                 175

Glu Gln Ser Val Pro Phe Lys Asp Val Asp Ser Asp Lys Tyr Ser Val
            180                 185                 190

Phe Pro Thr Leu Arg Gly Tyr His Trp Arg Gly Arg Asp Cys Asn Asp
        195                 200                 205

Ser Asp Glu Ser Val Tyr Pro Gly Arg Arg Pro Asn Asn Trp Asp Val
    210                 215                 220

His Gln Asp Ser Asn Cys Asn Gly Ile Trp Gly Val Asp Pro Lys Asp
225                 230                 235                 240

Gly Val Pro Tyr Glu Lys Lys Phe Cys Glu Gly Ser Gln Pro Arg Gly
                245                 250                 255
```

```
Ile Ile Leu Leu Gly Asp Ser Ala Gly Ala His Phe His Ile Ser Pro
            260                 265                 270

Glu Trp Ile Thr Ala Ser Gln Met Ser Leu Asn Ser Phe Ile Asn Leu
        275                 280                 285

Pro Thr Ala Leu Thr Asn Glu Leu Asp Trp Pro Gln Leu Ser Gly Ala
    290                 295                 300

Thr Gly Phe Leu Asp Ser Thr Val Gly Ile Lys Glu Lys Ser Ile Tyr
305                 310                 315                 320

Leu Arg Leu Trp Lys Arg Asn His Cys Asn His Arg Asp Tyr Gln Asn
                325                 330                 335

Ile Ser Arg Asn Gly Ala Ser Ser Arg Asn Leu Lys Lys Phe Ile Glu
            340                 345                 350

Ser Leu Ser Arg Asn Lys Val Leu Asp Tyr Pro Ala Ile Val Ile Tyr
        355                 360                 365

Ala Met Ile Gly Asn Asp Val Cys Ser Gly Lys Ser Asp Pro Val Pro
    370                 375                 380

Ala Met Thr Thr Pro Glu Lys Leu Tyr Ser Asn Val Met Gln Thr Leu
385                 390                 395                 400

Lys His Leu Asn Ser His Leu Pro Asn Gly Ser His Val Ile Leu Tyr
                405                 410                 415

Gly Leu Pro Asp Gly Thr Phe Leu Trp Asp Asn Leu His Asn Arg Tyr
            420                 425                 430

His Pro Leu Gly Gln Leu Asn Lys Asp Met Thr Tyr Ala Gln Leu Tyr
        435                 440                 445

Ser Phe Leu Asn Cys Leu Gln Val Ser Pro Cys His Gly Trp Met Ser
    450                 455                 460

Ser Asn Lys Thr Leu Arg Thr Leu Thr Ser Glu Arg Ala Glu Gln Leu
465                 470                 475                 480
```

```
Ser Asn Thr Leu Lys Lys Ile Ala Ala Ser Glu Lys Phe Thr Asn Phe
                485                 490                 495

Asn Leu Phe Tyr Met Asp Phe Ala Phe His Glu Ile Ile Gln Glu Trp
            500                 505                 510

Gln Lys Arg Gly Gly Gln Pro Trp Gln Leu Ile Glu Pro Val Asp Gly
        515                 520                 525

Phe His Pro Asn Glu Val Ala Leu Leu Leu Leu Ala Asp His Phe Trp
    530                 535                 540

Lys Lys Val Gln Leu Gln Trp Pro Gln Ile Leu Gly Lys Glu Asn Pro
545                 550                 555                 560

Phe Asn Pro Gln Ile Lys Gln Val Phe Gly Asp Gln Gly Gly His
                565                 570                 575


<210> 2113
<211> 543
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 532; "

<220>
<221> source
<223> /note="Gene Symbol: AOAH; "

<220>
<221> source
<223> /note="Gene Name:
      acyloxyacyl hydrolase (neutrophil); "

<220>
<221> source
<223> /note="Uniprot ID:  P28039; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484305"

<400> 2113
Met Gln Ser Pro Trp Lys Ile Leu Thr Val Ala Pro Leu Phe Leu Leu
1               5                   10                  15

Leu Ser Leu Gln Ser Ser Ala Ser Pro Ala Asn Asp Asp Gln Ser Arg
            20                  25                  30
```

```
Pro Ser Leu Ser Asn Gly His Thr Cys Val Glu Lys Leu Phe Leu Lys
        35                  40                  45

Thr Thr Cys Tyr Leu Val Ile Asp Lys Phe Gly Ser Asp Ile Ile Lys
    50                  55                  60

Leu Leu Ser Ala Asp Met Asn Ala Asp Val Val Cys His Thr Leu Glu
65                  70                  75                  80

Phe Cys Lys Gln Asn Thr Gly Gln Pro Leu Cys His Leu Tyr Pro Leu
                85                  90                  95

Pro Lys Glu Thr Trp Lys Phe Thr Leu Gln Lys Ala Arg Gln Ile Val
            100                 105                 110

Lys Lys Ser Pro Ile Leu Lys Tyr Ser Arg Ser Gly Ser Asp Ile Cys
        115                 120                 125

Ser Leu Pro Val Leu Ala Lys Ile Cys Gln Lys Ile Lys Leu Ala Met
    130                 135                 140

Glu Gln Ser Val Pro Phe Lys Asp Val Asp Ser Asp Lys Tyr Ser Val
145                 150                 155                 160

Phe Pro Thr Leu Arg Gly Tyr His Trp Arg Gly Arg Asp Cys Asn Asp
                165                 170                 175

Ser Asp Glu Ser Val Tyr Pro Gly Arg Arg Pro Asn Asn Trp Asp Val
            180                 185                 190

His Gln Asp Ser Asn Cys Asn Gly Ile Trp Gly Val Asp Pro Lys Asp
        195                 200                 205

Gly Val Pro Tyr Glu Lys Lys Phe Cys Glu Gly Ser Gln Pro Arg Gly
    210                 215                 220

Ile Ile Leu Leu Gly Asp Ser Ala Gly Ala His Phe His Ile Ser Pro
225                 230                 235                 240

Glu Trp Ile Thr Ala Ser Gln Met Ser Leu Asn Ser Phe Ile Asn Leu
                245                 250                 255
```

```
Pro Thr Ala Leu Thr Asn Glu Leu Asp Trp Pro Gln Leu Ser Gly Ala
            260                 265                 270

Thr Gly Phe Leu Asp Ser Thr Val Gly Ile Lys Glu Lys Ser Ile Tyr
        275                 280                 285

Leu Arg Leu Trp Lys Arg Asn His Cys Asn His Arg Asp Tyr Gln Asn
    290                 295                 300

Ile Ser Arg Asn Gly Ala Ser Ser Arg Asn Leu Lys Lys Phe Ile Glu
305                 310                 315                 320

Ser Leu Ser Arg Asn Lys Val Leu Asp Tyr Pro Ala Ile Val Ile Tyr
                325                 330                 335

Ala Met Ile Gly Asn Asp Val Cys Ser Gly Lys Ser Asp Pro Val Pro
            340                 345                 350

Ala Met Thr Thr Pro Glu Lys Leu Tyr Ser Asn Val Met Gln Thr Leu
        355                 360                 365

Lys His Leu Asn Ser His Leu Pro Asn Gly Ser His Val Ile Leu Tyr
    370                 375                 380

Gly Leu Pro Asp Gly Thr Phe Leu Trp Asp Asn Leu His Asn Arg Tyr
385                 390                 395                 400

His Pro Leu Gly Gln Leu Asn Lys Asp Met Thr Tyr Ala Gln Leu Tyr
                405                 410                 415

Ser Phe Leu Asn Cys Leu Gln Val Ser Pro Cys His Gly Trp Met Ser
            420                 425                 430

Ser Asn Lys Thr Leu Arg Thr Leu Thr Ser Glu Arg Ala Glu Gln Leu
        435                 440                 445

Ser Asn Thr Leu Lys Lys Ile Ala Ala Ser Glu Lys Phe Thr Asn Phe
    450                 455                 460

Asn Leu Phe Tyr Met Asp Phe Ala Phe His Glu Ile Ile Gln Glu Trp
465                 470                 475                 480
```

```
Gln Lys Arg Gly Gly Gln Pro Trp Gln Leu Ile Glu Pro Val Asp Gly
                485                 490                 495


Phe His Pro Asn Glu Val Ala Leu Leu Leu Leu Ala Asp His Phe Trp
            500                 505                 510


Lys Lys Val Gln Leu Gln Trp Pro Gln Ile Leu Gly Lys Glu Asn Pro
        515                 520                 525


Phe Asn Pro Gln Ile Lys Gln Val Phe Gly Asp Gln Gly Gly His
    530                 535                 540


<210> 2114
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 533; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP1; "

<220>
<221> source
<223> /note="Gene Name:
      acylphosphatase 1, erythrocyte (common) type; "

<220>
<221> source
<223> /note="Uniprot ID:  P07311; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000238618"

<400> 2114
Met Ala Glu Gly Asn Thr Leu Ile Ser Val Asp Tyr Glu Ile Phe Gly
1               5                   10                  15


Lys Val Gln Gly Val Phe Phe Arg Lys His Thr Gln Ala Glu Gly Lys
            20                  25                  30


Lys Leu Gly Leu Val Gly Trp Val Gln Asn Thr Asp Arg Gly Thr Val
        35                  40                  45


Gln Gly Gln Leu Gln Gly Pro Ile Ser Lys Val Arg His Met Gln Glu
    50                  55                  60
```

```
Trp Leu Glu Thr Arg Gly Ser Pro Lys Ser His Ile Asp Lys Ala Asn
65                  70                  75                  80


Phe Asn Asn Glu Lys Val Ile Leu Lys Leu Asp Tyr Ser Asp Phe Gln
                85                  90                  95


Ile Val Lys



<210> 2115
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 533; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP1; "

<220>
<221> source
<223> /note="Gene Name:
      acylphosphatase 1, erythrocyte (common) type; "

<220>
<221> source
<223> /note="Uniprot ID:  P07311; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000350655"

<400> 2115
Met Ala Glu Gly Asn Thr Leu Ile Ser Val Asp Tyr Glu Ile Phe Gly
1               5                   10                  15


Lys Val Gln Gly Val Phe Phe Arg Lys His Thr Gln Glu Met Thr Val
            20                  25                  30


Glu Asn Arg Ile Ala Glu Thr His Ser Lys Ser Cys Val Pro Val Ser
        35                  40                  45


Phe Ala Thr Ser Tyr Ala Gly
    50                  55
```

<210> 2116
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 533; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP1; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 1, erythrocyte (common) type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450873"

<400> 2116
Met Pro Ala Ser Ala Arg Leu Ala Gly Ala Gly Leu Leu Leu Ala Phe
1 5 10 15

Leu Arg Ala Leu Gly Cys Ala Gly Arg Ala Pro Gly Leu Ser Met Ala
20 25 30

Glu Gly Asn Thr Leu Ile Ser Val Asp Tyr Glu Ile Phe Gly Lys Val
35 40 45

Gln Gly Val Phe Phe Arg Lys His Thr Gln Ala Glu Gly Lys Lys Leu
50 55 60

Gly Leu Val Gly Trp Val Gln Asn Thr Asp Arg Gly Thr Val Gln Gly
65 70 75 80

Gln Leu Gln Gly Pro Ile Ser Lys Val Arg His Met Gln Glu Trp Leu
85 90 95

Glu Thr Arg Gly Ser Pro Lys Ser His Ile Asp Lys Ala Asn Phe Asn
100 105 110

Asn Glu Lys Val Ile Leu Lys Leu Asp Tyr Ser Asp Phe Gln Ile Val
115 120 125

Lys

<210> 2117
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 533; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP1; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 1, erythrocyte (common) type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451220"

<400> 2117
Met Ala Glu Gly Asn Thr Leu Ile Ser Val Asp Tyr Glu Ile Phe Gly
1 5 10 15

Lys Val Gln Gly Val Phe Phe Arg Lys His Thr Gln Val Cys Gly Leu
20 25 30

Gln Ala Leu Gly Trp
35

<210> 2118
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 533; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP1; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 1, erythrocyte (common) type; "

<220>
<221> source

<223> /note="Uniprot ID: P07311; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451581"

<400> 2118
Met Ala Glu Gly Asn Thr Leu Ile Ser Val Asp Tyr Glu Ile Phe Gly
1   5   10   15

Lys Val Gln Gly Val Phe Phe Arg Lys His Thr Gln Ala Glu Gly Lys
            20   25   30

Lys Leu Gly Leu Val Gly Trp Val Gln Asn Thr Asp Arg Gly Thr Val
        35   40   45

Gln Gly Gln Leu Gln Gly Pro Ile Ser Lys Val Arg His Met Gln Glu
    50   55   60

Trp Leu Glu Thr Arg Gly Ser Pro Lys Ser His Ile Asp Lys Ala Asn
65   70   75   80

Phe Asn Asn Glu Lys Val Ile Leu Lys Leu Asp Tyr Ser Asp Phe Gln
                85   90   95

Ile Val Lys

<210> 2119
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 533; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP1; "

<220>
<221> source
<223> /note="Gene Name:
      acylphosphatase 1, erythrocyte (common) type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452249"

<400> 2119
Met Ala Glu Gly Asn Thr Leu Ile Ser Val Asp Tyr Glu Ile Phe Gly
1   5   10   15

Lys Val Gln Gly Val Phe Phe Arg Lys His Thr Gln Glu Met Thr Val
            20   25   30

Glu Asn Arg Ile Ala Glu Thr His Ser Lys Ser Cys Val Pro Val Ser
        35   40   45

Phe Ala Thr Ser Tyr Ala Gly Ile Asn Glu Phe Lys Arg Ile
    50   55   60

<210> 2120
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
      acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000306448"

<400> 2120
Met Cys Pro Leu Pro Leu Ala Ala Ala Ala Val Ala Ala Pro Arg Ala
1   5   10   15

Pro Leu Arg Leu Leu Asn Arg Gly Leu Ala Ala Ala Met Ser Thr Ala
            20   25   30

Gln Ser Leu Lys Ser Val Asp Tyr Glu Val Phe Gly Arg Val Gln Gly
        35   40   45

Val Cys Phe Arg Met Tyr Thr Glu Asp Glu Ala Arg Lys Ile Gly Val
    50   55   60

Val Gly Trp Val Lys Asn Thr Ser Lys Gly Thr Val Thr Gly Gln Val

65 70 75 80

Gln Gly Pro Glu Asp Lys Val Asn Ser Met Asn Ser Ser Ala Pro Glu
85 90 95

Ala Gly

<210> 2121
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="Uniprot ID: P14621; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378161"

<400> 2121
Met Ser Thr Ala Gln Ser Leu Lys Ser Val Asp Tyr Glu Val Phe Gly
1 5 10 15

Arg Val Gln Gly Val Cys Phe Arg Met Tyr Thr Glu Asp Glu Ala Arg
20 25 30

Lys Ile Gly Val Val Gly Trp Val Lys Asn Thr Ser Lys Gly Thr Val
35 40 45

Thr Gly Gln Val Gln Gly Pro Glu Asp Lys Val Asn Ser Met Lys Ser
50 55 60

Trp Leu Ser Lys Val Gly Ser Pro Ser Ser Arg Ile Asp Arg Thr Asn
65 70 75 80

```
Phe Ser Asn Glu Lys Thr Ile Ser Lys Leu Glu Tyr Ser Asn Phe Ser
                85                  90                  95

Ile Arg Tyr



<210> 2122
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
      acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000385674"

<400> 2122
Met Cys Pro Leu Pro Leu Ala Ala Ala Ala Val Ala Ala Pro Arg Ala
1               5                  10                  15

Pro Leu Arg Leu Leu Asn Arg Gly Leu Ala Ala Ala Met Ser Thr Ala
            20                  25                  30

Gln Ser Leu Lys Ser Val Asp Tyr Glu Val Phe Gly Arg Val Gln Gly
        35                  40                  45

Val Cys Phe Arg Met Tyr Thr Glu Asp Glu Ala Arg Lys Ile Gly Val
    50                  55                  60

Val Gly Trp Val Lys Asn Thr Ser Lys Gly Thr Val Thr Gly Gln Val
65                  70                  75                  80

Gln Gly Pro Glu Asp Lys Val Asn Ser Met Leu Glu Cys Ser Gly Leu
                85                  90                  95

Ile
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<210> 2123
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
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<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475312"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2123
Xaa Ala Gln Ser Leu Lys Ser Val Asp Tyr Glu Val Phe Gly Arg Val
1 5 10 15

Gln Gly Val Cys Phe Arg Met Tyr Thr Glu Asp Glu Ala Arg Lys Ile
20 25 30

Gly Val Val Gly Trp Val Lys Asn Thr Ser Lys Gly Thr Val Thr Gly
35 40 45

Gln Val Gln Gly Pro Glu Asp Lys Val Asn Ser Ile Leu Ala Phe Pro
50 55 60

Phe Tyr
65

<210> 2124
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475333"

<400> 2124
Met Thr Ala Leu Val Leu Gln Ile Glu Tyr Thr Glu Asp Glu Ala Arg
1 5 10 15

Lys Ile Gly Val Val Gly Trp Val Lys Asn Thr Ser Lys Gly Thr Val
20 25 30

Thr Gly Gln Val Gln Gly Pro Glu Asp Lys Val Asn Ser Met Lys Ser
35 40 45

Trp Leu Ser Lys Val Gly Ser Pro Ser Ser Arg Ile Asp Arg Thr Asn
50 55 60

Phe Ser Asn Glu Lys Thr Ile Ser Lys Leu Glu Tyr Ser Asn Phe Ser
65 70 75 80

Ile Arg Tyr

<210> 2125
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source

<223> /note="Gene Name:
acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475424"

<400> 2125
Met Leu Leu Thr Gln Ser Leu Phe Gly Gly Leu Phe Pro Arg Thr Arg
1 5 10 15

Glu Thr Met Arg Arg Glu Ala Val Pro Asp Asp Asn Glu Leu Pro Arg
20 25 30

Asn Lys His Leu Asn Trp Lys Ser
35 40

<210> 2126
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475658"

<400> 2126
Met Leu Leu Thr Gln Ser Leu Phe Gly Gly Leu Phe Pro Arg Thr Arg
1 5 10 15

Glu Thr Met Arg Arg Tyr Lys Val Ser Leu Phe Tyr Leu Gly Cys Ser
20 25 30

Arg Thr Pro Asn Val Lys Leu Ser Ser Cys Leu Gly Leu Pro Cys Cys
35 40 45

Trp Asp Tyr Ser Tyr Lys Phe Ile Gln Leu Ser Glu Phe Gly Phe Gly
50 55 60

```
Gln Val Ile Ile Val Ser Glu Glu Pro Trp Lys Glu Asn Ile Ser Cys
65                  70                  75                  80


Ser Ser Thr Thr Phe Ile Lys Ser Thr Ile Cys Leu Asn Pro Asp Ser
                85                  90                  95


Glu Phe Arg Pro Cys Phe Asn Ala Trp Leu Ser Leu Ile Arg Glu Asn
            100                 105                 110


Ala Val Gly Leu
        115


<210> 2127
<211> 172
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 534; "

<220>
<221> source
<223> /note="Gene Symbol: ACYP2; "

<220>
<221> source
<223> /note="Gene Name:
      acylphosphatase 2, muscle type; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000475986"

<400> 2127
Met Leu Leu Thr Gln Ser Leu Phe Gly Gly Leu Phe Pro Arg Thr Arg
1               5                   10                  15


Glu Thr Met Arg Arg Tyr Lys Val Ser Leu Phe Tyr Leu Gly Cys Ser
            20                  25                  30


Arg Thr Pro Asn Val Lys Leu Ser Ser Cys Leu Gly Leu Pro Cys Cys
        35                  40                  45


Trp Asp Tyr Ser Tyr Lys Phe Ile Gln Leu Ser Glu Phe Gly Phe Gly
    50                  55                  60
```

```
Gln Val Ile Ile Val Ser Glu Glu Pro Trp Lys Glu Asn Ile Ser Cys
65                  70                  75                  80

Ser Ser Thr Thr Phe Ile Lys Ser Thr Ile Cys Leu Ser Val Cys Phe
                85                  90                  95

Arg Met Tyr Thr Glu Asp Glu Ala Arg Lys Ile Gly Val Val Gly Trp
            100                 105                 110

Val Lys Asn Thr Ser Lys Gly Thr Val Thr Gly Gln Val Gln Gly Pro
        115                 120                 125

Glu Asp Lys Val Asn Ser Met Lys Ser Trp Leu Ser Lys Val Gly Ser
    130                 135                 140

Pro Ser Ser Arg Ile Asp Arg Thr Asn Phe Ser Asn Glu Lys Thr Ile
145                 150                 155                 160

Ser Lys Leu Glu Tyr Ser Asn Phe Ser Ile Arg Tyr
                165                 170


<210> 2128
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 535; "

<220>
<221> source
<223> /note="Gene Symbol:; "

<220>
<221> source
<223> /note="Gene Name:
      AD000671.6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000472696"

<400> 2128
Met Ala Glu Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val
1               5                   10                  15

Asn Cys Ser Phe Tyr Phe Lys Ile Gly Val Cys Arg His Gly Asp Arg
            20                  25                  30
```

```
Cys Ser Arg Leu His Asn Lys Pro Thr Phe Ser Gln Pro Cys Pro Leu
        35                  40                  45

Ser Ser Gly Pro Ala Pro Phe Lys Phe Cys Ala Asp His Ser Ala Ala
    50                  55                  60

Gln Pro Val Pro Glu Ser Thr Glu His Ser Pro Asn Cys Arg Arg Ile
65                  70                  75                  80

Thr Leu Arg Cys Ser Gln Asn Cys Arg Arg Ser Met Gly Arg Leu Lys
                85                  90                  95

Arg
```

<210> 2129
<211> 748
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="Uniprot ID: O14672; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000260408"

<400> 2129

```
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1               5                   10                  15

Met Gly Gly Gln Tyr Gly Asn Pro Leu Asn Lys Tyr Ile Arg His Tyr
            20                  25                  30
```

```
Glu Gly Leu Ser Tyr Asn Val Asp Ser Leu His Gln Lys His Gln Arg
        35                  40                  45

Ala Lys Arg Ala Val Ser His Glu Asp Gln Phe Leu Arg Leu Asp Phe
    50                  55                  60

His Ala His Gly Arg His Phe Asn Leu Arg Met Lys Arg Asp Thr Ser
65                  70                  75                  80

Leu Phe Ser Asp Glu Phe Lys Val Glu Thr Ser Asn Lys Val Leu Asp
                85                  90                  95

Tyr Asp Thr Ser His Ile Tyr Thr Gly His Ile Tyr Gly Glu Glu Gly
            100                 105                 110

Ser Phe Ser His Gly Ser Val Ile Asp Gly Arg Phe Glu Gly Phe Ile
        115                 120                 125

Gln Thr Arg Gly Gly Thr Phe Tyr Val Glu Pro Ala Glu Arg Tyr Ile
    130                 135                 140

Lys Asp Arg Thr Leu Pro Phe His Ser Val Ile Tyr His Glu Asp Asp
145                 150                 155                 160

Ile Asn Tyr Pro His Lys Tyr Gly Pro Gln Gly Gly Cys Ala Asp His
                165                 170                 175

Ser Val Phe Glu Arg Met Arg Lys Tyr Gln Met Thr Gly Val Glu Glu
            180                 185                 190

Val Thr Gln Ile Pro Gln Glu Glu His Ala Ala Asn Gly Pro Glu Leu
        195                 200                 205

Leu Arg Lys Lys Arg Thr Thr Ser Ala Glu Lys Asn Thr Cys Gln Leu
    210                 215                 220

Tyr Ile Gln Thr Asp His Leu Phe Phe Lys Tyr Tyr Gly Thr Arg Glu
225                 230                 235                 240

Ala Val Ile Ala Gln Ile Ser Ser His Val Lys Ala Ile Asp Thr Ile
                245                 250                 255

Tyr Gln Thr Thr Asp Phe Ser Gly Ile Arg Asn Ile Ser Phe Met Val
```

```
            260                 265                 270

Lys Arg Ile Arg Ile Asn Thr Thr Ala Asp Glu Lys Asp Pro Thr Asn
        275                 280                 285

Pro Phe Arg Phe Pro Asn Ile Gly Val Glu Lys Phe Leu Glu Leu Asn
    290                 295                 300

Ser Glu Gln Asn His Asp Asp Tyr Cys Leu Ala Tyr Val Phe Thr Asp
305                 310                 315                 320

Arg Asp Phe Asp Asp Gly Val Leu Gly Leu Ala Trp Val Gly Ala Pro
                325                 330                 335

Ser Gly Ser Ser Gly Gly Ile Cys Glu Lys Ser Lys Leu Tyr Ser Asp
            340                 345                 350

Gly Lys Lys Lys Ser Leu Asn Thr Gly Ile Ile Thr Val Gln Asn Tyr
        355                 360                 365

Gly Ser His Val Pro Pro Lys Val Ser His Ile Thr Phe Ala His Glu
    370                 375                 380

Val Gly His Asn Phe Gly Ser Pro His Asp Ser Gly Thr Glu Cys Thr
385                 390                 395                 400

Pro Gly Glu Ser Lys Asn Leu Gly Gln Lys Glu Asn Gly Asn Tyr Ile
                405                 410                 415

Met Tyr Ala Arg Ala Thr Ser Gly Asp Lys Leu Asn Asn Asn Lys Phe
            420                 425                 430

Ser Leu Cys Ser Ile Arg Asn Ile Ser Gln Val Leu Glu Lys Lys Arg
        435                 440                 445

Asn Asn Cys Phe Val Glu Ser Gly Gln Pro Ile Cys Gly Asn Gly Met
    450                 455                 460

Val Glu Gln Gly Glu Glu Cys Asp Cys Gly Tyr Ser Asp Gln Cys Lys
465                 470                 475                 480

Asp Glu Cys Cys Phe Asp Ala Asn Gln Pro Glu Gly Arg Lys Cys Lys
                485                 490                 495
```

```
Leu Lys Pro Gly Lys Gln Cys Ser Pro Ser Gln Gly Pro Cys Cys Thr
            500                 505                 510

Ala Gln Cys Ala Phe Lys Ser Lys Ser Glu Lys Cys Arg Asp Asp Ser
        515                 520                 525

Asp Cys Ala Arg Glu Gly Ile Cys Asn Gly Phe Thr Ala Leu Cys Pro
    530                 535                 540

Ala Ser Asp Pro Lys Pro Asn Phe Thr Asp Cys Asn Arg His Thr Gln
545                 550                 555                 560

Val Cys Ile Asn Gly Gln Cys Ala Gly Ser Ile Cys Glu Lys Tyr Gly
                565                 570                 575

Leu Glu Glu Cys Thr Cys Ala Ser Ser Asp Gly Lys Asp Asp Lys Glu
            580                 585                 590

Leu Cys His Val Cys Cys Met Lys Lys Met Asp Pro Ser Thr Cys Ala
        595                 600                 605

Ser Thr Gly Ser Val Gln Trp Ser Arg His Phe Ser Gly Arg Thr Ile
    610                 615                 620

Thr Leu Gln Pro Gly Ser Pro Cys Asn Asp Phe Arg Gly Tyr Cys Asp
625                 630                 635                 640

Val Phe Met Arg Cys Arg Leu Val Asp Ala Asp Gly Pro Leu Ala Arg
                645                 650                 655

Leu Lys Lys Ala Ile Phe Ser Pro Glu Leu Tyr Glu Asn Ile Ala Glu
            660                 665                 670

Trp Ile Val Ala His Trp Trp Ala Val Leu Leu Met Gly Ile Ala Leu
        675                 680                 685

Ile Met Leu Met Ala Gly Phe Ile Lys Ile Cys Ser Val His Thr Pro
    690                 695                 700

Ser Ser Asn Pro Lys Leu Pro Pro Pro Lys Pro Leu Pro Gly Thr Leu
705                 710                 715                 720
```

```
Lys Arg Arg Arg Pro Pro Gln Pro Ile Gln Gln Pro Gln Arg Gln Arg
                725                 730                 735


Pro Arg Glu Ser Tyr Gln Met Gly His Met Arg Arg
            740                 745


<210> 2130
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000386056"

<400> 2130
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1               5                   10                  15


Met Gly Asp Arg Asp Phe Asp Asp Gly Val Leu Gly Leu Ala Trp Val
            20                  25                  30


Gly Ala Pro Ser Gly Ser Ser Gly Gly Ile Cys Glu Lys Ser Lys Leu
        35                  40                  45


Tyr Ser Asp Val Pro Thr Met Gly Lys Leu His Ser Lys Glu Lys Pro
    50                  55                  60


Ile Lys Ser Ser Ser Pro Asn
65                  70


<210> 2131
<211> 125
<212> PRT
<213> Homo sapiens
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<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
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<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391930"

<400> 2131
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1 5 10 15

Met Gly Gly Gln Tyr Gly Asn Pro Leu Asn Lys Tyr Ile Arg His Tyr
20 25 30

Glu Gly Leu Ser Tyr Asn Val Asp Ser Leu His Gln Lys His Gln Arg
35 40 45

Ala Lys Arg Ala Val Ser His Glu Asp Gln Phe Leu Arg Leu Asp Phe
50 55 60

His Ala His Gly Arg His Phe Asn Leu Arg Met Lys Arg Asp Thr Ser
65 70 75 80

Leu Phe Ser Asp Glu Phe Lys Val Glu Thr Ser Asn Lys Val Leu Asp
85 90 95

Tyr Asp Thr Ser His Ile Tyr Thr Gly His Ile Tyr Asp Tyr Pro His
100 105 110

Lys Tyr Gly Pro Gln Gly Gly Cys Ala Asp His Ser Val
115 120 125

<210> 2132
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452639"

<400> 2132
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1 5 10 15

Met Gly Val Pro Thr Met Gly Lys Leu His Ser Lys Glu Lys Pro Ile
20 25 30

Lys Ser Ser Ser Pro Asn
35

<210> 2133
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452704"

<400> 2133
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1 5 10 15

Met Gly Gly Gln Tyr Gly Asn Pro Leu Asn Lys Tyr Ile Arg His Tyr
20 25 30

Glu Gly Leu Ser Tyr Asn Val Asp Ser Leu His Gln Lys His Gln Arg
35 40 45

Ala Lys Arg Ala Val Ser His Glu Asp Gln Phe Leu Arg Leu Asp Phe
50 55 60

His Ala His Gly Arg Asp Gly Val Leu Pro Cys Cys Pro Gly Trp Ser
65 70 75 80

Gln Thr Pro Gly Leu Lys Arg Ser Thr Cys Leu Ser Leu Pro Gln Cys
85 90 95

Trp Asp Tyr Arg Cys Glu Pro Ser Pro Met Ile Ser Val Phe Asp Tyr
100 105 110

Pro His Lys
115

<210> 2134
<211> 148
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453952"

<400> 2134
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1 5 10 15

Met Gly Asp Arg Asp Phe Asp Asp Gly Val Leu Gly Leu Ala Trp Val
20 25 30

```
Gly Ala Pro Ser Gly Ser Ser Gly Gly Ile Cys Glu Lys Ser Lys Leu
        35                  40                  45

Tyr Ser Asp Gly Lys Lys Lys Ser Leu Asn Thr Gly Ile Ile Thr Val
    50                  55                  60

Gln Asn Tyr Gly Ser His Val Pro Pro Lys Val Ser His Ile Thr Phe
65                  70                  75                  80

Ala His Glu Val Gly His Asn Phe Gly Ser Pro His Asp Ser Gly Thr
                85                  90                  95

Glu Cys Thr Pro Gly Glu Ser Lys Asn Leu Gly Gln Lys Glu Asn Gly
            100                 105                 110

Asn Tyr Ile Met Tyr Ala Arg Ala Thr Ser Gly Asp Lys Leu Asn Asn
        115                 120                 125

Asn Lys Phe Ser Leu Cys Ser Ile Arg Asn Ile Ser Gln Val Leu Glu
    130                 135                 140

Lys Lys Arg Asn
145


<210> 2135
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456542"


<220>
<221> MOD_RES
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<222> (1)..(1)
<223> Any amino acid

<400> 2135
Xaa Glu Glu Gly Ser Phe Ser His Gly Ser Val Ile Asp Gly Arg Phe
1   5   10   15

Glu Gly Phe Ile Gln Thr Arg Gly Gly Thr Phe Tyr Val Glu Pro Ala
            20   25   30

Glu Arg Tyr Ile Lys Asp Arg Thr Leu Pro Phe His Ser Val Ile Tyr
        35   40   45

His Glu Asp Asp Ile Ser Glu Gly Leu Asn
    50   55

<210> 2136
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 536; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM10; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481779"

<400> 2136
Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1   5   10   15

Met Gly Ala Pro Ala Arg Trp Arg Ile Pro Lys Ser Ser Pro Pro Pro
            20   25   30

Arg Pro Ala Ala Gln Thr Arg Gly Lys Leu Cys Cys Leu Gln Leu Gly
        35   40   45

Ser Cys Ile Val Leu Tyr Pro Ala Arg Arg Ser
    50   55

<210> 2137
<211> 769
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 537; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM11; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 11; "

<220>
<221> source
<223> /note="Uniprot ID: O75078; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000200557"

<400> 2137
Met Arg Leu Leu Arg Arg Trp Ala Phe Ala Ala Leu Leu Leu Ser Leu
1   5   10   15

Leu Pro Thr Pro Gly Leu Gly Thr Gln Gly Pro Ala Gly Ala Leu Arg
            20   25   30

Trp Gly Gly Leu Pro Gln Leu Gly Gly Pro Gly Ala Pro Glu Val Thr
        35   40   45

Glu Pro Ser Arg Leu Val Arg Glu Ser Ser Gly Gly Glu Val Arg Lys
    50   55   60

Gln Gln Leu Asp Thr Arg Val Arg Gln Glu Pro Pro Gly Gly Pro Pro
65   70   75   80

Val His Leu Ala Gln Val Ser Phe Val Ile Pro Ala Phe Asn Ser Asn
                85   90   95

Phe Thr Leu Asp Leu Glu Leu Asn His His Leu Leu Ser Ser Gln Tyr
            100   105   110

```
Val Glu Arg His Phe Ser Arg Glu Gly Thr Thr Gln His Ser Thr Gly
        115                 120                 125

Ala Gly Asp His Cys Tyr Tyr Gln Gly Lys Leu Arg Gly Asn Pro His
    130                 135                 140

Ser Phe Ala Ala Leu Ser Thr Cys Gln Gly Leu His Gly Val Phe Ser
145                 150                 155                 160

Asp Gly Asn Leu Thr Tyr Ile Val Glu Pro Gln Glu Val Ala Gly Pro
                165                 170                 175

Trp Gly Ala Pro Gln Gly Pro Leu Pro His Leu Ile Tyr Arg Thr Pro
            180                 185                 190

Leu Leu Pro Asp Pro Leu Gly Cys Arg Glu Pro Gly Cys Leu Phe Ala
        195                 200                 205

Val Pro Ala Gln Ser Ala Pro Pro Asn Arg Pro Arg Leu Arg Arg Lys
    210                 215                 220

Arg Gln Val Arg Arg Gly His Pro Thr Val His Ser Glu Thr Lys Tyr
225                 230                 235                 240

Val Glu Leu Ile Val Ile Asn Asp His Gln Leu Phe Glu Gln Met Arg
                245                 250                 255

Gln Ser Val Val Leu Thr Ser Asn Phe Ala Lys Ser Val Val Asn Leu
            260                 265                 270

Ala Asp Val Ile Tyr Lys Glu Gln Leu Asn Thr Arg Ile Val Leu Val
        275                 280                 285

Ala Met Glu Thr Trp Ala Asp Gly Asp Lys Ile Gln Val Gln Asp Asp
    290                 295                 300

Leu Leu Glu Thr Leu Ala Arg Leu Met Val Tyr Arg Arg Glu Gly Leu
305                 310                 315                 320

Pro Glu Pro Ser Asp Ala Thr His Leu Phe Ser Gly Arg Thr Phe Gln
                325                 330                 335

Ser Thr Ser Ser Gly Ala Ala Tyr Val Gly Gly Ile Cys Ser Leu Ser
```

```
            340                 345                 350

His Gly Gly Gly Val Asn Glu Tyr Gly Asn Met Gly Ala Met Ala Val
        355                 360                 365

Thr Leu Ala Gln Thr Leu Gly Gln Asn Leu Gly Met Met Trp Asn Lys
    370                 375                 380

His Arg Ser Ser Ala Gly Asp Cys Lys Cys Pro Asp Ile Trp Leu Gly
385                 390                 395                 400

Cys Ile Met Glu Asp Thr Gly Phe Tyr Leu Pro Arg Lys Phe Ser Arg
                405                 410                 415

Cys Ser Ile Asp Glu Tyr Asn Gln Phe Leu Gln Glu Gly Gly Gly Ser
            420                 425                 430

Cys Leu Phe Asn Lys Pro Leu Lys Leu Leu Asp Pro Pro Glu Cys Gly
        435                 440                 445

Asn Gly Phe Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Ser Val Gln
    450                 455                 460

Glu Cys Ser Arg Ala Gly Gly Asn Cys Cys Lys Lys Cys Thr Leu Thr
465                 470                 475                 480

His Asp Ala Met Cys Ser Asp Gly Leu Cys Cys Arg Arg Cys Lys Tyr
                485                 490                 495

Glu Pro Arg Gly Val Ser Cys Arg Glu Ala Val Asn Glu Cys Asp Ile
            500                 505                 510

Ala Glu Thr Cys Thr Gly Asp Ser Ser Gln Cys Pro Pro Asn Leu His
        515                 520                 525

Lys Leu Asp Gly Tyr Tyr Cys Asp His Glu Gln Gly Arg Cys Tyr Gly
    530                 535                 540

Gly Arg Cys Lys Thr Arg Asp Arg Gln Cys Gln Val Leu Trp Gly His
545                 550                 555                 560

Ala Ala Ala Asp Arg Phe Cys Tyr Glu Lys Leu Asn Val Glu Gly Thr
                565                 570                 575
```

Glu Arg Gly Ser Cys Gly Arg Lys Gly Ser Gly Trp Val Gln Cys Ser
580 585 590

Lys Gln Asp Val Leu Cys Gly Phe Leu Leu Cys Val Asn Ile Ser Gly
595 600 605

Ala Pro Arg Leu Gly Asp Leu Val Gly Asp Ile Ser Ser Val Thr Phe
610 615 620

Tyr His Gln Gly Lys Glu Leu Asp Cys Arg Gly Gly His Val Gln Leu
625 630 635 640

Ala Asp Gly Ser Asp Leu Ser Tyr Val Glu Asp Gly Thr Ala Cys Gly
645 650 655

Pro Asn Met Leu Cys Leu Asp His Arg Cys Leu Pro Ala Ser Ala Phe
660 665 670

Asn Phe Ser Thr Cys Pro Gly Ser Gly Glu Arg Arg Ile Cys Ser His
675 680 685

His Gly Val Cys Ser Asn Glu Gly Lys Cys Ile Cys Gln Pro Asp Trp
690 695 700

Thr Gly Lys Asp Cys Ser Ile His Asn Pro Leu Pro Thr Ser Pro Pro
705 710 715 720

Thr Gly Glu Thr Glu Arg Tyr Lys Gly Pro Ser Gly Thr Asn Ile Ile
725 730 735

Ile Gly Ser Ile Ala Gly Ala Val Leu Val Ala Ala Ile Val Leu Gly
740 745 750

Gly Thr Gly Trp Gly Phe Lys Asn Ile Arg Arg Gly Arg Ser Gly Gly
755 760 765

Ala

<210> 2138
<211> 241
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 537; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM11; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000347856"

<400> 2138

```
Met Arg Leu Leu Arg Arg Trp Ala Phe Ala Ala Leu Leu Leu Ser Leu
1               5                  10                  15

Leu Pro Thr Pro Gly Leu Gly Thr Gln Gly Pro Ala Gly Ala Leu Arg
            20                  25                  30

Trp Gly Gly Leu Pro Gln Leu Gly Gly Pro Gly Ala Pro Glu Val Thr
        35                  40                  45

Glu Pro Ser Arg Leu Val Arg Glu Ser Ser Gly Gly Glu Val Arg Lys
    50                  55                  60

Gln Gln Leu Asp Thr Arg Val Arg Gln Glu Pro Pro Gly Gly Pro Pro
65                  70                  75                  80

Val His Leu Ala Gln Val Ser Phe Val Ile Pro Ala Phe Asn Ser Asn
                85                  90                  95

Phe Thr Leu Asp Leu Glu Leu Asn His His Leu Leu Ser Ser Gln Tyr
            100                 105                 110

Val Glu Arg His Phe Ser Arg Glu Gly Thr Thr Gln His Ser Thr Gly
        115                 120                 125

Ala Gly Asp His Cys Tyr Tyr Gln Gly Lys Leu Arg Gly Asn Pro His
    130                 135                 140

Ser Phe Ala Ala Leu Ser Thr Cys Gln Gly Leu His Gly Val Phe Ser
```

```
145                 150                 155                 160

Asp Gly Asn Leu Thr Tyr Ile Val Glu Pro Gln Glu Val Ala Gly Pro
                165                 170                 175

Trp Gly Ala Pro Gln Gly Pro Leu Pro His Leu Ile Tyr Arg Thr Pro
            180                 185                 190

Leu Leu Pro Asp Pro Leu Gly Cys Arg Glu Pro Gly Cys Leu Phe Ala
        195                 200                 205

Val Pro Ala Gln Ser Ala Pro Pro Asn Arg Pro Arg Leu Arg Arg Lys
    210                 215                 220

Arg Ser Ala Gly Ala Thr Leu Gln Cys Thr Val Lys Pro Ser Met Trp
225                 230                 235                 240

Ser
```

<210> 2139
<211> 569
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 537; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM11; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000443773"

<400> 2139

```
Met Gln Gly Thr Arg Leu Pro Val Cys Cys Ala Cys Pro Val Gly Ser
1               5                   10                  15

Ser Lys Pro Ala Glu Ala Glu Lys Glu Lys Val Arg Arg Gly His Pro
            20                  25                  30
```

```
Thr Val His Ser Glu Thr Lys Tyr Val Glu Leu Ile Val Ile Asn Asp
        35                  40                  45

His Gln Leu Phe Glu Gln Met Arg Gln Ser Val Val Leu Thr Ser Asn
    50                  55                  60

Phe Ala Lys Ser Val Val Asn Leu Ala Asp Val Ile Tyr Lys Glu Gln
65                  70                  75                  80

Leu Asn Thr Arg Ile Val Leu Val Ala Met Glu Thr Trp Ala Asp Gly
                85                  90                  95

Asp Lys Ile Gln Val Gln Asp Asp Leu Leu Glu Thr Leu Ala Arg Leu
            100                 105                 110

Met Val Tyr Arg Arg Glu Gly Leu Pro Glu Pro Ser Asp Ala Thr His
        115                 120                 125

Leu Phe Ser Gly Arg Thr Phe Gln Ser Thr Ser Ser Gly Ala Ala Tyr
    130                 135                 140

Val Gly Gly Ile Cys Ser Leu Ser His Gly Gly Gly Val Asn Glu Tyr
145                 150                 155                 160

Gly Asn Met Gly Ala Met Ala Val Thr Leu Ala Gln Thr Leu Gly Gln
                165                 170                 175

Asn Leu Gly Met Met Trp Asn Lys His Arg Ser Ser Ala Gly Asp Cys
            180                 185                 190

Lys Cys Pro Asp Ile Trp Leu Gly Cys Ile Met Glu Asp Thr Gly Phe
        195                 200                 205

Tyr Leu Pro Arg Lys Phe Ser Arg Cys Ser Ile Asp Glu Tyr Asn Gln
    210                 215                 220

Phe Leu Gln Glu Gly Gly Gly Ser Cys Leu Phe Asn Lys Pro Leu Lys
225                 230                 235                 240

Leu Leu Asp Pro Pro Glu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu
                245                 250                 255
```

```
Glu Cys Asp Cys Gly Ser Val Gln Glu Cys Ser Arg Ala Gly Gly Asn
            260                 265                 270

Cys Cys Lys Lys Cys Thr Leu Thr His Asp Ala Met Cys Ser Asp Gly
        275                 280                 285

Leu Cys Cys Arg Arg Cys Lys Tyr Glu Pro Arg Gly Val Ser Cys Arg
    290                 295                 300

Glu Ala Val Asn Glu Cys Asp Ile Ala Glu Thr Cys Thr Gly Asp Ser
305                 310                 315                 320

Ser Gln Cys Pro Pro Asn Leu His Lys Leu Asp Gly Tyr Tyr Cys Asp
                325                 330                 335

His Glu Gln Gly Arg Cys Tyr Gly Gly Arg Cys Lys Thr Arg Asp Arg
            340                 345                 350

Gln Cys Gln Val Leu Trp Gly His Ala Ala Ala Asp Arg Phe Cys Tyr
        355                 360                 365

Glu Lys Leu Asn Val Glu Gly Thr Glu Arg Gly Ser Cys Gly Arg Lys
    370                 375                 380

Gly Ser Gly Trp Val Gln Cys Ser Lys Gln Asp Val Leu Cys Gly Phe
385                 390                 395                 400

Leu Leu Cys Val Asn Ile Ser Gly Ala Pro Arg Leu Gly Asp Leu Val
                405                 410                 415

Gly Asp Ile Ser Ser Val Thr Phe Tyr His Gln Gly Lys Glu Leu Asp
            420                 425                 430

Cys Arg Gly Gly His Val Gln Leu Ala Asp Gly Ser Asp Leu Ser Tyr
        435                 440                 445

Val Glu Asp Gly Thr Ala Cys Gly Pro Asn Met Leu Cys Leu Asp His
    450                 455                 460

Arg Cys Leu Pro Ala Ser Ala Phe Asn Phe Ser Thr Cys Pro Gly Ser
465                 470                 475                 480

Gly Glu Arg Arg Ile Cys Ser His His Gly Val Cys Ser Asn Glu Gly
```

485 490 495

Lys Cys Ile Cys Gln Pro Asp Trp Thr Gly Lys Asp Cys Ser Ile His
500 505 510

Asn Pro Leu Pro Thr Ser Pro Pro Thr Gly Glu Thr Glu Arg Tyr Lys
515 520 525

Gly Pro Ser Gly Thr Asn Ile Ile Ile Gly Ser Ile Ala Gly Ala Val
530 535 540

Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe Lys Asn
545 550 555 560

Ile Arg Arg Gly Arg Ser Gly Gly Ala
565

<210> 2140
<211> 517
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 537; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM11; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465537"

<400> 2140
Leu Leu Ser Ser Gln Tyr Val Glu Arg His Phe Ser Arg Glu Gly Thr
1 5 10 15

Thr Gln His Ser Thr Gly Ala Gly Asp His Cys Tyr Tyr Gln Gly Lys
20 25 30

Leu Arg Gly Asn Pro His Ser Phe Ala Ala Leu Ser Thr Cys Gln Gly
35 40 45

```
Leu His Gly Val Phe Ser Asp Gly Asn Leu Thr Tyr Ile Val Glu Pro
    50                  55                  60

Gln Glu Val Ala Gly Pro Trp Gly Ala Pro Gln Gly Pro Leu Pro His
65                  70                  75                  80

Leu Ile Tyr Arg Thr Pro Leu Leu Pro Asp Pro Leu Gly Cys Arg Glu
                85                  90                  95

Pro Gly Cys Leu Phe Ala Val Pro Ala Gln Ser Ala Pro Pro Asn Arg
            100                 105                 110

Pro Arg Leu Arg Arg Lys Arg Gln Val Arg Arg Gly His Pro Thr Val
        115                 120                 125

His Ser Glu Thr Lys Tyr Val Glu Leu Ile Val Ile Asn Asp His Gln
    130                 135                 140

Leu Phe Glu Gln Met Arg Gln Ser Val Val Leu Thr Ser Asn Phe Ala
145                 150                 155                 160

Lys Ser Val Val Asn Leu Ala Asp Val Ile Tyr Lys Glu Gln Leu Asn
                165                 170                 175

Thr Arg Ile Val Leu Val Ala Met Glu Thr Trp Ala Asp Gly Asp Lys
            180                 185                 190

Ile Gln Val Gln Asp Asp Leu Leu Glu Thr Leu Ala Arg Leu Met Val
        195                 200                 205

Tyr Arg Arg Glu Gly Leu Pro Glu Pro Ser Asp Ala Thr His Leu Phe
    210                 215                 220

Ser Gly Arg Thr Phe Gln Ser Thr Ser Ser Gly Ala Ala Tyr Val Gly
225                 230                 235                 240

Gly Ile Cys Ser Leu Ser His Gly Gly Gly Val Asn Glu Tyr Gly Asn
                245                 250                 255

Met Gly Ala Met Ala Val Thr Leu Ala Gln Thr Leu Gly Gln Asn Leu
            260                 265                 270
```

```
Gly Met Met Trp Asn Lys His Arg Ser Ser Ala Gly Asp Cys Lys Cys
        275                 280                 285

Pro Asp Ile Trp Leu Gly Cys Ile Met Glu Asp Thr Gly Phe Tyr Leu
    290                 295                 300

Pro Arg Lys Phe Ser Arg Cys Ser Ile Asp Glu Tyr Asn Gln Phe Leu
305                 310                 315                 320

Gln Glu Gly Gly Gly Ser Cys Leu Phe Asn Lys Pro Leu Lys Leu Leu
                325                 330                 335

Asp Pro Pro Glu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Glu Cys
            340                 345                 350

Asp Cys Gly Ser Val Gln Glu Cys Ser Arg Ala Gly Gly Asn Cys Cys
        355                 360                 365

Lys Lys Cys Thr Leu Thr His Asp Ala Met Cys Ser Asp Gly Leu Cys
    370                 375                 380

Cys Arg Arg Cys Lys Tyr Glu Pro Arg Gly Val Ser Cys Arg Glu Ala
385                 390                 395                 400

Val Asn Glu Cys Asp Ile Ala Glu Thr Cys Thr Gly Asp Ser Ser Gln
                405                 410                 415

Cys Pro Pro Asn Leu His Lys Leu Asp Gly Tyr Tyr Cys Asp His Glu
            420                 425                 430

Gln Gly Arg Cys Tyr Gly Gly Arg Cys Lys Thr Arg Asp Arg Gln Cys
        435                 440                 445

Gln Val Leu Trp Gly His Ala Ala Ala Asp Arg Phe Cys Tyr Glu Lys
    450                 455                 460

Leu Asn Val Glu Gly Thr Glu Arg Gly Ser Cys Gly Arg Lys Gly Ser
465                 470                 475                 480

Gly Trp Val Gln Cys Ser Lys Gln Pro Gln Gln Gly Arg Ala Val Trp
                485                 490                 495

Leu Pro Pro Leu Cys Gln His Leu Trp Ser Ser Ser Ala Arg Gly Pro
```

```
            500                 505                 510

Gly Gly Arg His Gln
        515


<210> 2141
<211> 738
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 538; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM12; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 12; "

<220>
<221> source
<223> /note="Uniprot ID:  O43184; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000357665"

<400> 2141
Met Ala Ala Arg Pro Leu Pro Val Ser Pro Ala Arg Ala Leu Leu Leu
1               5                  10                  15


Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly Val Ser
            20                  25                  30


Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala Ser Val Gly
        35                  40                  45


Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp Ser Lys Asn His
    50                  55                  60


Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile
65                  70                  75                  80


Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu
                85                  90                  95
```

```
Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr
            100                 105                 110

Thr Val Ile Leu Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr
        115                 120                 125

Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu
    130                 135                 140

Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala
145                 150                 155                 160

Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg
                165                 170                 175

Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn
            180                 185                 190

Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu
        195                 200                 205

Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn
    210                 215                 220

Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg
225                 230                 235                 240

Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn
                245                 250                 255

Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys
            260                 265                 270

Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
        275                 280                 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln
    290                 295                 300

Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro
305                 310                 315                 320
```

```
Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp
                325                 330                 335

His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu
            340                 345                 350

Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser
        355                 360                 365

Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr
    370                 375                 380

Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu
385                 390                 395                 400

Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro
                405                 410                 415

Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val
            420                 425                 430

Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn
        435                 440                 445

Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys
    450                 455                 460

Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr
465                 470                 475                 480

Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr
                485                 490                 495

Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His
            500                 505                 510

Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
        515                 520                 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala
    530                 535                 540

Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly
```

545 550 555 560

Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg
565 570 575

Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser Arg Pro
580 585 590

Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln
595 600 605

Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp
610 615 620

Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys Ala Asp
625 630 635 640

Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly
645 650 655

Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys Asn Asn
660 665 670

Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp
675 680 685

Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala
690 695 700

Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly
705 710 715 720

Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr
725 730 735

Leu Ile

<210> 2142
<211> 909
<212> PRT
<213> Homo sapiens

<220>

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<223> /note="Payload ID: 538; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM12; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 12; "

<220>
<221> source
<223> /note="Uniprot ID: O43184; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000357668"

<400> 2142

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Met Ala Ala Arg Pro Leu Pro Val Ser Pro Ala Arg Ala Leu Leu Leu
1               5                   10                  15

Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly Val Ser
            20                  25                  30

Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala Ser Val Gly
        35                  40                  45

Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp Ser Lys Asn His
    50                  55                  60

Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile
65                  70                  75                  80

Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu
                85                  90                  95

Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr
            100                 105                 110

Thr Val Ile Leu Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr
        115                 120                 125

Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu
    130                 135                 140
```

```
Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala
145                 150                 155                 160

Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg
                165                 170                 175

Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn
            180                 185                 190

Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu
        195                 200                 205

Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn
    210                 215                 220

Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg
225                 230                 235                 240

Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn
                245                 250                 255

Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys
            260                 265                 270

Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
        275                 280                 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln
    290                 295                 300

Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro
305                 310                 315                 320

Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp
                325                 330                 335

His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu
            340                 345                 350

Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser
        355                 360                 365

Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr
```

```
    370                 375                 380

Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu
385                 390                 395                 400

Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro
                405                 410                 415

Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val
            420                 425                 430

Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn
        435                 440                 445

Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys
    450                 455                 460

Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr
465                 470                 475                 480

Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr
                485                 490                 495

Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His
            500                 505                 510

Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
        515                 520                 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala
    530                 535                 540

Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly
545                 550                 555                 560

Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg
                565                 570                 575

Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser Arg Pro
            580                 585                 590

Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln
        595                 600                 605
```

```
Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp
    610                 615                 620

Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys Ala Asp
625                 630                 635                 640

Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly
                645                 650                 655

Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys Asn Asn
            660                 665                 670

Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp
        675                 680                 685

Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala
    690                 695                 700

Asp Asn Gln Gly Leu Thr Ile Gly Ile Leu Val Thr Ile Leu Cys Leu
705                 710                 715                 720

Leu Ala Ala Gly Phe Val Val Tyr Leu Lys Arg Lys Thr Leu Ile Arg
                725                 730                 735

Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg Cys Val
            740                 745                 750

Arg Pro Ser Arg Pro Pro Arg Gly Phe Gln Pro Cys Gln Ala His Leu
        755                 760                 765

Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser Tyr Pro
    770                 775                 780

Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val Asp Ile
785                 790                 795                 800

Ser Arg Pro Leu Asn Gly Leu Asn Val Pro Gln Pro Gln Ser Thr Gln
                805                 810                 815

Arg Val Leu Pro Pro Leu His Arg Ala Pro Arg Ala Pro Ser Val Pro
            820                 825                 830
```

```
Ala Arg Pro Leu Pro Ala Lys Pro Ala Leu Arg Gln Ala Gln Gly Thr
        835                 840                 845

Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala
    850                 855                 860

Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp
865                 870                 875                 880

Glu Thr Gly Leu Arg Leu Ala Pro Leu Arg Pro Ala Pro Gln Tyr Pro
                885                 890                 895

His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys
            900                 905


<210> 2143
<211> 278
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 538; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM12; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000391268"

<400> 2143
Met Ala Ala Arg Pro Leu Pro Val Ser Pro Ala Arg Ala Leu Leu Leu
1               5                   10                  15

Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly Val Ser
            20                  25                  30

Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala Ser Val Gly
        35                  40                  45

Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp Ser Lys Asn His
```

50 55 60

Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile
65 70 75 80

Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu
85 90 95

Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr
100 105 110

Thr Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr Ser Asp Ser
115 120 125

Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu Ile Val Phe
130 135 140

Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala Thr Asn Arg
145 150 155 160

Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys
165 170 175

Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro
180 185 190

Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys
195 200 205

Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe
210 215 220

Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu
225 230 235 240

Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg Ile
245 250 255

Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys Ser Val
260 265 270

Ser Gln Asp Pro Phe Thr
275

<210> 2144
<211> 814
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 15; "

<220>
<221> source
<223> /note="Uniprot ID: Q13444; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000271836"

<400> 2144
Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1   5   10   15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20   25   30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35   40   45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50   55   60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65   70   75   80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85   90   95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100   105   110

```
Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115                 120                 125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130                 135                 140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145                 150                 155                 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165                 170                 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180                 185                 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
```

```
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575
```

```
Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
            740                 745                 750

Leu Leu Ala Arg Gly Thr Lys Ser Gln Gly Pro Ala Lys Pro Pro Pro
        755                 760                 765

Pro Arg Lys Pro Leu Pro Ala Asp Pro Gln Gly Arg Cys Pro Ser Gly
    770                 775                 780

Asp Leu Pro Gly Pro Gly Ala Gly Ile Pro Pro Leu Val Val Pro Ser
785                 790                 795                 800
```

```
Arg Pro Ala Pro Pro Pro Pro Thr Val Ser Ser Leu Tyr Leu
                805                 810


<210> 2145
<211> 839
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 15; "

<220>
<221> source
<223> /note="Uniprot ID:  Q13444; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000348227"

<400> 2145
Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1               5                  10                  15


Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20                  25                  30


Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35                  40                  45


Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50                  55                  60


Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65                  70                  75                  80


Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85                  90                  95


Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
```

```
            100                 105                 110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115                 120                 125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130                 135                 140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145                 150                 155                 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165                 170                 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180                 185                 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335
```

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
340 345 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
355 360 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
370 375 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385 390 395 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
405 410 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
420 425 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
435 440 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
450 455 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465 470 475 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
485 490 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
500 505 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
515 520 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
530 535 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545 550 555 560

```
Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
            740                 745                 750

Leu Leu Ala Arg Gly Thr Lys Gln Ala Ser Ala Leu Ser Phe Pro Ala
        755                 760                 765

Pro Pro Ser Arg Pro Leu Pro Pro Asp Pro Val Ser Lys Arg Leu Gln
    770                 775                 780
```

```
Ser Gln Gly Pro Ala Lys Pro Pro Pro Pro Arg Lys Pro Leu Pro Ala
785                 790                 795                 800


Asp Pro Gln Gly Arg Cys Pro Ser Gly Asp Leu Pro Gly Pro Gly Ala
                805                 810                 815


Gly Ile Pro Pro Leu Val Val Pro Ser Arg Pro Ala Pro Pro Pro Pro
            820                 825                 830


Thr Val Ser Ser Leu Tyr Leu
        835


<210> 2146
<211> 863
<212> PRT
<213> Homo sapiens

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<223> /note="Gene Name:
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<223> /note="Uniprot ID:  Q13444; "

<220>
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Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1               5                   10                  15


Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20                  25                  30


Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35                  40                  45


Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50                  55                  60
```

```
Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65                  70                  75                  80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85                  90                  95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100                 105                 110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115                 120                 125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130                 135                 140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145                 150                 155                 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165                 170                 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180                 185                 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285
```

```
Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510
```

```
Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
```

```
            740                 745                 750

Leu Leu Ala Arg Gly Thr Lys Gln Ala Ser Ala Leu Ser Phe Pro Ala
        755                 760                 765

Pro Pro Ser Arg Pro Leu Pro Pro Asp Pro Val Ser Lys Arg Leu Gln
    770                 775                 780

Ala Glu Leu Ala Asp Arg Pro Asn Pro Pro Thr Arg Pro Leu Pro Ala
785                 790                 795                 800

Asp Pro Val Val Arg Ser Pro Lys Ser Gln Gly Pro Ala Lys Pro Pro
                805                 810                 815

Pro Pro Arg Lys Pro Leu Pro Ala Asp Pro Gln Gly Arg Cys Pro Ser
            820                 825                 830

Gly Asp Leu Pro Gly Pro Gly Ala Gly Ile Pro Pro Leu Val Val Pro
        835                 840                 845

Ser Arg Pro Ala Pro Pro Pro Pro Thr Val Ser Ser Leu Tyr Leu
    850                 855                 860


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<400> 2147
Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1 5 10 15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
20 25 30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
35 40 45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
50 55 60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65 70 75 80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
85 90 95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
100 105 110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
115 120 125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
130 135 140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145 150 155 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
165 170 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
180 185 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
195 200 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
210 215 220

```
Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
```

```
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685
```

```
Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
            740                 745                 750

Leu Leu Ala Arg Gly Thr Lys Ala Glu Leu Ala Asp Arg Pro Asn Pro
        755                 760                 765

Pro Thr Arg Pro Leu Pro Ala Asp Pro Val Val Arg Ser Pro Lys Ser
    770                 775                 780

Gln Gly Pro Ala Lys Pro Pro Pro Pro Arg Lys Pro Leu Pro Ala Asp
785                 790                 795                 800

Pro Gln Gly Arg Cys Pro Ser Gly Asp Leu Pro Gly Pro Gly Ala Gly
                805                 810                 815

Ile Pro Pro Leu Val Val Pro Ser Arg Pro Ala Pro Pro Pro Pro Thr
            820                 825                 830

Val Ser Ser Leu Tyr Leu
        835


<210> 2148
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<400> 2148

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Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1               5                  10                  15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20                  25                  30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35                  40                  45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50                  55                  60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65                  70                  75                  80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85                  90                  95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100                 105                 110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115                 120                 125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130                 135                 140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145                 150                 155                 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165                 170                 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
```

```
            180                 185                 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415
```

```
Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640
```

```
Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Ser
                725                 730                 735

Leu Arg Gly Gln Pro Ser Pro His Pro Gln Gly Ser His Cys Leu Pro
            740                 745                 750

Thr Pro Arg Ala Gly Ala His Arg Val Thr Cys Pro Ala Gln Gly Leu
        755                 760                 765

Glu Ser Arg Pro
    770


<210> 2149
<211> 796
<212> PRT
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<223> /note="Uniprot ID: Q13444; "

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Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20   25   30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35   40   45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50   55   60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65   70   75   80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85   90   95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100   105   110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115   120   125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130   135   140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145   150   155   160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165   170   175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180   185   190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195   200   205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
210 215 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225 230 235 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
245 250 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
260 265 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
275 280 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
290 295 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305 310 315 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
325 330 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
340 345 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
355 360 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
370 375 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385 390 395 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
405 410 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
420 425 430

```
Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655
```

```
Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Leu Val Leu Ser Ala Ser Arg Pro Pro Leu Pro Gly Arg Cys Arg Leu
            740                 745                 750

Thr Leu Cys Pro Arg Asp Ser Ser Leu Arg Gly Gln Pro Ser Pro His
        755                 760                 765

Pro Gln Gly Ser His Cys Leu Pro Thr Pro Arg Ala Gly Ala His Arg
    770                 775                 780

Val Thr Cys Pro Ala Gln Gly Leu Glu Ser Arg Pro
785                 790                 795


<210> 2150
<211> 520
<212> PRT
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<220>
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Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1 5 10 15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
20 25 30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
35 40 45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
50 55 60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65 70 75 80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Leu Asn Phe
85 90 95

Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys Ala Leu Leu Asp Gly Met
100 105 110

Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser Leu Pro Pro Met Ala Ala
115 120 125

Phe Cys Gly Asn Met Phe Val Glu Pro Gly Glu Gln Cys Asp Cys Gly
130 135 140

Phe Leu Asp Asp Cys Val Asp Pro Cys Cys Asp Ser Leu Thr Cys Gln
145 150 155 160

Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp Gly Pro Cys Cys Gln Asn
165 170 175

Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys Arg Pro Thr Arg Gly Asp
180 185 190

Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp Ser Ser Gln Cys Pro Pro
195 200 205

```
Asp Val Ser Leu Gly Asp Gly Glu Pro Cys Ala Gly Gly Gln Ala Val
    210                 215                 220

Cys Met His Gly Arg Cys Ala Ser Tyr Ala Gln Gln Cys Gln Ser Leu
225                 230                 235                 240

Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro Leu Cys Leu Gln Thr Ala
                245                 250                 255

Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys Gly Arg Asn Pro Ser Gly
            260                 265                 270

Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala Ile Cys Gly Gln Leu Gln
        275                 280                 285

Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu Gly Ser Ile Arg Asp Leu
    290                 295                 300

Leu Trp Glu Thr Ile Asp Val Asn Gly Thr Glu Leu Asn Cys Ser Trp
305                 310                 315                 320

Val His Leu Asp Leu Gly Ser Asp Val Ala Gln Pro Leu Leu Thr Leu
                325                 330                 335

Pro Gly Thr Ala Cys Gly Pro Gly Leu Val Cys Ile Asp His Arg Cys
            340                 345                 350

Gln Arg Val Asp Leu Leu Gly Ala Gln Glu Cys Arg Ser Lys Cys His
        355                 360                 365

Gly His Gly Val Cys Asp Ser Asn Arg His Cys Tyr Cys Glu Glu Gly
    370                 375                 380

Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu Lys Ala Thr Ser Ser Leu
385                 390                 395                 400

Thr Thr Gly Leu Leu Leu Ser Leu Leu Val Leu Leu Val Leu Val Met
                405                 410                 415

Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg Leu His Gln Arg Leu Cys
            420                 425                 430
```

```
Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg Ala Ala Gln Ser Gly Pro
        435                 440                 445

Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala Leu Leu Ala Arg Gly Thr
    450                 455                 460

Lys Ser Gln Gly Pro Ala Lys Pro Pro Pro Pro Arg Lys Pro Leu Pro
465                 470                 475                 480

Ala Asp Pro Gln Gly Arg Cys Pro Ser Gly Asp Leu Pro Gly Pro Gly
                485                 490                 495

Ala Gly Ile Pro Pro Leu Val Val Pro Ser Arg Pro Ala Pro Pro Pro
            500                 505                 510

Pro Thr Val Ser Ser Leu Tyr Leu
        515                 520


<210> 2151
<211> 862
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 539; "

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<223> /note="Gene Name:
      ADAM metallopeptidase domain 15; "

<220>
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<223> /note="Uniprot ID:  Q13444; "

<220>
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<400> 2151
Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1               5                   10                  15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20                  25                  30
```

```
Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35                  40                  45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50                  55                  60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65                  70                  75                  80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85                  90                  95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100                 105                 110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115                 120                 125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130                 135                 140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145                 150                 155                 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165                 170                 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180                 185                 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255
```

```
Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480
```

```
Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
```

705 710 715 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
725 730 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
740 745 750

Leu Leu Ala Arg Gly Thr Lys Ala Ser Ala Leu Ser Phe Pro Ala Pro
755 760 765

Pro Ser Arg Pro Leu Pro Pro Asp Pro Val Ser Lys Arg Leu Gln Ala
770 775 780

Glu Leu Ala Asp Arg Pro Asn Pro Pro Thr Arg Pro Leu Pro Ala Asp
785 790 795 800

Pro Val Val Arg Ser Pro Lys Ser Gln Gly Pro Ala Lys Pro Pro Pro
805 810 815

Pro Arg Lys Pro Leu Pro Ala Asp Pro Gln Gly Arg Cys Pro Ser Gly
820 825 830

Asp Leu Pro Gly Pro Gly Ala Gly Ile Pro Pro Leu Val Val Pro Ser
835 840 845

Arg Pro Ala Pro Pro Pro Pro Thr Val Ser Ser Leu Tyr Leu
850 855 860

<210> 2152
<211> 822
<212> PRT
<213> Homo sapiens

<220>
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<221> source
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<223> /note="Gene Name:
ADAM metallopeptidase domain 15; "

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<223> /note="Uniprot ID: Q13444; "

<220>
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<223> /note="ENSP ID: ENSP00000432347"

<400> 2152
Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1   5   10   15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20   25   30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35   40   45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50   55   60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65   70   75   80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85   90   95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100   105   110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115   120   125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130   135   140

Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145   150   155   160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165   170   175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180   185   190

```
Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
```

```
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655
```

```
Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
            740                 745                 750

Leu Leu Ala Arg Gly Thr Lys Gln Ala Ser Ala Leu Ser Phe Pro Ala
        755                 760                 765

Pro Pro Ser Arg Pro Leu Pro Pro Asp Pro Val Ser Lys Arg Leu Gln
    770                 775                 780

Ala Glu Leu Ala Asp Arg Pro Asn Pro Pro Thr Arg Pro Leu Pro Ala
785                 790                 795                 800

Asp Pro Val Val Arg Ser Pro Lys Val Thr Val Gly Gly Glu Lys Gly
                805                 810                 815

Thr Ala Ser Pro Pro Thr
            820


<210> 2153
<211> 824
<212> PRT
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<223> /note="Gene Name:
ADAM metallopeptidase domain 15; "

<220>
<221> source
<223> /note="Uniprot ID: Q13444; "

<220>
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<223> /note="ENSP ID: ENSP00000432927"

<400> 2153

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Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1               5                  10                  15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Val Leu Ser Trp Gly Val
            20                  25                  30

Leu Gly Pro Ala Gly Gly Thr Glu Glu Gln Gln Ala Glu Ser Glu Lys
        35                  40                  45

Ala Pro Arg Glu Pro Leu Glu Pro Gln Val Leu Gln Asp Asp Leu Pro
    50                  55                  60

Ile Ser Leu Lys Lys Val Leu Gln Thr Ser Leu Pro Glu Pro Leu Arg
65                  70                  75                  80

Ile Lys Leu Glu Leu Asp Gly Asp Ser His Ile Leu Glu Leu Leu Gln
                85                  90                  95

Asn Arg Glu Leu Val Pro Gly Arg Pro Thr Leu Val Trp Tyr Gln Pro
            100                 105                 110

Asp Gly Thr Arg Val Val Ser Glu Gly His Thr Leu Glu Asn Cys Cys
        115                 120                 125

Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly Ser Trp Val Ser Ile Cys
    130                 135                 140

Thr Cys Ser Gly Leu Arg Gly Leu Val Val Leu Thr Pro Glu Arg Ser
145                 150                 155                 160

Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu Gln Gly Pro Pro Ile Ile
```

```
                165                 170                 175

Ser Arg Ile Gln Asp Leu His Leu Pro Gly His Thr Cys Ala Leu Ser
            180                 185                 190

Trp Arg Glu Ser Val His Thr Gln Lys Pro Pro Glu His Pro Leu Gly
        195                 200                 205

Gln Arg His Ile Arg Arg Arg Arg Asp Val Val Thr Glu Thr Lys Thr
    210                 215                 220

Val Glu Leu Val Ile Val Ala Asp His Ser Glu Ala Gln Lys Tyr Arg
225                 230                 235                 240

Asp Phe Gln His Leu Leu Asn Arg Thr Leu Glu Val Ala Leu Leu Leu
                245                 250                 255

Asp Thr Phe Phe Arg Pro Leu Asn Val Arg Val Ala Leu Val Gly Leu
            260                 265                 270

Glu Ala Trp Thr Gln Arg Asp Leu Val Glu Ile Ser Pro Asn Pro Ala
        275                 280                 285

Val Thr Leu Glu Asn Phe Leu His Trp Arg Arg Ala His Leu Leu Pro
    290                 295                 300

Arg Leu Pro His Asp Ser Ala Gln Leu Val Thr Gly Thr Ser Phe Ser
305                 310                 315                 320

Gly Pro Thr Val Gly Met Ala Ile Gln Asn Ser Ile Cys Ser Pro Asp
                325                 330                 335

Phe Ser Gly Gly Val Asn Met Asp His Ser Thr Ser Ile Leu Gly Val
            340                 345                 350

Ala Ser Ser Ile Ala His Glu Leu Gly His Ser Leu Gly Leu Asp His
        355                 360                 365

Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro Gly Pro Ala Pro Ala Lys
    370                 375                 380

Thr Cys Ile Met Glu Ala Ser Thr Asp Phe Leu Pro Gly Leu Asn Phe
385                 390                 395                 400
```

```
Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys Ala Leu Leu Asp Gly Met
                405                 410                 415

Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser Leu Pro Pro Met Ala Ala
            420                 425                 430

Phe Cys Gly Asn Met Phe Val Glu Pro Gly Glu Gln Cys Asp Cys Gly
        435                 440                 445

Phe Leu Asp Asp Cys Val Asp Pro Cys Cys Asp Ser Leu Thr Cys Gln
    450                 455                 460

Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp Gly Pro Cys Cys Gln Asn
465                 470                 475                 480

Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys Arg Pro Thr Arg Gly Asp
                485                 490                 495

Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp Ser Ser Gln Cys Pro Pro
            500                 505                 510

Asp Val Ser Leu Gly Asp Gly Glu Pro Cys Ala Gly Gly Gln Ala Val
        515                 520                 525

Cys Met His Gly Arg Cys Ala Ser Tyr Ala Gln Gln Cys Gln Ser Leu
    530                 535                 540

Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro Leu Cys Leu Gln Thr Ala
545                 550                 555                 560

Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys Gly Arg Asn Pro Ser Gly
                565                 570                 575

Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala Ile Cys Gly Gln Leu Gln
            580                 585                 590

Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu Gly Ser Ile Arg Asp Leu
        595                 600                 605

Leu Trp Glu Thr Ile Asp Val Asn Gly Thr Glu Leu Asn Cys Ser Trp
    610                 615                 620
```

```
Val His Leu Asp Leu Gly Ser Asp Val Ala Gln Pro Leu Leu Thr Leu
625                 630                 635                 640

Pro Gly Thr Ala Cys Gly Pro Gly Leu Val Cys Ile Asp His Arg Cys
                645                 650                 655

Gln Arg Val Asp Leu Leu Gly Ala Gln Glu Cys Arg Ser Lys Cys His
            660                 665                 670

Gly His Gly Val Cys Asp Ser Asn Arg His Cys Tyr Cys Glu Glu Gly
        675                 680                 685

Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu Lys Ala Thr Ser Ser Leu
    690                 695                 700

Thr Thr Gly Leu Leu Leu Ser Leu Leu Val Leu Leu Val Leu Val Met
705                 710                 715                 720

Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg Leu His Gln Arg Leu Cys
                725                 730                 735

Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg Ala Ala Gln Ser Gly Pro
            740                 745                 750

Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala Leu Leu Ala Arg Gly Thr
        755                 760                 765

Lys Ser Gln Gly Pro Ala Lys Pro Pro Pro Pro Arg Lys Pro Leu Pro
    770                 775                 780

Ala Asp Pro Gln Gly Arg Cys Pro Ser Gly Asp Leu Pro Gly Pro Gly
785                 790                 795                 800

Ala Gly Ile Pro Pro Leu Val Val Pro Ser Arg Pro Ala Pro Pro Pro
                805                 810                 815

Pro Thr Val Ser Ser Leu Tyr Leu
            820
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<210> 2154
<211> 797
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 15; "

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<221> source
<223> /note="Uniprot ID: Q13444; "

<220>
<221> source
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Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1   5   10   15

Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Gly Gly Thr Glu Glu Gln
            20   25   30

Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln Val
        35   40   45

Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr Ser
    50   55   60

Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser His
65   70   75   80

Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro Thr
                85   90   95

Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
            100   105   110

Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
        115   120   125

Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
    130   135   140

```
Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
145                 150                 155                 160

Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
                165                 170                 175

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
            180                 185                 190

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
        195                 200                 205

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
    210                 215                 220

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
225                 230                 235                 240

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
                245                 250                 255

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
            260                 265                 270

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
        275                 280                 285

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
    290                 295                 300

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
305                 310                 315                 320

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
                325                 330                 335

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
            340                 345                 350

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
        355                 360                 365
```

```
Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
    370                 375                 380

Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
385                 390                 395                 400

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
                405                 410                 415

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
            420                 425                 430

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
        435                 440                 445

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
    450                 455                 460

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
465                 470                 475                 480

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
                485                 490                 495

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
            500                 505                 510

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
        515                 520                 525

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
    530                 535                 540

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
545                 550                 555                 560

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
                565                 570                 575

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
            580                 585                 590
```

```
Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
        595                 600                 605

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
    610                 615                 620

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
625                 630                 635                 640

Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln Glu
                645                 650                 655

Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg His
            660                 665                 670

Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln Leu
        675                 680                 685

Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu Val
    690                 695                 700

Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala Arg
705                 710                 715                 720

Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr Arg
                725                 730                 735

Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg Ala
            740                 745                 750

Leu Leu Ala Arg Gly Thr Lys Ala Glu Leu Ala Asp Arg Pro Asn Pro
        755                 760                 765

Pro Thr Arg Pro Leu Pro Ala Asp Pro Val Val Arg Ser Pro Lys Val
    770                 775                 780

Thr Val Gly Gly Glu Lys Gly Thr Ala Ser Pro Pro Thr
785                 790                 795
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<210> 2155
<211> 633
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 15; "

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<220>
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<400> 2155

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Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
1               5                   10                  15


Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Val Ser Ala Cys Asn Val
            20                  25                  30


Glu Ala Pro Gln Val Ala Leu Arg Ser Ser Arg Gln Ser Gln Arg Arg
        35                  40                  45


Pro Arg Gly Ser Pro Trp Ser Pro Arg Ser Phe Arg Thr Ile Ser Gln
    50                  55                  60


Leu Ala Ser Lys Arg Cys Phe Arg Glu Leu Val Pro Gly Arg Pro Thr
65                  70                  75                  80


Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly His
                85                  90                  95


Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala Gly
            100                 105                 110


Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val Val
        115                 120                 125


Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp Leu
    130                 135                 140
```

```
Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro Gly
145                 150                 155                 160

His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Lys Pro
                165                 170                 175

Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Arg Asp Val
            180                 185                 190

Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His Ser
        195                 200                 205

Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr Leu
    210                 215                 220

Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val Arg
225                 230                 235                 240

Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val Glu
                245                 250                 255

Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp Arg
            260                 265                 270

Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu Val
        275                 280                 285

Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln Asn
    290                 295                 300

Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His Ser
305                 310                 315                 320

Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly His
                325                 330                 335

Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys Pro
            340                 345                 350

Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp Phe
        355                 360                 365
```

```
Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu Lys
    370                 375                 380

Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro Ser
385                 390                 395                 400

Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro Gly
                405                 410                 415

Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys Cys
            420                 425                 430

Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser Asp
        435                 440                 445

Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln Cys
    450                 455                 460

Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly Asp
465                 470                 475                 480

Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro Cys
                485                 490                 495

Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr Ala
            500                 505                 510

Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala Pro
        515                 520                 525

Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser Cys
    530                 535                 540

Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp Ala
545                 550                 555                 560

Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu Leu
                565                 570                 575

Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly Thr
            580                 585                 590

Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val Ala
```

595 600 605

Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu Val
610 615 620

Ser Ser Leu Gly Gly Gln Asp Gln Val
625 630

<210> 2156
<211> 824
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 540; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 17; "

<220>
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<223> /note="Uniprot ID: P78536; "

<220>
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<400> 2156
Met Arg Gln Ser Leu Leu Phe Leu Thr Ser Val Val Pro Phe Val Leu
1 5 10 15

Ala Pro Arg Pro Pro Asp Asp Pro Gly Phe Gly Pro His Gln Arg Leu
20 25 30

Glu Lys Leu Asp Ser Leu Leu Ser Asp Tyr Asp Ile Leu Ser Leu Ser
35 40 45

Asn Ile Gln Gln His Ser Val Arg Lys Arg Asp Leu Gln Thr Ser Thr
50 55 60

His Val Glu Thr Leu Leu Thr Phe Ser Ala Leu Lys Arg His Phe Lys
65 70 75 80

```
Leu Tyr Leu Thr Ser Ser Thr Glu Arg Phe Ser Gln Asn Phe Lys Val
                85                  90                  95

Val Val Val Asp Gly Lys Asn Glu Ser Glu Tyr Thr Val Lys Trp Gln
            100                 105                 110

Asp Phe Phe Thr Gly His Val Val Gly Glu Pro Asp Ser Arg Val Leu
        115                 120                 125

Ala His Ile Arg Asp Asp Asp Val Ile Ile Arg Ile Asn Thr Asp Gly
    130                 135                 140

Ala Glu Tyr Asn Ile Glu Pro Leu Trp Arg Phe Val Asn Asp Thr Lys
145                 150                 155                 160

Asp Lys Arg Met Leu Val Tyr Lys Ser Glu Asp Ile Lys Asn Val Ser
                165                 170                 175

Arg Leu Gln Ser Pro Lys Val Cys Gly Tyr Leu Lys Val Asp Asn Glu
            180                 185                 190

Glu Leu Leu Pro Lys Gly Leu Val Asp Arg Glu Pro Pro Glu Glu Leu
        195                 200                 205

Val His Arg Val Lys Arg Arg Ala Asp Pro Asp Pro Met Lys Asn Thr
    210                 215                 220

Cys Lys Leu Leu Val Val Ala Asp His Arg Phe Tyr Arg Tyr Met Gly
225                 230                 235                 240

Arg Gly Glu Glu Ser Thr Thr Thr Asn Tyr Leu Ile Glu Leu Ile Asp
                245                 250                 255

Arg Val Asp Asp Ile Tyr Arg Asn Thr Ser Trp Asp Asn Ala Gly Phe
            260                 265                 270

Lys Gly Tyr Gly Ile Gln Ile Glu Gln Ile Arg Ile Leu Lys Ser Pro
        275                 280                 285

Gln Glu Val Lys Pro Gly Glu Lys His Tyr Asn Met Ala Lys Ser Tyr
    290                 295                 300
```

```
Pro Asn Glu Glu Lys Asp Ala Trp Asp Val Lys Met Leu Leu Glu Gln
305                 310                 315                 320

Phe Ser Phe Asp Ile Ala Glu Glu Ala Ser Lys Val Cys Leu Ala His
                325                 330                 335

Leu Phe Thr Tyr Gln Asp Phe Asp Met Gly Thr Leu Gly Leu Ala Tyr
            340                 345                 350

Val Gly Ser Pro Arg Ala Asn Ser His Gly Gly Val Cys Pro Lys Ala
        355                 360                 365

Tyr Tyr Ser Pro Val Gly Lys Lys Asn Ile Tyr Leu Asn Ser Gly Leu
    370                 375                 380

Thr Ser Thr Lys Asn Tyr Gly Lys Thr Ile Leu Thr Lys Glu Ala Asp
385                 390                 395                 400

Leu Val Thr Thr His Glu Leu Gly His Asn Phe Gly Ala Glu His Asp
                405                 410                 415

Pro Asp Gly Leu Ala Glu Cys Ala Pro Asn Glu Asp Gln Gly Gly Lys
            420                 425                 430

Tyr Val Met Tyr Pro Ile Ala Val Ser Gly Asp His Glu Asn Asn Lys
        435                 440                 445

Met Phe Ser Asn Cys Ser Lys Gln Ser Ile Tyr Lys Thr Ile Glu Ser
    450                 455                 460

Lys Ala Gln Glu Cys Phe Gln Glu Arg Ser Asn Lys Val Cys Gly Asn
465                 470                 475                 480

Ser Arg Val Asp Glu Gly Glu Glu Cys Asp Pro Gly Ile Met Tyr Leu
                485                 490                 495

Asn Asn Asp Thr Cys Cys Asn Ser Asp Cys Thr Leu Lys Glu Gly Val
            500                 505                 510

Gln Cys Ser Asp Arg Asn Ser Pro Cys Cys Lys Asn Cys Gln Phe Glu
        515                 520                 525

Thr Ala Gln Lys Lys Cys Gln Glu Ala Ile Asn Ala Thr Cys Lys Gly
```

530 535 540

Val Ser Tyr Cys Thr Gly Asn Ser Ser Glu Cys Pro Pro Pro Gly Asn
545 550 555 560

Ala Glu Asp Asp Thr Val Cys Leu Asp Leu Gly Lys Cys Lys Asp Gly
565 570 575

Lys Cys Ile Pro Phe Cys Glu Arg Glu Gln Gln Leu Glu Ser Cys Ala
580 585 590

Cys Asn Glu Thr Asp Asn Ser Cys Lys Val Cys Cys Arg Asp Leu Ser
595 600 605

Gly Arg Cys Val Pro Tyr Val Asp Ala Glu Gln Lys Asn Leu Phe Leu
610 615 620

Arg Lys Gly Lys Pro Cys Thr Val Gly Phe Cys Asp Met Asn Gly Lys
625 630 635 640

Cys Glu Lys Arg Val Gln Asp Val Ile Glu Arg Phe Trp Asp Phe Ile
645 650 655

Asp Gln Leu Ser Ile Asn Thr Phe Gly Lys Phe Leu Ala Asp Asn Ile
660 665 670

Val Gly Ser Val Leu Val Phe Ser Leu Ile Phe Trp Ile Pro Phe Ser
675 680 685

Ile Leu Val His Cys Val Asp Lys Lys Leu Asp Lys Gln Tyr Glu Ser
690 695 700

Leu Ser Leu Phe His Pro Ser Asn Val Glu Met Leu Ser Ser Met Asp
705 710 715 720

Ser Ala Ser Val Arg Ile Ile Lys Pro Phe Pro Ala Pro Gln Thr Pro
725 730 735

Gly Arg Leu Gln Pro Ala Pro Val Ile Pro Ser Ala Pro Ala Ala Pro
740 745 750

Lys Leu Asp His Gln Arg Met Asp Thr Ile Gln Glu Asp Pro Ser Thr
755 760 765

```
Asp Ser His Met Asp Glu Asp Gly Phe Glu Lys Asp Pro Phe Pro Asn
    770                 775                 780

Ser Ser Thr Ala Ala Lys Ser Phe Glu Asp Leu Thr Asp His Pro Val
785                 790                 795                 800

Thr Arg Ser Glu Lys Ala Ala Ser Phe Lys Leu Gln Arg Gln Asn Arg
                805                 810                 815

Val Asp Ser Lys Glu Thr Glu Cys
            820


<210> 2157
<211> 285
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 540; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM17; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 17; "

<220>
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<223> /note="ENSP ID: ENSP00000418728"

<400> 2157
Met Arg Gln Ser Leu Leu Phe Leu Thr Ser Val Val Pro Phe Val Leu
1               5                   10                  15

Ala Pro Arg Pro Pro Asp Asp Pro Gly Phe Gly Pro His Gln Arg Leu
            20                  25                  30

Glu Lys Leu Asp Ser Leu Leu Ser Asp Tyr Asp Ile Leu Ser Leu Ser
        35                  40                  45

Asn Ile Gln Gln His Ser Val Arg Lys Arg Asp Leu Gln Thr Ser Thr
    50                  55                  60
```

His Val Glu Thr Leu Leu Thr Phe Ser Ala Leu Lys Arg His Phe Lys
65 70 75 80

Leu Tyr Leu Thr Ser Ser Thr Glu Arg Phe Ser Gln Asn Phe Lys Val
85 90 95

Val Val Val Asp Gly Lys Asn Glu Ser Glu Tyr Thr Val Lys Trp Gln
100 105 110

Asp Phe Phe Thr Gly His Val Val Gly Glu Pro Asp Ser Arg Val Leu
115 120 125

Ala His Ile Arg Asp Asp Asp Val Ile Ile Arg Ile Asn Thr Asp Gly
130 135 140

Ala Glu Tyr Asn Ile Glu Pro Leu Trp Arg Phe Val Asn Asp Thr Lys
145 150 155 160

Asp Lys Arg Met Leu Val Tyr Lys Ser Glu Asp Ile Lys Asn Val Ser
165 170 175

Arg Leu Gln Ser Pro Lys Val Cys Gly Tyr Leu Lys Val Asp Asn Glu
180 185 190

Glu Leu Leu Pro Lys Gly Leu Val Asp Arg Glu Pro Pro Glu Glu Leu
195 200 205

Val His Arg Val Lys Arg Arg Ala Asp Pro Asp Pro Met Lys Asn Thr
210 215 220

Cys Lys Leu Leu Val Val Ala Asp His Arg Phe Tyr Arg Tyr Met Gly
225 230 235 240

Arg Gly Glu Glu Ser Thr Thr Thr Asn Tyr Leu Ile Glu Leu Ile Asp
245 250 255

Arg Val Asp Asp Ile Tyr Arg Asn Thr Ser Trp Asp Asn Ala Gly Phe
260 265 270

Lys Gly Tyr Gly Ile Gln Ile Glu Gln Leu Leu Phe Glu
275 280 285

<210> 2158

<211> 258
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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ADAM metallopeptidase domain 17; "

<220>
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<400> 2158

Met	Arg	Gln	Ser	Leu	Leu	Phe	Leu	Thr	Ser	Val	Val	Pro	Phe	Val	Leu
1				5					10					15	
Ala	Pro	Arg	Pro	Pro	Asp	Asp	Pro	Gly	Phe	Gly	Pro	His	Gln	Arg	Leu
			20					25					30		
Glu	Lys	Leu	Asp	Ser	Leu	Leu	Ser	Asp	Tyr	Asp	Ile	Leu	Ser	Leu	Ser
		35					40					45			
Asn	Ile	Gln	Gln	His	Ser	Val	Arg	Lys	Arg	Asp	Leu	Gln	Thr	Ser	Thr
	50					55					60				
His	Val	Glu	Thr	Leu	Leu	Thr	Phe	Ser	Ala	Leu	Lys	Arg	His	Phe	Lys
65					70					75					80
Leu	Tyr	Leu	Thr	Ser	Ser	Thr	Glu	Arg	Phe	Ser	Gln	Asn	Phe	Lys	Val
				85					90					95	
Val	Val	Val	Asp	Gly	Lys	Asn	Glu	Ser	Glu	Tyr	Thr	Val	Lys	Trp	Gln
			100					105					110		
Asp	Phe	Phe	Thr	Gly	His	Val	Val	Gly	Glu	Pro	Asp	Ser	Arg	Val	Leu
		115					120					125			
Ala	His	Ile	Arg	Asp	Asp	Asp	Val	Ile	Ile	Arg	Ile	Asn	Thr	Asp	Gly
	130					135					140				

```
Ala Glu Tyr Asn Ile Glu Pro Leu Trp Arg Phe Val Asn Asp Thr Lys
145                 150                 155                 160

Asp Lys Arg Met Leu Val Tyr Lys Ser Glu Asp Ile Lys Asn Val Ser
                165                 170                 175

Arg Leu Gln Ser Pro Lys Val Cys Gly Tyr Leu Lys Val Asp Asn Glu
            180                 185                 190

Glu Leu Leu Pro Lys Gly Leu Val Asp Arg Glu Pro Pro Glu Glu Leu
        195                 200                 205

Val His Arg Val Lys Arg Arg Ala Asp Pro Asp Pro Met Lys Asn Thr
    210                 215                 220

Cys Lys Leu Leu Val Val Ala Asp His Arg Phe Tyr Arg Tyr Met Gly
225                 230                 235                 240

Arg Gly Glu Glu Ser Thr Thr Thr Asn Tyr Leu Ile His Thr Asp Arg
                245                 250                 255

Ala Asn
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<210> 2159
<211> 739
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 541; "

<220>
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<223> /note="Gene Symbol: ADAM18; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 18; "

<220>
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<223> /note="Uniprot ID: Q9Y3Q7; "

<220>
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<223> /note="ENSP ID: ENSP00000265707"

<400> 2159

```
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1               5                  10                  15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20                  25                  30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
        35                  40                  45

Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
    50                  55                  60

Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65                  70                  75                  80

Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
            100                 105                 110

Gly Leu Arg Gly Phe Leu Gln Phe Glu Asn Ile Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Val Glu Ser Ser Ala Arg Phe Glu His Ile Ile Tyr Gln Met Lys
    130                 135                 140

Asn Asn Asp Pro Asn Val Ser Ile Leu Ala Val Asn Tyr Ser His Ile
145                 150                 155                 160

Trp Gln Lys Asp Gln Pro Tyr Lys Val Pro Leu Asn Ser Gln Ile Lys
                165                 170                 175

Asn Leu Ser Lys Leu Leu Pro Gln Tyr Leu Glu Ile Tyr Ile Ile Val
            180                 185                 190

Glu Lys Ala Leu Tyr Asp Tyr Met Gly Ser Glu Met Met Ala Val Thr
        195                 200                 205

Gln Lys Ile Val Gln Val Ile Gly Leu Val Asn Thr Met Phe Thr Gln
    210                 215                 220
```

```
Phe Lys Leu Thr Val Ile Leu Ser Ser Leu Glu Leu Trp Ser Asn Glu
225                 230                 235                 240

Asn Gln Ile Ser Thr Ser Gly Asp Ala Asp Asp Ile Leu Gln Arg Phe
                245                 250                 255

Leu Ala Trp Lys Arg Asp Tyr Leu Ile Leu Arg Pro His Asp Ile Ala
            260                 265                 270

Tyr Leu Leu Val Tyr Arg Lys His Pro Lys Tyr Val Gly Ala Thr Phe
        275                 280                 285

Pro Gly Thr Val Cys Asn Lys Ser Tyr Asp Ala Gly Ile Ala Met Tyr
    290                 295                 300

Pro Asp Ala Ile Gly Leu Glu Gly Phe Ser Val Ile Ile Ala Gln Leu
305                 310                 315                 320

Leu Gly Leu Asn Val Gly Leu Thr Tyr Asp Asp Ile Thr Gln Cys Phe
                325                 330                 335

Cys Leu Arg Ala Thr Cys Ile Met Asn His Glu Ala Val Ser Ala Ser
            340                 345                 350

Gly Arg Lys Ile Phe Ser Asn Cys Ser Met His Asp Tyr Arg Tyr Phe
        355                 360                 365

Val Ser Lys Phe Glu Thr Lys Cys Leu Gln Lys Leu Ser Asn Leu Gln
    370                 375                 380

Pro Leu His Gln Asn Gln Pro Val Cys Gly Asn Gly Ile Leu Glu Ser
385                 390                 395                 400

Asn Glu Glu Cys Asp Cys Gly Asn Lys Asn Glu Cys Gln Phe Lys Lys
                405                 410                 415

Cys Cys Asp Tyr Asn Thr Cys Lys Leu Lys Gly Ser Val Lys Cys Gly
            420                 425                 430

Ser Gly Pro Cys Cys Thr Ser Lys Cys Glu Leu Ser Ile Ala Gly Thr
        435                 440                 445
```

```
Pro Cys Arg Lys Ser Ile Asp Pro Glu Cys Asp Phe Thr Glu Tyr Cys
    450                 455                 460

Asn Gly Thr Ser Ser Asn Cys Val Pro Asp Thr Tyr Ala Leu Asn Gly
465                 470                 475                 480

Arg Leu Cys Lys Leu Gly Thr Ala Tyr Cys Tyr Asn Gly Gln Cys Gln
                485                 490                 495

Thr Thr Asp Asn Gln Cys Ala Lys Ile Phe Gly Lys Gly Ala Gln Gly
            500                 505                 510

Ala Pro Phe Ala Cys Phe Lys Glu Val Asn Ser Leu His Glu Arg Ser
        515                 520                 525

Glu Asn Cys Gly Phe Lys Asn Ser Gln Pro Leu Pro Cys Glu Arg Lys
    530                 535                 540

Asp Val Leu Cys Gly Lys Leu Ala Cys Val Gln Pro His Lys Asn Ala
545                 550                 555                 560

Asn Lys Ser Asp Ala Gln Ser Thr Val Tyr Ser Tyr Ile Gln Asp His
                565                 570                 575

Val Cys Val Ser Ile Ala Thr Gly Ser Ser Met Arg Ser Asp Gly Thr
            580                 585                 590

Asp Asn Ala Tyr Val Ala Asp Gly Thr Met Cys Gly Pro Glu Met Tyr
        595                 600                 605

Cys Val Asn Lys Thr Cys Arg Lys Val His Leu Met Gly Tyr Asn Cys
    610                 615                 620

Asn Ala Thr Thr Lys Cys Lys Gly Lys Gly Ile Cys Asn Asn Phe Gly
625                 630                 635                 640

Asn Cys Gln Cys Phe Pro Gly His Arg Pro Pro Asp Cys Lys Phe Gln
                645                 650                 655

Phe Gly Ser Pro Gly Gly Ser Ile Asp Asp Gly Asn Phe Gln Lys Ser
            660                 665                 670
```

```
Gly Asp Phe Tyr Thr Glu Lys Gly Tyr Asn Thr His Trp Asn Asn Trp
        675                 680                 685

Phe Ile Leu Ser Phe Cys Ile Phe Leu Pro Phe Phe Ile Val Phe Thr
    690                 695                 700

Thr Val Ile Phe Lys Arg Asn Glu Ile Ser Lys Ser Cys Asn Arg Glu
705                 710                 715                 720

Asn Ala Glu Tyr Asn Arg Asn Ser Ser Val Val Ser Glu Ser Asp Asp
                725                 730                 735

Val Gly His
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<210> 2160
<211> 715
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 541; "

<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 18; "

<220>
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<223> /note="Uniprot ID: Q9Y3Q7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369195"

<400> 2160

```
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1               5                   10                  15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20                  25                  30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
        35                  40                  45
```

```
Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
    50                  55                  60

Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65                  70                  75                  80

Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
            100                 105                 110

Gly Leu Arg Gly Phe Leu Gln Phe Glu Asn Ile Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Val Glu Ser Ser Ala Arg Phe Glu His Ile Ile Tyr Gln Met Lys
    130                 135                 140

Asn Asn Asp Pro Asn Val Ser Ile Leu Ala Val Asn Tyr Ser His Ile
145                 150                 155                 160

Trp Gln Lys Asp Gln Pro Tyr Lys Val Pro Leu Asn Ser Gln Ile Lys
                165                 170                 175

Asn Leu Ser Lys Leu Leu Pro Gln Tyr Leu Glu Ile Tyr Ile Ile Val
            180                 185                 190

Glu Lys Ala Leu Met Phe Thr Gln Phe Lys Leu Thr Val Ile Leu Ser
        195                 200                 205

Ser Leu Glu Leu Trp Ser Asn Glu Asn Gln Ile Ser Thr Ser Gly Asp
    210                 215                 220

Ala Asp Asp Ile Leu Gln Arg Phe Leu Ala Trp Lys Arg Asp Tyr Leu
225                 230                 235                 240

Ile Leu Arg Pro His Asp Ile Ala Tyr Leu Leu Val Tyr Arg Lys His
                245                 250                 255

Pro Lys Tyr Val Gly Ala Thr Phe Pro Gly Thr Val Cys Asn Lys Ser
            260                 265                 270
```

```
Tyr Asp Ala Gly Ile Ala Met Tyr Pro Asp Ala Ile Gly Leu Glu Gly
        275                 280                 285

Phe Ser Val Ile Ile Ala Gln Leu Leu Gly Leu Asn Val Gly Leu Thr
    290                 295                 300

Tyr Asp Asp Ile Thr Gln Cys Phe Cys Leu Arg Ala Thr Cys Ile Met
305                 310                 315                 320

Asn His Glu Ala Val Ser Ala Ser Gly Arg Lys Ile Phe Ser Asn Cys
                325                 330                 335

Ser Met His Asp Tyr Arg Tyr Phe Val Ser Lys Phe Glu Thr Lys Cys
            340                 345                 350

Leu Gln Lys Leu Ser Asn Leu Gln Pro Leu His Gln Asn Gln Pro Val
        355                 360                 365

Cys Gly Asn Gly Ile Leu Glu Ser Asn Glu Glu Cys Asp Cys Gly Asn
    370                 375                 380

Lys Asn Glu Cys Gln Phe Lys Lys Cys Cys Asp Tyr Asn Thr Cys Lys
385                 390                 395                 400

Leu Lys Gly Ser Val Lys Cys Gly Ser Gly Pro Cys Cys Thr Ser Lys
                405                 410                 415

Cys Glu Leu Ser Ile Ala Gly Thr Pro Cys Arg Lys Ser Ile Asp Pro
            420                 425                 430

Glu Cys Asp Phe Thr Glu Tyr Cys Asn Gly Thr Ser Ser Asn Cys Val
        435                 440                 445

Pro Asp Thr Tyr Ala Leu Asn Gly Arg Leu Cys Lys Leu Gly Thr Ala
    450                 455                 460

Tyr Cys Tyr Asn Gly Gln Cys Gln Thr Thr Asp Asn Gln Cys Ala Lys
465                 470                 475                 480

Ile Phe Gly Lys Gly Ala Gln Gly Ala Pro Phe Ala Cys Phe Lys Glu
                485                 490                 495
```

```
Val Asn Ser Leu His Glu Arg Ser Glu Asn Cys Gly Phe Lys Asn Ser
            500                 505                 510

Gln Pro Leu Pro Cys Glu Arg Lys Asp Val Leu Cys Gly Lys Leu Ala
        515                 520                 525

Cys Val Gln Pro His Lys Asn Ala Asn Lys Ser Asp Ala Gln Ser Thr
    530                 535                 540

Val Tyr Ser Tyr Ile Gln Asp His Val Cys Val Ser Ile Ala Thr Gly
545                 550                 555                 560

Ser Ser Met Arg Ser Asp Gly Thr Asp Asn Ala Tyr Val Ala Asp Gly
                565                 570                 575

Thr Met Cys Gly Pro Glu Met Tyr Cys Val Asn Lys Thr Cys Arg Lys
            580                 585                 590

Val His Leu Met Gly Tyr Asn Cys Asn Ala Thr Thr Lys Cys Lys Gly
        595                 600                 605

Lys Gly Ile Cys Asn Asn Phe Gly Asn Cys Gln Cys Phe Pro Gly His
    610                 615                 620

Arg Pro Pro Asp Cys Lys Phe Gln Phe Gly Ser Pro Gly Gly Ser Ile
625                 630                 635                 640

Asp Asp Gly Asn Phe Gln Lys Ser Gly Asp Phe Tyr Thr Glu Lys Gly
                645                 650                 655

Tyr Asn Thr His Trp Asn Asn Trp Phe Ile Leu Ser Phe Cys Ile Phe
            660                 665                 670

Leu Pro Phe Phe Ile Val Phe Thr Thr Val Ile Phe Lys Arg Asn Glu
        675                 680                 685

Ile Ser Lys Ser Cys Asn Arg Glu Asn Ala Glu Tyr Asn Arg Asn Ser
    690                 695                 700

Ser Val Val Ser Glu Ser Asp Asp Val Gly His
705                 710                 715
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<210> 2161

<211> 115
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428083"

<400> 2161

Met	Phe	Leu	Leu	Leu	Ala	Leu	Leu	Thr	Glu	Leu	Gly	Arg	Leu	Gln	Ala
1				5				10					15		
His	Glu	Gly	Ser	Glu	Gly	Ile	Phe	Leu	His	Val	Thr	Val	Pro	Arg	Lys
			20					25					30		
Ile	Lys	Ser	Asn	Asp	Ser	Glu	Val	Ser	Glu	Arg	Lys	Met	Ile	Tyr	Ile
		35					40					45			
Ile	Thr	Ile	Asp	Gly	Gln	Pro	Tyr	Thr	Leu	His	Leu	Gly	Lys	Gln	Ser
	50					55					60				
Phe	Leu	Pro	Gln	Asn	Phe	Leu	Val	Tyr	Thr	Tyr	Asn	Glu	Thr	Gly	Ser
65					70					75					80
Leu	His	Ser	Val	Ser	Pro	Tyr	Phe	Met	Met	His	Cys	His	Tyr	Gln	Gly
				85					90					95	
Tyr	Ala	Ala	Glu	Phe	Pro	Asn	Ser	Phe	Val	Thr	Leu	Ser	Ile	Cys	Ser
			100					105					110		
Gly	Leu	Arg													
		115													

<210> 2162
<211> 62
<212> PRT

<213> Homo sapiens

<220>
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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000429335"

<400> 2162
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1 5 10 15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
20 25 30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Val Phe Gly Glu
35 40 45

Gln Val Val Phe Gly Tyr Met Asn Asp Leu His His Tyr Asn
50 55 60

<210> 2163
<211> 182
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000429908"

<400> 2163
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1   5   10   15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20   25   30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
        35   40   45

Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
    50   55   60

Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65   70   75   80

Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
                85   90   95

Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
            100   105   110

Gly Leu Arg Gly Phe Leu Gln Phe Glu Asn Ile Ser Tyr Gly Ile Glu
        115   120   125

Pro Val Glu Ser Ser Ala Arg Phe Glu His Ile Ile Tyr Gln Met Lys
    130   135   140

Asn Asn Asp Pro Asn Val Ser Ile Leu Ala Val Asn Tyr Ser His Ile
145   150   155   160

Trp Gln Lys Asp Gln Pro Tyr Lys Val Pro Leu Asn Ser Gln Val Thr
                165   170   175

Val Ile Ile Leu Met Leu
            180

<210> 2164
<211> 739
<212> PRT

<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID: Q9Y3Q7; "

<220>
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<223> /note="ENSP ID: ENSP00000482348"

<400> 2164

```
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1               5                   10                  15


His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20                  25                  30


Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
        35                  40                  45


Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
    50                  55                  60


Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65                  70                  75                  80


Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
                85                  90                  95


Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
            100                 105                 110


Gly Leu Arg Gly Phe Leu Gln Phe Glu Asn Ile Ser Tyr Gly Ile Glu
        115                 120                 125


Pro Val Glu Ser Ser Ala Arg Phe Glu His Ile Ile Tyr Gln Met Lys
```

```
    130                 135                 140

Asn Asn Asp Pro Asn Val Ser Ile Leu Ala Val Asn Tyr Ser His Ile
145                 150                 155                 160

Trp Gln Lys Asp Gln Pro Tyr Lys Val Pro Leu Asn Ser Gln Ile Lys
                165                 170                 175

Asn Leu Ser Lys Leu Leu Pro Gln Tyr Leu Glu Ile Tyr Ile Ile Val
            180                 185                 190

Glu Lys Ala Leu Tyr Asp Tyr Met Gly Ser Glu Met Met Ala Val Thr
        195                 200                 205

Gln Lys Ile Val Gln Val Ile Gly Leu Val Asn Thr Met Phe Thr Gln
    210                 215                 220

Phe Lys Leu Thr Val Ile Leu Ser Ser Leu Glu Leu Trp Ser Asn Glu
225                 230                 235                 240

Asn Gln Ile Ser Thr Ser Gly Asp Ala Asp Asp Ile Leu Gln Arg Phe
                245                 250                 255

Leu Ala Trp Lys Arg Asp Tyr Leu Ile Leu Arg Pro His Asp Ile Ala
            260                 265                 270

Tyr Leu Leu Val Tyr Arg Lys His Pro Lys Tyr Val Gly Ala Thr Phe
        275                 280                 285

Pro Gly Thr Val Cys Asn Lys Ser Tyr Asp Ala Gly Ile Ala Met Tyr
    290                 295                 300

Pro Asp Ala Ile Gly Leu Glu Gly Phe Ser Val Ile Ile Ala Gln Leu
305                 310                 315                 320

Leu Gly Leu Asn Val Gly Leu Thr Tyr Asp Asp Ile Thr Gln Cys Phe
                325                 330                 335

Cys Leu Arg Ala Thr Cys Ile Met Asn His Glu Ala Val Ser Ala Ser
            340                 345                 350

Gly Arg Lys Ile Phe Ser Asn Cys Ser Met His Asp Tyr Arg Tyr Phe
        355                 360                 365
```

```
Val Ser Lys Phe Glu Thr Lys Cys Leu Gln Lys Leu Ser Asn Leu Gln
    370                 375                 380

Pro Leu His Gln Asn Gln Pro Val Cys Gly Asn Gly Ile Leu Glu Ser
385                 390                 395                 400

Asn Glu Glu Cys Asp Cys Gly Asn Lys Asn Glu Cys Gln Phe Lys Lys
                405                 410                 415

Cys Cys Asp Tyr Asn Thr Cys Lys Leu Lys Gly Ser Val Lys Cys Gly
            420                 425                 430

Ser Gly Pro Cys Cys Thr Ser Lys Cys Glu Leu Ser Ile Ala Gly Thr
        435                 440                 445

Pro Cys Arg Lys Ser Ile Asp Pro Glu Cys Asp Phe Thr Glu Tyr Cys
    450                 455                 460

Asn Gly Thr Ser Ser Asn Cys Val Pro Asp Thr Tyr Ala Leu Asn Gly
465                 470                 475                 480

Arg Leu Cys Lys Leu Gly Thr Ala Tyr Cys Tyr Asn Gly Gln Cys Gln
                485                 490                 495

Thr Thr Asp Asn Gln Cys Ala Lys Ile Phe Gly Lys Gly Ala Gln Gly
            500                 505                 510

Ala Pro Phe Ala Cys Phe Lys Glu Val Asn Ser Leu His Glu Arg Ser
        515                 520                 525

Glu Asn Cys Gly Phe Lys Asn Ser Gln Pro Leu Pro Cys Glu Arg Lys
    530                 535                 540

Asp Val Leu Cys Gly Lys Leu Ala Cys Val Gln Pro His Lys Asn Ala
545                 550                 555                 560

Asn Lys Ser Asp Ala Gln Ser Thr Val Tyr Ser Tyr Ile Gln Asp His
                565                 570                 575

Val Cys Val Ser Ile Ala Thr Gly Ser Ser Met Arg Ser Asp Gly Thr
            580                 585                 590
```

```
Asp Asn Ala Tyr Val Ala Asp Gly Thr Met Cys Gly Pro Glu Met Tyr
        595                 600                 605

Cys Val Asn Lys Thr Cys Arg Lys Val His Leu Met Gly Tyr Asn Cys
    610                 615                 620

Asn Ala Thr Thr Lys Cys Lys Gly Lys Gly Ile Cys Asn Asn Phe Gly
625                 630                 635                 640

Asn Cys Gln Cys Phe Pro Gly His Arg Pro Pro Asp Cys Lys Phe Gln
                645                 650                 655

Phe Gly Ser Pro Gly Gly Ser Ile Asp Asp Gly Asn Phe Gln Lys Ser
            660                 665                 670

Gly Asp Phe Tyr Thr Glu Lys Gly Tyr Asn Thr His Trp Asn Asn Trp
        675                 680                 685

Phe Ile Leu Ser Phe Cys Ile Phe Leu Pro Phe Phe Ile Val Phe Thr
    690                 695                 700

Thr Val Ile Phe Lys Arg Asn Glu Ile Ser Lys Ser Cys Asn Arg Glu
705                 710                 715                 720

Asn Ala Glu Tyr Asn Arg Asn Ser Ser Val Val Ser Glu Ser Asp Asp
                725                 730                 735

Val Gly His
```

<210> 2165
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 541; "

<220>
<221> source
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<220>
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<223> /note="Gene Name:

ADAM metallopeptidase domain 18; "

<220>
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<400> 2165
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1 5 10 15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
20 25 30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
35 40 45

Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
50 55 60

Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65 70 75 80

Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
85 90 95

Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
100 105 110

Gly Leu Arg
115

<210> 2166
<211> 182
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000488128"

<400> 2166
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1   5   10   15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20   25   30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
        35   40   45

Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
    50   55   60

Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65   70   75   80

Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
                85   90   95

Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
            100   105   110

Gly Leu Arg Gly Phe Leu Gln Phe Glu Asn Ile Ser Tyr Gly Ile Glu
        115   120   125

Pro Val Glu Ser Ser Ala Arg Phe Glu His Ile Ile Tyr Gln Met Lys
    130   135   140

Asn Asn Asp Pro Asn Val Ser Ile Leu Ala Val Asn Tyr Ser His Ile
145   150   155   160

Trp Gln Lys Asp Gln Pro Tyr Lys Val Pro Leu Asn Ser Gln Val Thr
                165   170   175

Val Ile Ile Leu Met Leu
            180

<210> 2167
<211> 715
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000488176"

<400> 2167
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1   5   10   15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20   25   30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Met Ile Tyr Ile
        35   40   45

Ile Thr Ile Asp Gly Gln Pro Tyr Thr Leu His Leu Gly Lys Gln Ser
    50   55   60

Phe Leu Pro Gln Asn Phe Leu Val Tyr Thr Tyr Asn Glu Thr Gly Ser
65   70   75   80

Leu His Ser Val Ser Pro Tyr Phe Met Met His Cys His Tyr Gln Gly
                85   90   95

Tyr Ala Ala Glu Phe Pro Asn Ser Phe Val Thr Leu Ser Ile Cys Ser
            100   105   110

Gly Leu Arg Gly Phe Leu Gln Phe Glu Asn Ile Ser Tyr Gly Ile Glu
        115   120   125

```
Pro Val Glu Ser Ser Ala Arg Phe Glu His Ile Ile Tyr Gln Met Lys
    130                 135                 140

Asn Asn Asp Pro Asn Val Ser Ile Leu Ala Val Asn Tyr Ser His Ile
145                 150                 155                 160

Trp Gln Lys Asp Gln Pro Tyr Lys Val Pro Leu Asn Ser Gln Ile Lys
                165                 170                 175

Asn Leu Ser Lys Leu Leu Pro Gln Tyr Leu Glu Ile Tyr Ile Ile Val
            180                 185                 190

Glu Lys Ala Leu Met Phe Thr Gln Phe Lys Leu Thr Val Ile Leu Ser
        195                 200                 205

Ser Leu Glu Leu Trp Ser Asn Glu Asn Gln Ile Ser Thr Ser Gly Asp
    210                 215                 220

Ala Asp Asp Ile Leu Gln Arg Phe Leu Ala Trp Lys Arg Asp Tyr Leu
225                 230                 235                 240

Ile Leu Arg Pro His Asp Ile Ala Tyr Leu Leu Val Tyr Arg Lys His
                245                 250                 255

Pro Lys Tyr Val Gly Ala Thr Phe Pro Gly Thr Val Cys Asn Lys Ser
            260                 265                 270

Tyr Asp Ala Gly Ile Ala Met Tyr Pro Asp Ala Ile Gly Leu Glu Gly
        275                 280                 285

Phe Ser Val Ile Ile Ala Gln Leu Leu Gly Leu Asn Val Gly Leu Thr
    290                 295                 300

Tyr Asp Asp Ile Thr Gln Cys Phe Cys Leu Arg Ala Thr Cys Ile Met
305                 310                 315                 320

Asn His Glu Ala Val Ser Ala Ser Gly Arg Lys Ile Phe Ser Asn Cys
                325                 330                 335

Ser Met His Asp Tyr Arg Tyr Phe Val Ser Lys Phe Glu Thr Lys Cys
            340                 345                 350
```

```
Leu Gln Lys Leu Ser Asn Leu Gln Pro Leu His Gln Asn Gln Pro Val
        355                 360                 365

Cys Gly Asn Gly Ile Leu Glu Ser Asn Glu Glu Cys Asp Cys Gly Asn
    370                 375                 380

Lys Asn Glu Cys Gln Phe Lys Lys Cys Cys Asp Tyr Asn Thr Cys Lys
385                 390                 395                 400

Leu Lys Gly Ser Val Lys Cys Gly Ser Gly Pro Cys Cys Thr Ser Lys
                405                 410                 415

Cys Glu Leu Ser Ile Ala Gly Thr Pro Cys Arg Lys Ser Ile Asp Pro
            420                 425                 430

Glu Cys Asp Phe Thr Glu Tyr Cys Asn Gly Thr Ser Ser Asn Cys Val
        435                 440                 445

Pro Asp Thr Tyr Ala Leu Asn Gly Arg Leu Cys Lys Leu Gly Thr Ala
    450                 455                 460

Tyr Cys Tyr Asn Gly Gln Cys Gln Thr Thr Asp Asn Gln Cys Ala Lys
465                 470                 475                 480

Ile Phe Gly Lys Gly Ala Gln Gly Ala Pro Phe Ala Cys Phe Lys Glu
                485                 490                 495

Val Asn Ser Leu His Glu Arg Ser Glu Asn Cys Gly Phe Lys Asn Ser
            500                 505                 510

Gln Pro Leu Pro Cys Glu Arg Lys Asp Val Leu Cys Gly Lys Leu Ala
        515                 520                 525

Cys Val Gln Pro His Lys Asn Ala Asn Lys Ser Asp Ala Gln Ser Thr
    530                 535                 540

Val Tyr Ser Tyr Ile Gln Asp His Val Cys Val Ser Ile Ala Thr Gly
545                 550                 555                 560

Ser Ser Met Arg Ser Asp Gly Thr Asp Asn Ala Tyr Val Ala Asp Gly
                565                 570                 575
```

```
Thr Met Cys Gly Pro Glu Met Tyr Cys Val Asn Lys Thr Cys Arg Lys
            580                 585                 590

Val His Leu Met Gly Tyr Asn Cys Asn Ala Thr Thr Lys Cys Lys Gly
        595                 600                 605

Lys Gly Ile Cys Asn Asn Phe Gly Asn Cys Gln Cys Phe Pro Gly His
    610                 615                 620

Arg Pro Pro Asp Cys Lys Phe Gln Phe Gly Ser Pro Gly Gly Ser Ile
625                 630                 635                 640

Asp Asp Gly Asn Phe Gln Lys Ser Gly Asp Phe Tyr Thr Glu Lys Gly
                645                 650                 655

Tyr Asn Thr His Trp Asn Asn Trp Phe Ile Leu Ser Phe Cys Ile Phe
            660                 665                 670

Leu Pro Phe Phe Ile Val Phe Thr Thr Val Ile Phe Lys Arg Asn Glu
        675                 680                 685

Ile Ser Lys Ser Cys Asn Arg Glu Asn Ala Glu Tyr Asn Arg Asn Ser
    690                 695                 700

Ser Val Val Ser Glu Ser Asp Asp Val Gly His
705                 710                 715


<210> 2168
<211> 62
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 541; "

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<220>
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<400> 2168
Met Phe Leu Leu Leu Ala Leu Leu Thr Glu Leu Gly Arg Leu Gln Ala
1   5   10   15

His Glu Gly Ser Glu Gly Ile Phe Leu His Val Thr Val Pro Arg Lys
            20   25   30

Ile Lys Ser Asn Asp Ser Glu Val Ser Glu Arg Lys Val Phe Gly Glu
        35   40   45

Gln Val Val Phe Gly Tyr Met Asn Asp Leu His His Tyr Asn
    50   55   60

<210> 2169
<211> 918
<212> PRT
<213> Homo sapiens

<220>
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<221> source
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<220>
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<223> /note="Gene Name:
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<223> /note="Uniprot ID: Q9H013; "

<220>
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<223> /note="ENSP ID: ENSP00000257527"

<400> 2169
Met Pro Gly Gly Ala Gly Ala Ala Arg Leu Cys Leu Leu Ala Phe Ala
1   5   10   15

Leu Gln Pro Leu Arg Pro Arg Ala Ala Arg Glu Pro Gly Trp Thr Arg
            20   25   30

Gly Ser Glu Glu Gly Ser Pro Lys Leu Gln His Glu Leu Ile Ile Pro
        35   40   45

```
Gln Trp Lys Thr Ser Glu Ser Pro Val Arg Glu Lys His Pro Leu Lys
    50                  55                  60

Ala Glu Leu Arg Val Met Ala Glu Gly Arg Glu Leu Ile Leu Asp Leu
65                  70                  75                  80

Glu Lys Asn Glu Gln Leu Phe Ala Pro Ser Tyr Thr Glu Thr His Tyr
                85                  90                  95

Thr Ser Ser Gly Asn Pro Gln Thr Thr Thr Arg Lys Leu Glu Asp His
            100                 105                 110

Cys Phe Tyr His Gly Thr Val Arg Glu Thr Glu Leu Ser Ser Val Thr
        115                 120                 125

Leu Ser Thr Cys Arg Gly Ile Arg Gly Leu Ile Thr Val Ser Ser Asn
    130                 135                 140

Leu Ser Tyr Val Ile Glu Pro Leu Pro Asp Ser Lys Gly Gln His Leu
145                 150                 155                 160

Ile Tyr Arg Ser Glu His Leu Lys Pro Pro Pro Gly Asn Cys Gly Phe
                165                 170                 175

Glu His Ser Lys Pro Thr Thr Arg Asp Trp Ala Leu Gln Phe Thr Gln
            180                 185                 190

Gln Thr Lys Lys Arg Pro Arg Arg Met Lys Arg Glu Asp Leu Asn Ser
        195                 200                 205

Met Lys Tyr Val Glu Leu Tyr Leu Val Ala Asp Tyr Leu Glu Phe Gln
    210                 215                 220

Lys Asn Arg Arg Asp Gln Asp Ala Thr Lys His Lys Leu Ile Glu Ile
225                 230                 235                 240

Ala Asn Tyr Val Asp Lys Phe Tyr Arg Ser Leu Asn Ile Arg Ile Ala
                245                 250                 255

Leu Val Gly Leu Glu Val Trp Thr His Gly Asn Met Cys Glu Val Ser
            260                 265                 270

Glu Asn Pro Tyr Ser Thr Leu Trp Ser Phe Leu Ser Trp Arg Arg Lys
```

```
        275                 280                 285

Leu Leu Ala Gln Lys Tyr His Asp Asn Ala Gln Leu Ile Thr Gly Met
    290                 295                 300

Ser Phe His Gly Thr Thr Ile Gly Leu Ala Pro Leu Met Ala Met Cys
305                 310                 315                 320

Ser Val Tyr Gln Ser Gly Gly Val Asn Met Asp His Ser Glu Asn Ala
                325                 330                 335

Ile Gly Val Ala Ala Thr Met Ala His Glu Met Gly His Asn Phe Gly
            340                 345                 350

Met Thr His Asp Ser Ala Asp Cys Cys Ser Ala Ser Ala Ala Asp Gly
        355                 360                 365

Gly Cys Ile Met Ala Ala Ala Thr Gly His Pro Phe Pro Lys Val Phe
    370                 375                 380

Asn Gly Cys Asn Arg Arg Glu Leu Asp Arg Tyr Leu Gln Ser Gly Gly
385                 390                 395                 400

Gly Met Cys Leu Ser Asn Met Pro Asp Thr Arg Met Leu Tyr Gly Gly
                405                 410                 415

Arg Arg Cys Gly Asn Gly Tyr Leu Glu Asp Gly Glu Glu Cys Asp Cys
            420                 425                 430

Gly Glu Glu Glu Glu Cys Asn Asn Pro Cys Cys Asn Ala Ser Asn Cys
        435                 440                 445

Thr Leu Arg Pro Gly Ala Glu Cys Ala His Gly Ser Cys Cys His Gln
    450                 455                 460

Cys Lys Leu Leu Ala Pro Gly Thr Leu Cys Arg Glu Gln Ala Arg Gln
465                 470                 475                 480

Cys Asp Leu Pro Glu Phe Cys Thr Gly Lys Ser Pro His Cys Pro Thr
                485                 490                 495

Asn Phe Tyr Gln Met Asp Gly Thr Pro Cys Glu Gly Gly Gln Ala Tyr
            500                 505                 510
```

```
Cys Tyr Asn Gly Met Cys Leu Thr Tyr Gln Glu Gln Cys Gln Gln Leu
        515                 520                 525

Trp Gly Pro Gly Ala Arg Pro Ala Pro Asp Leu Cys Phe Glu Lys Val
    530                 535                 540

Asn Val Ala Gly Asp Thr Phe Gly Asn Cys Gly Lys Asp Met Asn Gly
545                 550                 555                 560

Glu His Arg Lys Cys Asn Met Arg Asp Ala Lys Cys Gly Lys Ile Gln
                565                 570                 575

Cys Gln Ser Ser Glu Ala Arg Pro Leu Glu Ser Asn Ala Val Pro Ile
            580                 585                 590

Asp Thr Thr Ile Ile Met Asn Gly Arg Gln Ile Gln Cys Arg Gly Thr
        595                 600                 605

His Val Tyr Arg Gly Pro Glu Glu Glu Gly Asp Met Leu Asp Pro Gly
    610                 615                 620

Leu Val Met Thr Gly Thr Lys Cys Gly Tyr Asn His Ile Cys Phe Glu
625                 630                 635                 640

Gly Gln Cys Arg Asn Thr Ser Phe Phe Glu Thr Glu Gly Cys Gly Lys
                645                 650                 655

Lys Cys Asn Gly His Gly Val Cys Asn Asn Asn Gln Asn Cys His Cys
            660                 665                 670

Leu Pro Gly Trp Ala Pro Pro Phe Cys Asn Thr Pro Gly His Gly Gly
        675                 680                 685

Ser Ile Asp Ser Gly Pro Met Pro Pro Glu Ser Val Gly Pro Val Val
    690                 695                 700

Ala Gly Val Leu Val Ala Ile Leu Val Leu Ala Val Leu Met Leu Met
705                 710                 715                 720

Tyr Tyr Cys Cys Arg Gln Asn Asn Lys Leu Gly Gln Leu Lys Pro Ser
                725                 730                 735
```

```
Ala Leu Pro Ser Lys Leu Arg Gln Gln Phe Ser Cys Pro Phe Arg Val
            740                 745                 750

Ser Gln Asn Ser Gly Thr Gly His Ala Asn Pro Thr Phe Lys Leu Gln
        755                 760                 765

Thr Pro Gln Gly Lys Arg Lys Val Ile Asn Thr Pro Glu Ile Leu Arg
    770                 775                 780

Lys Pro Ser Gln Pro Pro Pro Arg Pro Pro Pro Asp Tyr Leu Arg Gly
785                 790                 795                 800

Gly Ser Pro Pro Ala Pro Leu Pro Ala His Leu Ser Arg Ala Ala Arg
                805                 810                 815

Asn Ser Pro Gly Pro Gly Ser Gln Ile Glu Arg Thr Glu Ser Ser Arg
            820                 825                 830

Arg Pro Pro Pro Ser Arg Pro Ile Pro Pro Ala Pro Asn Cys Ile Val
        835                 840                 845

Ser Gln Asp Phe Ser Arg Pro Arg Pro Pro Gln Lys Ala Leu Pro Ala
    850                 855                 860

Asn Pro Val Pro Gly Arg Arg Ser Leu Pro Arg Pro Gly Gly Ala Ser
865                 870                 875                 880

Pro Leu Arg Pro Pro Gly Ala Gly Pro Gln Gln Ser Arg Pro Leu Ala
                885                 890                 895

Ala Leu Ala Pro Lys Phe Pro Glu Tyr Arg Ser Gln Arg Ala Gly Gly
            900                 905                 910

Met Ile Ser Ser Lys Ile
        915


<210> 2170
<211> 272
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 542; "
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<220>
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<223> /note="Gene Symbol: ADAM19; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 19; "

<220>
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<223> /note="ENSP ID: ENSP00000428376"

<400> 2170

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Met Pro Gly Gly Ala Gly Ala Ala Arg Leu Cys Leu Leu Ala Phe Ala
1               5                   10                  15

Leu Gln Pro Leu Arg Pro Arg Ala Ala Arg Glu Pro Gly Trp Thr Arg
            20                  25                  30

Gly Ser Glu Glu Gly Ser Pro Lys Leu Gln His Glu Leu Ile Ile Pro
        35                  40                  45

Gln Trp Lys Thr Ser Glu Ser Pro Val Arg Glu Lys His Pro Leu Lys
    50                  55                  60

Ala Glu Leu Arg Val Met Ala Glu Gly Arg Glu Leu Ile Leu Asp Leu
65                  70                  75                  80

Glu Lys Asn Glu Gln Leu Phe Ala Pro Ser Tyr Thr Glu Thr His Tyr
                85                  90                  95

Thr Ser Ser Gly Asn Pro Gln Thr Thr Thr Arg Lys Leu Glu Asp His
            100                 105                 110

Cys Phe Tyr His Gly Thr Val Arg Glu Thr Glu Leu Ser Ser Val Thr
        115                 120                 125

Leu Ser Thr Cys Arg Gly Ile Arg Gly Leu Ile Thr Val Ser Ser Asn
    130                 135                 140

Leu Ser Tyr Val Ile Glu Pro Leu Pro Asp Ser Lys Gly Gln His Leu
145                 150                 155                 160

Ile Tyr Arg Ser Glu His Leu Lys Pro Pro Pro Gly Asn Cys Gly Phe
                165                 170                 175
```

```
Glu His Ser Lys Pro Thr Thr Arg Asp Trp Ala Leu Gln Phe Thr Gln
            180                 185                 190

Gln Thr Lys Lys Arg Pro Arg Arg Met Lys Arg Glu Asp Leu Asn Ser
        195                 200                 205

Met Lys Tyr Val Glu Leu Tyr Leu Val Ala Asp Tyr Leu Glu Phe Gln
    210                 215                 220

Lys Asn Arg Arg Asp Gln Asp Ala Thr Lys His Lys Leu Ile Glu Ile
225                 230                 235                 240

Ala Asn Tyr Val Asp Lys Val Arg Pro Val Leu Pro Ile Leu Glu His
                245                 250                 255

Pro Asp Cys Ser Arg Gly Leu Gly Ser Val Asp Pro Arg Glu His Val
            260                 265                 270


<210> 2171
<211> 955
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Uniprot ID:  Q9H013; "

<220>
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<223> /note="ENSP ID: ENSP00000428654"

<400> 2171
Met Pro Gly Gly Ala Gly Ala Ala Arg Leu Cys Leu Leu Ala Phe Ala
1               5                   10                  15
```

```
Leu Gln Pro Leu Arg Pro Arg Ala Ala Arg Glu Pro Gly Trp Thr Arg
            20                  25                  30

Gly Ser Glu Glu Gly Ser Pro Lys Leu Gln His Glu Leu Ile Ile Pro
        35                  40                  45

Gln Trp Lys Thr Ser Glu Ser Pro Val Arg Glu Lys His Pro Leu Lys
    50                  55                  60

Ala Glu Leu Arg Val Met Ala Glu Gly Arg Glu Leu Ile Leu Asp Leu
65                  70                  75                  80

Glu Lys Asn Glu Gln Leu Phe Ala Pro Ser Tyr Thr Glu Thr His Tyr
                85                  90                  95

Thr Ser Ser Gly Asn Pro Gln Thr Thr Thr Arg Lys Leu Glu Asp His
            100                 105                 110

Cys Phe Tyr His Gly Thr Val Arg Glu Thr Glu Leu Ser Ser Val Thr
        115                 120                 125

Leu Ser Thr Cys Arg Gly Ile Arg Gly Leu Ile Thr Val Ser Ser Asn
    130                 135                 140

Leu Ser Tyr Val Ile Glu Pro Leu Pro Asp Ser Lys Gly Gln His Leu
145                 150                 155                 160

Ile Tyr Arg Ser Glu His Leu Lys Pro Pro Pro Gly Asn Cys Gly Phe
                165                 170                 175

Glu His Ser Lys Pro Thr Thr Arg Asp Trp Ala Leu Gln Phe Thr Gln
            180                 185                 190

Gln Thr Lys Lys Arg Pro Arg Arg Met Lys Arg Glu Asp Leu Asn Ser
        195                 200                 205

Met Lys Tyr Val Glu Leu Tyr Leu Val Ala Asp Tyr Leu Glu Phe Gln
    210                 215                 220

Lys Asn Arg Arg Asp Gln Asp Ala Thr Lys His Lys Leu Ile Glu Ile
225                 230                 235                 240

Ala Asn Tyr Val Asp Lys Phe Tyr Arg Ser Leu Asn Ile Arg Ile Ala
```

```
                245                 250                 255

Leu Val Gly Leu Glu Val Trp Thr His Gly Asn Met Cys Glu Val Ser
            260                 265                 270

Glu Asn Pro Tyr Ser Thr Leu Trp Ser Phe Leu Ser Trp Arg Arg Lys
        275                 280                 285

Leu Leu Ala Gln Lys Tyr His Asp Asn Ala Gln Leu Ile Thr Gly Met
    290                 295                 300

Ser Phe His Gly Thr Thr Ile Gly Leu Ala Pro Leu Met Ala Met Cys
305                 310                 315                 320

Ser Val Tyr Gln Ser Gly Gly Val Asn Met Asp His Ser Glu Asn Ala
                325                 330                 335

Ile Gly Val Ala Ala Thr Met Ala His Glu Met Gly His Asn Phe Gly
            340                 345                 350

Met Thr His Asp Ser Ala Asp Cys Cys Ser Ala Ser Ala Ala Asp Gly
        355                 360                 365

Gly Cys Ile Met Ala Ala Ala Thr Gly His Pro Phe Pro Lys Val Phe
    370                 375                 380

Asn Gly Cys Asn Arg Arg Glu Leu Asp Arg Tyr Leu Gln Ser Gly Gly
385                 390                 395                 400

Gly Met Cys Leu Ser Asn Met Pro Asp Thr Arg Met Leu Tyr Gly Gly
                405                 410                 415

Arg Arg Cys Gly Asn Gly Tyr Leu Glu Asp Gly Glu Glu Cys Asp Cys
            420                 425                 430

Gly Glu Glu Glu Glu Cys Asn Asn Pro Cys Cys Asn Ala Ser Asn Cys
        435                 440                 445

Thr Leu Arg Pro Gly Ala Glu Cys Ala His Gly Ser Cys Cys His Gln
    450                 455                 460

Cys Lys Leu Leu Ala Pro Gly Thr Leu Cys Arg Glu Gln Ala Arg Gln
465                 470                 475                 480
```

```
Cys Asp Leu Pro Glu Phe Cys Thr Gly Lys Ser Pro His Cys Pro Thr
                485                 490                 495

Asn Phe Tyr Gln Met Asp Gly Thr Pro Cys Glu Gly Gly Gln Ala Tyr
            500                 505                 510

Cys Tyr Asn Gly Met Cys Leu Thr Tyr Gln Glu Gln Cys Gln Gln Leu
        515                 520                 525

Trp Gly Pro Gly Ala Arg Pro Ala Pro Asp Leu Cys Phe Glu Lys Val
    530                 535                 540

Asn Val Ala Gly Asp Thr Phe Gly Asn Cys Gly Lys Asp Met Asn Gly
545                 550                 555                 560

Glu His Arg Lys Cys Asn Met Arg Asp Ala Lys Cys Gly Lys Ile Gln
                565                 570                 575

Cys Gln Ser Ser Glu Ala Arg Pro Leu Glu Ser Asn Ala Val Pro Ile
            580                 585                 590

Asp Thr Thr Ile Ile Met Asn Gly Arg Gln Ile Gln Cys Arg Gly Thr
        595                 600                 605

His Val Tyr Arg Gly Pro Glu Glu Glu Gly Asp Met Leu Asp Pro Gly
    610                 615                 620

Leu Val Met Thr Gly Thr Lys Cys Gly Tyr Asn His Ile Cys Phe Glu
625                 630                 635                 640

Gly Gln Cys Arg Asn Thr Ser Phe Phe Glu Thr Glu Gly Cys Gly Lys
                645                 650                 655

Lys Cys Asn Gly His Gly Val Cys Asn Asn Asn Gln Asn Cys His Cys
            660                 665                 670

Leu Pro Gly Trp Ala Pro Pro Phe Cys Asn Thr Pro Gly His Gly Gly
        675                 680                 685

Ser Ile Asp Ser Gly Pro Met Pro Pro Glu Ser Val Gly Pro Val Val
    690                 695                 700
```

```
Ala Gly Val Leu Val Ala Ile Leu Val Leu Ala Val Leu Met Leu Met
705                 710                 715                 720

Tyr Tyr Cys Cys Arg Gln Asn Asn Lys Leu Gly Gln Leu Lys Pro Ser
                725                 730                 735

Ala Leu Pro Ser Lys Leu Arg Gln Gln Phe Ser Cys Pro Phe Arg Val
            740                 745                 750

Ser Gln Asn Ser Gly Thr Gly His Ala Asn Pro Thr Phe Lys Leu Gln
        755                 760                 765

Thr Pro Gln Gly Lys Arg Lys Val Ile Asn Thr Pro Glu Ile Leu Arg
    770                 775                 780

Lys Pro Ser Gln Pro Pro Pro Arg Pro Pro Pro Asp Tyr Leu Arg Gly
785                 790                 795                 800

Gly Ser Pro Pro Ala Pro Leu Pro Ala His Leu Ser Arg Ala Ala Arg
                805                 810                 815

Asn Ser Pro Gly Pro Gly Ser Gln Ile Glu Arg Thr Glu Ser Ser Arg
            820                 825                 830

Arg Pro Pro Pro Ser Arg Pro Ile Pro Pro Ala Pro Asn Cys Ile Val
        835                 840                 845

Ser Gln Asp Phe Ser Arg Pro Arg Pro Pro Gln Lys Ala Leu Pro Ala
    850                 855                 860

Asn Pro Val Pro Gly Arg Arg Ser Leu Pro Arg Pro Gly Gly Ala Ser
865                 870                 875                 880

Pro Leu Arg Pro Pro Gly Ala Gly Pro Gln Gln Ser Arg Pro Leu Ala
                885                 890                 895

Ala Leu Ala Pro Lys Val Ser Pro Arg Glu Ala Leu Lys Val Lys Ala
            900                 905                 910

Gly Thr Arg Gly Leu Gln Gly Gly Arg Cys Arg Val Glu Lys Thr Lys
        915                 920                 925
```

```
Gln Phe Met Leu Leu Val Val Trp Thr Glu Leu Pro Glu Gln Lys Pro
    930                 935                 940

Arg Ala Lys His Ser Cys Phe Leu Val Pro Ala
945                 950                 955


<210> 2172
<211> 489
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 542; "

<220>
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<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 19; "

<220>
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 2172
Xaa Asp Cys Gly Glu Glu Glu Glu Cys Asn Asn Pro Cys Cys Asn Ala
1               5                   10                  15

Ser Asn Cys Thr Leu Arg Pro Gly Ala Glu Cys Ala His Gly Ser Cys
            20                  25                  30

Cys His Gln Cys Lys Leu Leu Ala Pro Gly Thr Leu Cys Arg Glu Gln
        35                  40                  45

Ala Arg Gln Cys Asp Leu Pro Glu Phe Cys Thr Gly Lys Ser Pro His
    50                  55                  60

Cys Pro Thr Asn Phe Tyr Gln Met Asp Gly Thr Pro Cys Glu Gly Gly
65                  70                  75                  80
```

```
Gln Ala Tyr Cys Tyr Asn Gly Met Cys Leu Thr Tyr Gln Glu Gln Cys
                85                  90                  95

Gln Gln Leu Trp Gly Pro Gly Ala Arg Pro Ala Pro Asp Leu Cys Phe
            100                 105                 110

Glu Lys Val Asn Val Ala Gly Asp Thr Phe Gly Asn Cys Gly Lys Asp
        115                 120                 125

Met Asn Gly Glu His Arg Lys Cys Asn Met Arg Asp Ala Lys Cys Gly
    130                 135                 140

Lys Ile Gln Cys Gln Ser Ser Glu Ala Arg Pro Leu Glu Ser Asn Ala
145                 150                 155                 160

Val Pro Ile Asp Thr Thr Ile Ile Met Asn Gly Arg Gln Ile Gln Cys
                165                 170                 175

Arg Gly Thr His Val Tyr Arg Gly Pro Glu Glu Glu Gly Asp Met Leu
            180                 185                 190

Asp Pro Gly Leu Val Met Thr Gly Thr Lys Cys Gly Tyr Asn His Ile
        195                 200                 205

Cys Phe Glu Gly Gln Cys Arg Asn Thr Ser Phe Phe Glu Thr Glu Gly
    210                 215                 220

Cys Gly Lys Lys Cys Asn Gly His Gly Val Cys Asn Asn Asn Gln Asn
225                 230                 235                 240

Cys His Cys Leu Pro Gly Trp Ala Pro Pro Phe Cys Asn Thr Pro Gly
                245                 250                 255

His Gly Gly Ser Ile Asp Ser Gly Pro Met Pro Pro Glu Ser Val Gly
            260                 265                 270

Pro Val Val Ala Gly Val Leu Val Ala Ile Leu Val Leu Ala Val Leu
        275                 280                 285

Met Leu Met Tyr Tyr Cys Cys Arg Gln Asn Asn Lys Leu Gly Gln Leu
    290                 295                 300

Lys Pro Ser Ala Leu Pro Ser Lys Leu Arg Gln Gln Phe Ser Cys Pro
```

```
305                 310                 315                 320

Phe Arg Val Ser Gln Asn Ser Gly Thr Gly His Ala Asn Pro Thr Phe
                325                 330                 335

Lys Leu Gln Thr Pro Gln Gly Lys Arg Lys Val Ile Asn Thr Pro Glu
            340                 345                 350

Ile Leu Arg Lys Pro Ser Gln Pro Pro Pro Arg Pro Pro Pro Asp Tyr
        355                 360                 365

Leu Arg Gly Gly Ser Pro Pro Ala Pro Leu Pro Ala His Leu Ser Arg
    370                 375                 380

Ala Ala Arg Asn Ser Pro Gly Pro Gly Ser Gln Ile Glu Arg Thr Glu
385                 390                 395                 400

Ser Ser Arg Arg Pro Pro Pro Ser Arg Pro Ile Pro Pro Ala Pro Asn
                405                 410                 415

Cys Ile Val Ser Gln Asp Phe Ser Arg Pro Arg Pro Pro Gln Lys Ala
            420                 425                 430

Leu Pro Ala Asn Pro Val Pro Gly Arg Arg Ser Leu Pro Arg Pro Gly
        435                 440                 445

Gly Ala Ser Pro Leu Arg Pro Pro Gly Ala Gly Pro Gln Gln Ser Arg
    450                 455                 460

Pro Leu Ala Ala Leu Ala Pro Lys Arg Val Trp Lys Thr Cys Asn Leu
465                 470                 475                 480

Lys Thr Gly Asp Gln Phe Gln Ser Gln
                485

<210> 2173
<211> 735
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 543; "

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<221> source
<223> /note="Gene Symbol: ADAM2; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q99965; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000265708"

<400> 2173

Met	Trp	Arg	Val	Leu	Phe	Leu	Leu	Ser	Gly	Leu	Gly	Gly	Leu	Arg	Met
1				5				10						15	

Asp	Ser	Asn	Phe	Asp	Ser	Leu	Pro	Val	Gln	Ile	Thr	Val	Pro	Glu	Lys
		20					25					30			

Ile	Arg	Ser	Ile	Ile	Lys	Glu	Gly	Ile	Glu	Ser	Gln	Ala	Ser	Tyr	Lys
	35					40					45				

Ile	Val	Ile	Glu	Gly	Lys	Pro	Tyr	Thr	Val	Asn	Leu	Met	Gln	Lys	Asn
50						55					60				

Phe	Leu	Pro	His	Asn	Phe	Arg	Val	Tyr	Ser	Tyr	Ser	Gly	Thr	Gly	Ile
65					70					75					80

Met	Lys	Pro	Leu	Asp	Gln	Asp	Phe	Gln	Asn	Phe	Cys	His	Tyr	Gln	Gly
			85					90					95		

Tyr	Ile	Glu	Gly	Tyr	Pro	Lys	Ser	Val	Val	Met	Val	Ser	Thr	Cys	Thr
		100					105					110			

Gly	Leu	Arg	Gly	Val	Leu	Gln	Phe	Glu	Asn	Val	Ser	Tyr	Gly	Ile	Glu
	115					120					125				

Pro	Leu	Glu	Ser	Ser	Val	Gly	Phe	Glu	His	Val	Ile	Tyr	Gln	Val	Lys
130						135					140				

His	Lys	Lys	Ala	Asp	Val	Ser	Leu	Tyr	Asn	Glu	Lys	Asp	Ile	Glu	Ser
145					150					155					160

```
Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Pro Gln Gln Asp Phe
                165                 170                 175

Ala Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn
            180                 185                 190

His Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu
        195                 200                 205

Ile Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile
    210                 215                 220

Leu Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr
225                 230                 235                 240

Gly Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser
                245                 250                 255

Tyr Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg
            260                 265                 270

Glu Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp
        275                 280                 285

Ala Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu
    290                 295                 300

Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly
305                 310                 315                 320

Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys
                325                 330                 335

Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser
            340                 345                 350

Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser
        355                 360                 365

Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln
    370                 375                 380

Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys
```

385 390 395 400

Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile
405 410 415

Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys
420 425 430

Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser
435 440 445

Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser
450 455 460

Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn
465 470 475 480

Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys
485 490 495

Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr
500 505 510

Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser
515 520 525

Asp Ser Gly Tyr Thr Gln Cys Glu Ala Asp Asn Leu Gln Cys Gly Lys
530 535 540

Leu Ile Cys Lys Tyr Val Gly Lys Phe Leu Leu Gln Ile Pro Arg Ala
545 550 555 560

Thr Ile Ile Tyr Ala Asn Ile Ser Gly His Leu Cys Ile Ala Val Glu
565 570 575

Phe Ala Ser Asp His Ala Asp Ser Gln Lys Met Trp Ile Lys Asp Gly
580 585 590

Thr Ser Cys Gly Ser Asn Lys Val Cys Arg Asn Gln Arg Cys Val Ser
595 600 605

Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp Arg
610 615 620

```
Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr Leu
625                 630                 635                 640

Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser Ile
                645                 650                 655

Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro Glu
            660                 665                 670

Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp Pro
        675                 680                 685

Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile Ala
    690                 695                 700

Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu Asp
705                 710                 715                 720

Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
                725                 730                 735


<210> 2174
<211> 716
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 543; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM2; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="Uniprot ID:  Q99965; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000343854"

<400> 2174
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```
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                  10                  15

Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Tyr Asn His Met Gly
                165                 170                 175

Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu Ile Gly Leu
            180                 185                 190

Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile Leu Ser Ser
        195                 200                 205

Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr Gly Glu Ala
    210                 215                 220

Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser Tyr Leu Val
```

225 230 235 240

Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg Glu Lys Ser
245 250 255

Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp Ala Asn Tyr
260 265 270

Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu Glu Ser Leu
275 280 285

Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly Ile Thr Tyr
290 295 300

Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys Ile Met Asn
305 310 315 320

Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser Asn Cys Ser
325 330 335

Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser Gln Cys Leu
340 345 350

His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln Ala Val Cys
355 360 365

Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys Gly Thr Glu
370 375 380

Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile Ala Thr Cys
385 390 395 400

Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys Cys Glu Asn
405 410 415

Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser Phe Glu Glu
420 425 430

Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser Cys Pro Glu
435 440 445

Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn Gln Trp Ile
450 455 460

```
Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys Thr Asp Thr
465                 470                 475                 480

Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr Ser His Leu
                485                 490                 495

Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser Asp Ser Gly
            500                 505                 510

Tyr Thr Gln Cys Glu Ala Asp Asn Leu Gln Cys Gly Lys Leu Ile Cys
        515                 520                 525

Lys Tyr Val Gly Lys Phe Leu Leu Gln Ile Pro Arg Ala Thr Ile Ile
    530                 535                 540

Tyr Ala Asn Ile Ser Gly His Leu Cys Ile Ala Val Glu Phe Ala Ser
545                 550                 555                 560

Asp His Ala Asp Ser Gln Lys Met Trp Ile Lys Asp Gly Thr Ser Cys
                565                 570                 575

Gly Ser Asn Lys Val Cys Arg Asn Gln Arg Cys Val Ser Ser Ser Tyr
            580                 585                 590

Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp Arg Gly Val Cys
        595                 600                 605

Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr Leu Pro Pro Asp
    610                 615                 620

Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser Ile Asp Ser Gly
625                 630                 635                 640

Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro Glu Arg Arg Tyr
                645                 650                 655

Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp Pro Phe Phe Leu
            660                 665                 670

Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile Ala Ile Met Val
        675                 680                 685
```

```
Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu Asp Tyr Ser Ser
    690                 695                 700

Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
705                 710                 715


<210> 2175
<211> 579
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 543; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM2; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369182"

<400> 2175
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                   10                  15

Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
```

```
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu His Pro Arg Thr Ile
                165                 170                 175

Ser Leu Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser
            180                 185                 190

Met Gly Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala
        195                 200                 205

Val Cys Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile
    210                 215                 220

Phe Ser Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln
225                 230                 235                 240

Lys Ser Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys
                245                 250                 255

Gln Gln Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys
            260                 265                 270

Asp Cys Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys
        275                 280                 285

Asp Ile Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly
    290                 295                 300

Pro Cys Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg
305                 310                 315                 320

Pro Ser Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser
                325                 330                 335
```

```
Ala Ser Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly
            340                 345                 350

Leu Asn Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys
        355                 360                 365

Gln Cys Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu
    370                 375                 380

Cys Tyr Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly
385                 390                 395                 400

Ile Ser Asp Ser Gly Tyr Thr Gln Cys Glu Ala Asp Gly His Leu Cys
                405                 410                 415

Ile Ala Val Glu Phe Ala Ser Asp His Ala Asp Ser Gln Lys Met Trp
            420                 425                 430

Ile Lys Asp Gly Thr Ser Cys Gly Ser Asn Lys Val Cys Arg Asn Gln
        435                 440                 445

Arg Cys Val Ser Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys
    450                 455                 460

Cys Asn Asp Arg Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser
465                 470                 475                 480

Ala Ser Tyr Leu Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro
                485                 490                 495

Gly Gly Ser Ile Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala
            500                 505                 510

Arg Leu Pro Glu Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro
        515                 520                 525

Met Arg Trp Pro Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys
    530                 535                 540

Val Leu Ile Ala Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp
545                 550                 555                 560
```

```
Arg Thr Glu Asp Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu
                565                 570                 575


Pro Lys Gly
```

<210> 2176
<211> 672
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429352"

<400> 2176

```
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                   10                  15


Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30


Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45


Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60


Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80


Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95


Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
```

```
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Pro Gln Gln Asp Phe
                165                 170                 175

Ala Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn
            180                 185                 190

His Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu
        195                 200                 205

Ile Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile
    210                 215                 220

Leu Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr
225                 230                 235                 240

Gly Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser
                245                 250                 255

Tyr Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg
            260                 265                 270

Glu Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp
        275                 280                 285

Ala Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu
    290                 295                 300

Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly
305                 310                 315                 320

Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys
                325                 330                 335
```

```
Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser
            340                 345                 350

Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser
        355                 360                 365

Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln
    370                 375                 380

Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys
385                 390                 395                 400

Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile
                405                 410                 415

Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys
            420                 425                 430

Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser
        435                 440                 445

Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser
    450                 455                 460

Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn
465                 470                 475                 480

Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys
                485                 490                 495

Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr
            500                 505                 510

Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser
        515                 520                 525

Asp Ser Gly Tyr Thr Gln Cys Glu Val Cys Arg Asn Gln Arg Cys Val
    530                 535                 540

Ser Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp
545                 550                 555                 560
```

```
Arg Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr
                565                 570                 575

Leu Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser
            580                 585                 590

Ile Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro
        595                 600                 605

Glu Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp
    610                 615                 620

Pro Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile
625                 630                 635                 640

Ala Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu
                645                 650                 655

Asp Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
            660                 665                 670


<210> 2177
<211> 672
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 2; "

<220>
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<400> 2177
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                   10                  15

Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
```

```
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Pro Gln Gln Asp Phe
                165                 170                 175

Ala Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn
            180                 185                 190

His Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu
        195                 200                 205

Ile Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile
    210                 215                 220

Leu Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr
225                 230                 235                 240

Gly Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser
                245                 250                 255
```

```
Tyr Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg
            260                 265                 270

Glu Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp
        275                 280                 285

Ala Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu
    290                 295                 300

Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly
305                 310                 315                 320

Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys
                325                 330                 335

Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser
            340                 345                 350

Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser
        355                 360                 365

Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln
    370                 375                 380

Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys
385                 390                 395                 400

Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile
                405                 410                 415

Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys
            420                 425                 430

Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser
        435                 440                 445

Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser
    450                 455                 460

Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn
465                 470                 475                 480
```

```
Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys
                485                 490                 495

Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr
            500                 505                 510

Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser
        515                 520                 525

Asp Ser Gly Tyr Thr Gln Cys Glu Val Cys Arg Asn Gln Arg Cys Val
    530                 535                 540

Ser Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp
545                 550                 555                 560

Arg Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr
                565                 570                 575

Leu Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser
            580                 585                 590

Ile Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro
        595                 600                 605

Glu Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp
    610                 615                 620

Pro Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile
625                 630                 635                 640

Ala Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu
                645                 650                 655

Asp Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
            660                 665                 670


<210> 2178
<211> 579
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 543; "
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<220>
<221> source
<223> /note="Gene Symbol: ADAM2; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000480574"

<400> 2178

```
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                  10                  15

Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu His Pro Arg Thr Ile
                165                 170                 175
```

```
Ser Leu Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser
            180                 185                 190

Met Gly Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala
        195                 200                 205

Val Cys Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile
    210                 215                 220

Phe Ser Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln
225                 230                 235                 240

Lys Ser Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys
                245                 250                 255

Gln Gln Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys
            260                 265                 270

Asp Cys Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys
        275                 280                 285

Asp Ile Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly
    290                 295                 300

Pro Cys Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg
305                 310                 315                 320

Pro Ser Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser
                325                 330                 335

Ala Ser Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly
            340                 345                 350

Leu Asn Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys
        355                 360                 365

Gln Cys Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu
    370                 375                 380

Cys Tyr Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly
385                 390                 395                 400
```

```
Ile Ser Asp Ser Gly Tyr Thr Gln Cys Glu Ala Asp Gly His Leu Cys
                405                 410                 415

Ile Ala Val Glu Phe Ala Ser Asp His Ala Asp Ser Gln Lys Met Trp
            420                 425                 430

Ile Lys Asp Gly Thr Ser Cys Gly Ser Asn Lys Val Cys Arg Asn Gln
        435                 440                 445

Arg Cys Val Ser Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys
    450                 455                 460

Cys Asn Asp Arg Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser
465                 470                 475                 480

Ala Ser Tyr Leu Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro
                485                 490                 495

Gly Gly Ser Ile Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala
            500                 505                 510

Arg Leu Pro Glu Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro
        515                 520                 525

Met Arg Trp Pro Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys
    530                 535                 540

Val Leu Ile Ala Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp
545                 550                 555                 560

Arg Thr Glu Asp Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu
                565                 570                 575

Pro Lys Gly
```

<210> 2179
<211> 735
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 543; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q99965; "

<220>
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<400> 2179
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1   5   10   15

Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20   25   30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35   40   45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50   55   60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65   70   75   80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85   90   95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100   105   110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115   120   125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130   135   140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145   150   155   160

```
Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Pro Gln Gln Asp Phe
                165                 170                 175

Ala Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn
            180                 185                 190

His Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu
        195                 200                 205

Ile Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile
    210                 215                 220

Leu Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr
225                 230                 235                 240

Gly Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser
                245                 250                 255

Tyr Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg
            260                 265                 270

Glu Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp
        275                 280                 285

Ala Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu
    290                 295                 300

Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly
305                 310                 315                 320

Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys
                325                 330                 335

Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser
            340                 345                 350

Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser
        355                 360                 365

Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln
    370                 375                 380
```

Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys
385 390 395 400

Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile
405 410 415

Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys
420 425 430

Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser
435 440 445

Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser
450 455 460

Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn
465 470 475 480

Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys
485 490 495

Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr
500 505 510

Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser
515 520 525

Asp Ser Gly Tyr Thr Gln Cys Glu Ala Asp Asn Leu Gln Cys Gly Lys
530 535 540

Leu Ile Cys Lys Tyr Val Gly Lys Phe Leu Leu Gln Ile Pro Arg Ala
545 550 555 560

Thr Ile Ile Tyr Ala Asn Ile Ser Gly His Leu Cys Ile Ala Val Glu
565 570 575

Phe Ala Ser Asp His Ala Asp Ser Gln Lys Met Trp Ile Lys Asp Gly
580 585 590

Thr Ser Cys Gly Ser Asn Lys Val Cys Arg Asn Gln Arg Cys Val Ser
595 600 605

```
Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp Arg
    610                 615                 620

Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr Leu
625                 630                 635                 640

Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser Ile
                645                 650                 655

Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro Glu
            660                 665                 670

Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp Pro
        675                 680                 685

Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile Ala
    690                 695                 700

Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu Asp
705                 710                 715                 720

Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
                725                 730                 735


<210> 2180
<211> 672
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 543; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM2; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483607"

<400> 2180
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                   10                  15
```

```
Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Pro Gln Gln Asp Phe
                165                 170                 175

Ala Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn
            180                 185                 190

His Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu
        195                 200                 205

Ile Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile
    210                 215                 220

Leu Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr
225                 230                 235                 240
```

```
Gly Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser
                245                 250                 255

Tyr Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg
            260                 265                 270

Glu Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp
        275                 280                 285

Ala Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu
    290                 295                 300

Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly
305                 310                 315                 320

Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys
                325                 330                 335

Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser
            340                 345                 350

Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser
        355                 360                 365

Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln
    370                 375                 380

Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys
385                 390                 395                 400

Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile
                405                 410                 415

Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys
            420                 425                 430

Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser
        435                 440                 445

Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser
    450                 455                 460
```

```
Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn
465                 470                 475                 480

Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys
                485                 490                 495

Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr
            500                 505                 510

Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser
        515                 520                 525

Asp Ser Gly Tyr Thr Gln Cys Glu Val Cys Arg Asn Gln Arg Cys Val
    530                 535                 540

Ser Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp
545                 550                 555                 560

Arg Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr
                565                 570                 575

Leu Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser
            580                 585                 590

Ile Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro
        595                 600                 605

Glu Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp
    610                 615                 620

Pro Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile
625                 630                 635                 640

Ala Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu
                645                 650                 655

Asp Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
            660                 665                 670
```

<210> 2181
<211> 716
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 543; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM2; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q99965; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484999"

<400> 2181

```
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1               5                  10                  15

Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140
```

```
His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Tyr Asn His Met Gly
                165                 170                 175

Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu Ile Gly Leu
            180                 185                 190

Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile Leu Ser Ser
        195                 200                 205

Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr Gly Glu Ala
    210                 215                 220

Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser Tyr Leu Val
225                 230                 235                 240

Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg Glu Lys Ser
                245                 250                 255

Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp Ala Asn Tyr
            260                 265                 270

Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu Glu Ser Leu
        275                 280                 285

Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly Ile Thr Tyr
    290                 295                 300

Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys Ile Met Asn
305                 310                 315                 320

Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser Asn Cys Ser
                325                 330                 335

Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser Gln Cys Leu
            340                 345                 350

His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln Ala Val Cys
        355                 360                 365
```

```
Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys Gly Thr Glu
    370                 375                 380

Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile Ala Thr Cys
385                 390                 395                 400

Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys Cys Glu Asn
                405                 410                 415

Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser Phe Glu Glu
            420                 425                 430

Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser Cys Pro Glu
        435                 440                 445

Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn Gln Trp Ile
    450                 455                 460

Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys Thr Asp Thr
465                 470                 475                 480

Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr Ser His Leu
                485                 490                 495

Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser Asp Ser Gly
            500                 505                 510

Tyr Thr Gln Cys Glu Ala Asp Asn Leu Gln Cys Gly Lys Leu Ile Cys
        515                 520                 525

Lys Tyr Val Gly Lys Phe Leu Leu Gln Ile Pro Arg Ala Thr Ile Ile
    530                 535                 540

Tyr Ala Asn Ile Ser Gly His Leu Cys Ile Ala Val Glu Phe Ala Ser
545                 550                 555                 560

Asp His Ala Asp Ser Gln Lys Met Trp Ile Lys Asp Gly Thr Ser Cys
                565                 570                 575

Gly Ser Asn Lys Val Cys Arg Asn Gln Arg Cys Val Ser Ser Ser Tyr
            580                 585                 590

Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp Arg Gly Val Cys
```

595 600 605

Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr Leu Pro Pro Asp
610 615 620

Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser Ile Asp Ser Gly
625 630 635 640

Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro Glu Arg Arg Tyr
645 650 655

Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp Pro Phe Phe Leu
660 665 670

Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile Ala Ile Met Val
675 680 685

Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu Asp Tyr Ser Ser
690 695 700

Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
705 710 715

<210> 2182
<211> 672
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 543; "

<220>
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ADAM metallopeptidase domain 2; "

<220>
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<400> 2182
Met Trp Arg Val Leu Phe Leu Leu Ser Gly Leu Gly Gly Leu Arg Met
1 5 10 15

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Asp Ser Asn Phe Asp Ser Leu Pro Val Gln Ile Thr Val Pro Glu Lys
            20                  25                  30

Ile Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys
        35                  40                  45

Ile Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn
    50                  55                  60

Phe Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile
65                  70                  75                  80

Met Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly
                85                  90                  95

Tyr Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr
            100                 105                 110

Gly Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu
        115                 120                 125

Pro Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys
    130                 135                 140

His Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser
145                 150                 155                 160

Arg Asp Leu Ser Phe Lys Leu Gln Ser Val Glu Pro Gln Gln Asp Phe
                165                 170                 175

Ala Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn
            180                 185                 190

His Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu
        195                 200                 205

Ile Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile
    210                 215                 220

Leu Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr
225                 230                 235                 240
```

```
Gly Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser
                245                 250                 255

Tyr Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg
            260                 265                 270

Glu Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp
        275                 280                 285

Ala Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu
    290                 295                 300

Glu Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly
305                 310                 315                 320

Ile Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys
                325                 330                 335

Ile Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser
            340                 345                 350

Asn Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser
        355                 360                 365

Gln Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln
    370                 375                 380

Ala Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys
385                 390                 395                 400

Gly Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile
                405                 410                 415

Ala Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys
            420                 425                 430

Cys Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser
        435                 440                 445

Phe Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser
    450                 455                 460

Cys Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn
```

465 470 475 480

Gln Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys
485 490 495

Thr Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr
500 505 510

Ser His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser
515 520 525

Asp Ser Gly Tyr Thr Gln Cys Glu Val Cys Arg Asn Gln Arg Cys Val
530 535 540

Ser Ser Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp
545 550 555 560

Arg Gly Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr
565 570 575

Leu Pro Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser
580 585 590

Ile Asp Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro
595 600 605

Glu Arg Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp
610 615 620

Pro Phe Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile
625 630 635 640

Ala Ile Met Val Lys Val Asn Phe Gln Arg Lys Lys Trp Arg Thr Glu
645 650 655

Asp Tyr Ser Ser Asp Glu Gln Pro Glu Ser Glu Ser Glu Pro Lys Gly
660 665 670

<210> 2183
<211> 776
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<213> Homo sapiens

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<223> /note="Uniprot ID: O43506; "

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<400> 2183

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Met Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln
1               5                  10                  15

Pro Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro
            20                  25                  30

His Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser
        35                  40                  45

Phe Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu
    50                  55                  60

Leu Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln
65                  70                  75                  80

Ala Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu
                85                  90                  95

Lys Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser
            100                 105                 110

Tyr Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val
        115                 120                 125

Asn Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu
    130                 135                 140
```

```
Gln His Ala Leu Leu Gln Asp Gln Pro Phe Ile Gln Asp Asp Cys Tyr
145                 150                 155                 160

Tyr His Gly Tyr Val Glu Gly Val Pro Glu Ser Leu Val Ala Leu Ser
                165                 170                 175

Thr Cys Ser Gly Gly Phe Leu Gly Met Leu Gln Ile Asn Asp Leu Val
            180                 185                 190

Tyr Glu Ile Lys Pro Ile Ser Val Ser Ala Thr Phe Glu His Leu Val
        195                 200                 205

Tyr Lys Ile Asp Ser Asp Asp Thr Gln Phe Pro Pro Met Arg Cys Gly
    210                 215                 220

Leu Thr Glu Glu Lys Ile Ala His Gln Met Glu Leu Gln Leu Ser Tyr
225                 230                 235                 240

Asn Phe Thr Leu Lys Gln Ser Ser Phe Val Gly Trp Trp Thr His Gln
                245                 250                 255

Arg Phe Val Glu Leu Val Val Val Val Asp Asn Ile Arg Tyr Leu Phe
            260                 265                 270

Ser Gln Ser Asn Ala Thr Thr Val Gln His Glu Val Phe Asn Val Val
        275                 280                 285

Asn Ile Val Asp Ser Phe Tyr His Pro Leu Glu Val Asp Val Ile Leu
    290                 295                 300

Thr Gly Ile Asp Ile Trp Thr Ala Ser Asn Pro Leu Pro Thr Ser Gly
305                 310                 315                 320

Asp Leu Asp Asn Val Leu Glu Asp Phe Ser Ile Trp Lys Asn Tyr Asn
                325                 330                 335

Leu Asn Asn Arg Leu Gln His Asp Val Ala His Leu Phe Ile Lys Asp
            340                 345                 350

Thr Gln Gly Met Lys Leu Gly Val Ala Tyr Val Lys Gly Ile Cys Gln
        355                 360                 365

Asn Pro Phe Asn Thr Gly Val Asp Val Phe Glu Asp Asn Arg Leu Val
```

370 375 380

Val Phe Ala Ile Thr Leu Gly His Glu Leu Gly His Asn Leu Gly Met
385 390 395 400

Gln His Asp Thr Gln Trp Cys Val Cys Glu Leu Gln Trp Cys Ile Met
405 410 415

His Ala Tyr Arg Lys Val Thr Thr Lys Phe Ser Asn Cys Ser Tyr Ala
420 425 430

Gln Tyr Trp Asp Ser Thr Ile Ser Ser Gly Leu Cys Ile Gln Pro Pro
435 440 445

Pro Tyr Pro Gly Asn Ile Phe Arg Leu Lys Tyr Cys Gly Asn Leu Val
450 455 460

Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Thr Ile Arg Gln Cys Ala
465 470 475 480

Lys Asp Pro Cys Cys Leu Leu Asn Cys Thr Leu His Pro Gly Ala Ala
485 490 495

Cys Ala Phe Gly Ile Cys Cys Lys Asp Cys Lys Phe Leu Pro Ser Gly
500 505 510

Thr Leu Cys Arg Gln Gln Val Gly Glu Cys Asp Leu Pro Glu Trp Cys
515 520 525

Asn Gly Thr Ser His Gln Cys Pro Asp Asp Val Tyr Val Gln Asp Gly
530 535 540

Ile Ser Cys Asn Val Asn Ala Phe Cys Tyr Glu Lys Thr Cys Asn Asn
545 550 555 560

His Asp Ile Gln Cys Lys Glu Ile Phe Gly Gln Asp Ala Arg Ser Ala
565 570 575

Ser Gln Ser Cys Tyr Gln Glu Ile Asn Thr Gln Gly Asn Arg Phe Gly
580 585 590

His Cys Gly Ile Val Gly Thr Thr Tyr Val Lys Cys Trp Thr Pro Asp
595 600 605

```
Ile Met Cys Gly Arg Val Gln Cys Glu Asn Val Gly Val Ile Pro Asn
    610                 615                 620

Leu Ile Glu His Ser Thr Val Gln Gln Phe His Leu Asn Asp Thr Thr
625                 630                 635                 640

Cys Trp Gly Thr Asp Tyr His Leu Gly Met Ala Ile Pro Asp Ile Gly
                645                 650                 655

Glu Val Lys Asp Gly Thr Val Cys Gly Pro Glu Lys Ile Cys Ile Arg
            660                 665                 670

Lys Lys Cys Ala Ser Met Val His Leu Ser Gln Ala Cys Gln Pro Lys
        675                 680                 685

Thr Cys Asn Met Arg Gly Ile Cys Asn Asn Lys Gln His Cys His Cys
    690                 695                 700

Asn His Glu Trp Ala Pro Pro Tyr Cys Lys Asp Lys Gly Tyr Gly Gly
705                 710                 715                 720

Ser Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn
                725                 730                 735

Val Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu
            740                 745                 750

Val Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr
        755                 760                 765

Lys Ser Lys Glu Asp Glu Glu Gly
    770                 775


<210> 2184
<211> 722
<212> PRT
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<220>
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<223> /note="Gene Symbol: ADAM21; "

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ADAM metallopeptidase domain 21; "

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<223> /note="Uniprot ID: Q9UKJ8; "

<220>
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<400> 2184

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Met Ala Val Asp Gly Thr Leu Val Tyr Ile Arg Val Thr Leu Leu Leu
1               5                   10                  15

Leu Trp Leu Gly Val Phe Leu Ser Ile Ser Gly Tyr Cys Gln Ala Gly
            20                  25                  30

Pro Ser Gln His Phe Thr Ser Pro Glu Val Val Ile Pro Leu Lys Val
        35                  40                  45

Ile Ser Arg Gly Arg Ser Ala Lys Ala Pro Gly Trp Leu Ser Tyr Ser
    50                  55                  60

Leu Arg Phe Gly Gly Gln Lys His Val Val His Met Arg Val Lys Lys
65                  70                  75                  80

Leu Leu Val Ser Arg His Leu Pro Val Phe Thr Tyr Thr Asp Asp Arg
                85                  90                  95

Ala Leu Leu Glu Asp Gln Leu Phe Ile Pro Asp Asp Cys Tyr Tyr His
            100                 105                 110

Gly Tyr Val Glu Ala Ala Pro Glu Ser Leu Val Val Phe Ser Ala Cys
        115                 120                 125

Phe Gly Gly Phe Arg Gly Val Leu Lys Ile Ser Gly Leu Thr Tyr Glu
    130                 135                 140

Ile Glu Pro Ile Arg His Ser Ala Thr Phe Glu His Leu Val Tyr Lys
145                 150                 155                 160

Ile Asn Ser Asn Glu Thr Gln Phe Pro Ala Met Arg Cys Gly Leu Thr
```

```
                165                 170                 175

Glu Lys Glu Val Ala Arg Gln Gln Leu Glu Phe Glu Glu Ala Glu Asn
            180                 185                 190

Ser Ala Leu Glu Pro Lys Ser Ala Gly Asp Trp Trp Thr His Ala Trp
        195                 200                 205

Phe Leu Glu Leu Val Val Val Val Asn His Asp Phe Phe Ile Tyr Ser
    210                 215                 220

Gln Ser Asn Ile Ser Lys Val Gln Glu Asp Val Phe Leu Val Val Asn
225                 230                 235                 240

Ile Val Asp Ser Met Tyr Lys Gln Leu Gly Thr Tyr Ile Ile Leu Ile
                245                 250                 255

Gly Ile Glu Ile Trp Asn Gln Gly Asn Val Phe Pro Met Thr Ser Ile
            260                 265                 270

Glu Gln Val Leu Asn Asp Phe Ser Gln Trp Lys Gln Ile Ser Leu Ser
        275                 280                 285

Gln Leu Gln His Asp Ala Ala His Met Phe Ile Lys Asn Ser Leu Ile
    290                 295                 300

Ser Ile Leu Gly Leu Ala Tyr Val Ala Gly Ile Cys Arg Pro Pro Ile
305                 310                 315                 320

Asp Cys Gly Val Asp Asn Phe Gln Gly Asp Thr Trp Ser Leu Phe Ala
                325                 330                 335

Asn Thr Val Ala His Glu Leu Gly His Thr Leu Gly Met Gln His Asp
            340                 345                 350

Glu Glu Phe Cys Phe Cys Gly Glu Arg Gly Cys Ile Met Asn Thr Phe
        355                 360                 365

Arg Val Pro Ala Glu Lys Phe Thr Asn Cys Ser Tyr Ala Asp Phe Met
    370                 375                 380

Lys Thr Thr Leu Asn Gln Gly Ser Cys Leu His Asn Pro Pro Arg Leu
385                 390                 395                 400
```

```
Gly Glu Ile Phe Met Leu Lys Arg Cys Gly Asn Gly Val Val Glu Arg
                405                 410                 415

Glu Glu Gln Cys Asp Cys Gly Ser Val Gln Gln Cys Glu Gln Asp Ala
            420                 425                 430

Cys Cys Leu Leu Asn Cys Thr Leu Arg Pro Gly Ala Ala Cys Ala Phe
        435                 440                 445

Gly Leu Cys Cys Lys Asp Cys Lys Phe Met Pro Ser Gly Glu Leu Cys
    450                 455                 460

Arg Gln Glu Val Asn Glu Cys Asp Leu Pro Glu Trp Cys Asn Gly Thr
465                 470                 475                 480

Ser His Gln Cys Pro Glu Asp Arg Tyr Val Gln Asp Gly Ile Pro Cys
                485                 490                 495

Ser Asp Ser Ala Tyr Cys Tyr Gln Lys Arg Cys Asn Asn His Asp Gln
            500                 505                 510

His Cys Arg Glu Ile Phe Gly Lys Asp Ala Lys Ser Ala Ser Gln Asn
        515                 520                 525

Cys Tyr Lys Glu Ile Asn Ser Gln Gly Asn Arg Phe Gly His Cys Gly
    530                 535                 540

Ile Asn Gly Thr Thr Tyr Leu Lys Cys His Ile Ser Asp Val Phe Cys
545                 550                 555                 560

Gly Arg Val Gln Cys Glu Asn Val Arg Asp Ile Pro Leu Leu Gln Asp
                565                 570                 575

His Phe Thr Leu Gln His Thr His Ile Asn Gly Val Thr Cys Trp Gly
            580                 585                 590

Ile Asp Tyr His Leu Arg Met Asn Ile Ser Asp Ile Gly Glu Val Lys
        595                 600                 605

Asp Gly Thr Val Cys Gly Pro Gly Lys Ile Cys Ile His Lys Lys Cys
    610                 615                 620
```

```
Val Ser Leu Ser Val Leu Ser His Val Cys Leu Pro Glu Thr Cys Asn
625                 630                 635                 640

Met Lys Gly Ile Cys Asn Asn Lys His His Cys His Cys Gly Tyr Gly
                645                 650                 655

Trp Ser Pro Pro Tyr Cys Gln His Arg Gly Tyr Gly Gly Ser Ile Asp
            660                 665                 670

Ser Gly Pro Ala Ser Ala Lys Arg Gly Val Phe Leu Pro Leu Ile Val
        675                 680                 685

Ile Pro Ser Leu Ser Val Leu Thr Phe Leu Phe Thr Val Gly Leu Leu
    690                 695                 700

Met Tyr Leu Arg Gln Cys Ser Gly Pro Lys Glu Thr Lys Ala His Ser
705                 710                 715                 720

Ser Gly
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<210> 2185
<211> 906
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 22; "

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<223> /note="Uniprot ID: Q9P0K1; "

<220>
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<223> /note="ENSP ID: ENSP00000265727"

<400> 2185
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Met Gln Ala Ala Val Ala Val Ser Val Pro Phe Leu Leu Leu Cys Val
```

```
1               5                   10                  15

Leu Gly Thr Cys Pro Pro Ala Arg Cys Gly Gln Ala Gly Asp Ala Ser
            20                  25                  30

Leu Met Glu Leu Glu Lys Arg Lys Glu Asn Arg Phe Val Glu Arg Gln
        35                  40                  45

Ser Ile Val Pro Leu Arg Leu Ile Tyr Arg Ser Gly Gly Glu Asp Glu
    50                  55                  60

Ser Arg His Asp Ala Leu Asp Thr Arg Val Arg Gly Asp Leu Gly Gly
65                  70                  75                  80

Pro Gln Leu Thr His Val Asp Gln Ala Ser Phe Gln Val Asp Ala Phe
                85                  90                  95

Gly Thr Ser Phe Ile Leu Asp Val Val Leu Asn His Asp Leu Leu Ser
            100                 105                 110

Ser Glu Tyr Ile Glu Arg His Ile Glu His Gly Gly Lys Thr Val Glu
        115                 120                 125

Val Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly Asn
    130                 135                 140

Pro Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly Met
145                 150                 155                 160

Phe Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn Asp
                165                 170                 175

Thr Thr Gln Glu Asp Phe His Phe His Ser Val Tyr Lys Ser Arg Leu
            180                 185                 190

Phe Glu Phe Ser Leu Asp Asp Leu Pro Ser Glu Phe Gln Gln Val Asn
        195                 200                 205

Ile Thr Pro Ser Lys Phe Ile Leu Lys Pro Arg Pro Lys Arg Ser Lys
    210                 215                 220

Arg Gln Leu Arg Arg Tyr Pro Arg Asn Val Glu Glu Glu Thr Lys Tyr
225                 230                 235                 240
```

```
Ile Glu Leu Met Ile Val Asn Asp His Leu Met Phe Lys Lys His Arg
                245                 250                 255

Leu Ser Val Val His Thr Asn Thr Tyr Ala Lys Ser Val Val Asn Met
            260                 265                 270

Ala Asp Leu Ile Tyr Lys Asp Gln Leu Lys Thr Arg Ile Val Leu Val
        275                 280                 285

Ala Met Glu Thr Trp Ala Thr Asp Asn Lys Phe Ala Ile Ser Glu Asn
    290                 295                 300

Pro Leu Ile Thr Leu Arg Glu Phe Met Lys Tyr Arg Arg Asp Phe Ile
305                 310                 315                 320

Lys Glu Lys Ser Asp Ala Val His Leu Phe Ser Gly Ser Gln Phe Glu
                325                 330                 335

Ser Ser Arg Ser Gly Ala Ala Tyr Ile Gly Gly Ile Cys Ser Leu Leu
            340                 345                 350

Lys Gly Gly Gly Val Asn Glu Phe Gly Lys Thr Asp Leu Met Ala Val
        355                 360                 365

Thr Leu Ala Gln Ser Leu Ala His Asn Ile Gly Ile Ile Ser Asp Lys
    370                 375                 380

Arg Lys Leu Ala Ser Gly Glu Cys Lys Cys Glu Asp Thr Trp Ser Gly
385                 390                 395                 400

Cys Ile Met Gly Asp Thr Gly Tyr Tyr Leu Pro Lys Lys Phe Thr Gln
                405                 410                 415

Cys Asn Ile Glu Glu Tyr His Asp Phe Leu Asn Ser Gly Gly Gly Ala
            420                 425                 430

Cys Leu Phe Asn Lys Pro Ser Lys Leu Leu Asp Pro Pro Glu Cys Gly
        435                 440                 445

Asn Gly Phe Ile Glu Thr Gly Glu Glu Cys Asp Cys Gly Thr Pro Ala
    450                 455                 460
```

```
Glu Cys Val Leu Glu Gly Ala Glu Cys Cys Lys Lys Cys Thr Leu Thr
465                 470                 475                 480

Gln Asp Ser Gln Cys Ser Asp Gly Leu Cys Cys Lys Lys Cys Lys Phe
                485                 490                 495

Gln Pro Met Gly Thr Val Cys Arg Glu Ala Val Asn Asp Cys Asp Ile
            500                 505                 510

Arg Glu Thr Cys Ser Gly Asn Ser Ser Gln Cys Ala Pro Asn Ile His
        515                 520                 525

Lys Met Asp Gly Tyr Ser Cys Asp Gly Val Gln Gly Ile Cys Phe Gly
    530                 535                 540

Gly Arg Cys Lys Thr Arg Asp Arg Gln Cys Lys Tyr Ile Trp Gly Gln
545                 550                 555                 560

Lys Val Thr Ala Ser Asp Lys Tyr Cys Tyr Glu Lys Leu Asn Ile Glu
                565                 570                 575

Gly Thr Glu Lys Gly Asn Cys Gly Lys Asp Lys Asp Thr Trp Ile Gln
            580                 585                 590

Cys Asn Lys Arg Asp Val Leu Cys Gly Tyr Leu Leu Cys Thr Asn Ile
        595                 600                 605

Gly Asn Ile Pro Arg Leu Gly Glu Leu Asp Gly Glu Ile Thr Ser Thr
    610                 615                 620

Leu Val Val Gln Gln Gly Arg Thr Leu Asn Cys Ser Gly Gly His Val
625                 630                 635                 640

Lys Leu Glu Glu Asp Val Asp Leu Gly Tyr Val Glu Asp Gly Thr Pro
                645                 650                 655

Cys Gly Pro Gln Met Met Cys Leu Glu His Arg Cys Leu Pro Val Ala
            660                 665                 670

Ser Phe Asn Phe Ser Thr Cys Leu Ser Ser Lys Glu Gly Thr Ile Cys
        675                 680                 685
```

```
Ser Gly Asn Gly Val Cys Ser Asn Glu Leu Lys Cys Val Cys Asn Arg
    690                 695                 700

His Trp Ile Gly Ser Asp Cys Asn Thr Tyr Phe Pro His Asn Asp Asp
705                 710                 715                 720

Ala Lys Thr Gly Ile Thr Leu Ser Gly Asn Gly Val Ala Gly Thr Asn
                725                 730                 735

Ile Ile Ile Gly Ile Ile Ala Gly Thr Ile Leu Val Leu Ala Leu Ile
            740                 745                 750

Leu Gly Ile Thr Ala Trp Gly Tyr Lys Asn Tyr Arg Glu Gln Arg Gln
        755                 760                 765

Leu Pro Gln Gly Asp Tyr Val Lys Lys Pro Gly Asp Gly Asp Ser Phe
    770                 775                 780

Tyr Ser Asp Ile Pro Pro Gly Val Ser Thr Asn Ser Ala Ser Ser Ser
785                 790                 795                 800

Lys Lys Arg Ser Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile Pro
                805                 810                 815

Asp Thr Lys His Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg Ser
            820                 825                 830

Asn Ser Trp Gln Gly Asn Leu Gly Gly Asn Lys Lys Lys Ile Arg Gly
        835                 840                 845

Lys Arg Phe Arg Pro Arg Ser Asn Ser Thr Glu Thr Leu Ser Pro Ala
    850                 855                 860

Lys Ser Pro Ser Ser Ser Thr Gly Ser Ile Ala Ser Ser Arg Lys Tyr
865                 870                 875                 880

Pro Tyr Pro Met Pro Pro Leu Pro Asp Glu Asp Lys Lys Val Asn Arg
                885                 890                 895

Gln Ser Ala Arg Leu Trp Glu Thr Ser Ile
            900                 905
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<210> 2186

<211> 859
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
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<223> /note="Uniprot ID: Q9P0K1; "

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<400> 2186

Met	Gln	Ala	Ala	Val	Ala	Val	Ser	Val	Pro	Phe	Leu	Leu	Leu	Cys	Val
1				5					10					15	

Leu	Gly	Thr	Cys	Pro	Pro	Ala	Arg	Cys	Gly	Gln	Ala	Gly	Asp	Ala	Ser
			20					25					30		

Leu	Met	Glu	Leu	Glu	Lys	Arg	Lys	Glu	Asn	Arg	Phe	Val	Glu	Arg	Gln
		35					40					45			

Ser	Ile	Val	Pro	Leu	Arg	Leu	Ile	Tyr	Arg	Ser	Gly	Gly	Glu	Asp	Glu
	50					55					60				

Ser	Arg	His	Asp	Ala	Leu	Asp	Thr	Arg	Val	Arg	Gly	Asp	Leu	Gly	Gly
65				70					75					80	

Pro	Gln	Leu	Thr	His	Val	Asp	Gln	Ala	Ser	Phe	Gln	Val	Asp	Ala	Phe
				85					90					95	

Gly	Thr	Ser	Phe	Ile	Leu	Asp	Val	Val	Leu	Asn	His	Asp	Leu	Leu	Ser
			100					105					110		

Ser	Glu	Tyr	Ile	Glu	Arg	His	Ile	Glu	His	Gly	Gly	Lys	Thr	Val	Glu
		115					120					125			

```
Val Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly Asn
    130                 135                 140

Pro Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly Met
145                 150                 155                 160

Phe Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn Asp
                165                 170                 175

Thr Thr Gln Glu Asp Phe His Phe His Ser Val Tyr Lys Ser Arg Leu
            180                 185                 190

Phe Glu Phe Ser Leu Asp Asp Leu Pro Ser Glu Phe Gln Gln Val Asn
        195                 200                 205

Ile Thr Pro Ser Lys Phe Ile Leu Lys Pro Arg Pro Lys Arg Ser Lys
    210                 215                 220

Arg Gln Leu Arg Arg Tyr Pro Arg Asn Val Glu Glu Glu Thr Lys Tyr
225                 230                 235                 240

Ile Glu Leu Met Ile Val Asn Asp His Leu Met Phe Lys Lys His Arg
                245                 250                 255

Leu Ser Val Val His Thr Asn Thr Tyr Ala Lys Ser Val Val Asn Met
            260                 265                 270

Ala Asp Leu Ile Tyr Lys Asp Gln Leu Lys Thr Arg Ile Val Leu Val
        275                 280                 285

Ala Met Glu Thr Trp Ala Thr Asp Asn Lys Phe Ala Ile Ser Glu Asn
    290                 295                 300

Pro Leu Ile Thr Leu Arg Glu Phe Met Lys Tyr Arg Arg Asp Phe Ile
305                 310                 315                 320

Lys Glu Lys Ser Asp Ala Val His Leu Phe Ser Gly Ser Gln Phe Glu
                325                 330                 335

Ser Ser Arg Ser Gly Ala Ala Tyr Ile Gly Gly Ile Cys Ser Leu Leu
            340                 345                 350
```

```
Lys Gly Gly Gly Val Asn Glu Phe Gly Lys Thr Asp Leu Met Ala Val
        355                 360                 365

Thr Leu Ala Gln Ser Leu Ala His Asn Ile Gly Ile Ile Ser Asp Lys
    370                 375                 380

Arg Lys Leu Ala Ser Gly Glu Cys Lys Cys Glu Asp Thr Trp Ser Gly
385                 390                 395                 400

Cys Ile Met Gly Asp Thr Gly Tyr Tyr Leu Pro Lys Lys Phe Thr Gln
                405                 410                 415

Cys Asn Ile Glu Glu Tyr His Asp Phe Leu Asn Ser Gly Gly Gly Ala
            420                 425                 430

Cys Leu Phe Asn Lys Pro Ser Lys Leu Leu Asp Pro Pro Glu Cys Gly
        435                 440                 445

Asn Gly Phe Ile Glu Thr Gly Glu Glu Cys Asp Cys Gly Thr Pro Ala
    450                 455                 460

Glu Cys Val Leu Glu Gly Ala Glu Cys Cys Lys Lys Cys Thr Leu Thr
465                 470                 475                 480

Gln Asp Ser Gln Cys Ser Asp Gly Leu Cys Cys Lys Lys Cys Lys Phe
                485                 490                 495

Gln Pro Met Gly Thr Val Cys Arg Glu Ala Val Asn Asp Cys Asp Ile
            500                 505                 510

Arg Glu Thr Cys Ser Gly Asn Ser Ser Gln Cys Ala Pro Asn Ile His
        515                 520                 525

Lys Met Asp Gly Tyr Ser Cys Asp Gly Val Gln Gly Ile Cys Phe Gly
    530                 535                 540

Gly Arg Cys Lys Thr Arg Asp Arg Gln Cys Lys Tyr Ile Trp Gly Gln
545                 550                 555                 560

Lys Val Thr Ala Ser Asp Lys Tyr Cys Tyr Glu Lys Leu Asn Ile Glu
                565                 570                 575

Gly Thr Glu Lys Gly Asn Cys Gly Lys Asp Lys Asp Thr Trp Ile Gln
```

580 585 590

Cys Asn Lys Arg Asp Val Leu Cys Gly Tyr Leu Leu Cys Thr Asn Ile
595 600 605

Gly Asn Ile Pro Arg Leu Gly Glu Leu Asp Gly Glu Ile Thr Ser Thr
610 615 620

Leu Val Val Gln Gln Gly Arg Thr Leu Asn Cys Ser Gly Gly His Val
625 630 635 640

Lys Leu Glu Glu Asp Val Asp Leu Gly Tyr Val Glu Asp Gly Thr Pro
645 650 655

Cys Gly Pro Gln Met Met Cys Leu Glu His Arg Cys Leu Pro Val Ala
660 665 670

Ser Phe Asn Phe Ser Thr Cys Leu Ser Ser Lys Glu Gly Thr Ile Cys
675 680 685

Ser Gly Asn Gly Val Cys Ser Asn Glu Leu Lys Cys Val Cys Asn Arg
690 695 700

His Trp Ile Gly Ser Asp Cys Asn Thr Tyr Phe Pro His Asn Asp Asp
705 710 715 720

Ala Lys Thr Gly Ile Thr Leu Ser Gly Asn Gly Val Ala Gly Thr Asn
725 730 735

Ile Ile Ile Gly Ile Ile Ala Gly Thr Ile Leu Val Leu Ala Leu Ile
740 745 750

Leu Gly Ile Thr Ala Trp Gly Tyr Lys Asn Tyr Arg Glu Gln Arg Gln
755 760 765

Leu Pro Gln Gly Asp Tyr Val Lys Lys Pro Gly Asp Gly Asp Ser Phe
770 775 780

Tyr Ser Asp Ile Pro Pro Gly Val Ser Thr Asn Ser Ala Ser Ser Ser
785 790 795 800

Lys Lys Arg Ser Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile Pro
805 810 815

```
Asp Thr Lys His Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg Ser
            820                 825                 830

Asn Ser Trp Gln Gly Asn Leu Gly Gly Asn Lys Lys Lys Ile Arg Gly
        835                 840                 845

Lys Arg Phe Arg Pro Arg Ser Asn Ser Thr Glu
    850                 855


<210> 2187
<211> 804
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 546; "

<220>
<221> source
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 22; "

<220>
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<223> /note="ENSP ID: ENSP00000381261"

<400> 2187
Met Glu Leu Glu Lys Arg Lys Glu Asn Arg Phe Val Glu Arg Gln Ser
1               5                   10                  15

Ile Val Pro Leu Arg Leu Ile Tyr Arg Ser Gly Gly Glu Asp Glu Ser
            20                  25                  30

Arg His Asp Ala Leu Asp Thr Arg Val Arg Gly Asp Leu Gly Gly Pro
        35                  40                  45

Gln Leu Thr His Val Asp Gln Ala Ser Phe Gln Val Asp Ala Phe Gly
    50                  55                  60

Thr Ser Phe Ile Leu Asp Val Val Leu Asn His Asp Leu Leu Ser Ser
65                  70                  75                  80
```

```
Glu Tyr Ile Glu Arg His Ile Glu His Gly Gly Lys Thr Val Glu Val
                85                  90                  95

Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly Asn Pro
            100                 105                 110

Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly Met Phe
        115                 120                 125

Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn Asp Thr
    130                 135                 140

Thr Gln Glu Asp Phe His Phe His Ser Val Tyr Lys Ser Arg Leu Phe
145                 150                 155                 160

Glu Phe Ser Leu Asp Asp Leu Pro Ser Glu Phe Gln Gln Val Asn Ile
                165                 170                 175

Thr Pro Ser Lys Phe Ile Leu Lys Pro Arg Pro Lys Arg Ser Lys Arg
            180                 185                 190

Gln Leu Arg Arg Tyr Pro Arg Asn Val Glu Glu Glu Thr Lys Tyr Ile
        195                 200                 205

Glu Leu Met Ile Val Asn Asp His Leu Met Phe Lys Lys His Arg Leu
    210                 215                 220

Ser Val Val His Thr Asn Thr Tyr Ala Lys Ser Val Val Asn Met Ala
225                 230                 235                 240

Asp Leu Ile Tyr Lys Asp Gln Leu Lys Thr Arg Ile Val Leu Val Ala
                245                 250                 255

Met Glu Thr Trp Ala Thr Asp Asn Lys Phe Ala Ile Ser Glu Asn Pro
            260                 265                 270

Leu Ile Thr Leu Arg Glu Phe Met Lys Tyr Arg Arg Asp Phe Ile Lys
        275                 280                 285

Glu Lys Ser Asp Ala Val His Leu Phe Ser Gly Ser Gln Phe Glu Ser
    290                 295                 300

Ser Arg Ser Gly Ala Ala Tyr Ile Gly Gly Ile Cys Ser Leu Leu Lys
```

```
305                 310                 315                 320

Gly Gly Gly Val Asn Glu Phe Gly Lys Thr Asp Leu Met Ala Val Thr
                325                 330                 335

Leu Ala Gln Ser Leu Ala His Asn Ile Gly Ile Ile Ser Asp Lys Arg
            340                 345                 350

Lys Leu Ala Ser Gly Glu Cys Lys Cys Glu Asp Thr Trp Ser Gly Cys
        355                 360                 365

Ile Met Gly Asp Thr Gly Tyr Tyr Leu Pro Lys Lys Phe Thr Gln Cys
    370                 375                 380

Asn Ile Glu Glu Tyr His Asp Phe Leu Asn Ser Gly Gly Gly Ala Cys
385                 390                 395                 400

Leu Phe Asn Lys Pro Ser Lys Leu Leu Asp Pro Pro Glu Cys Gly Asn
                405                 410                 415

Gly Phe Ile Glu Thr Gly Glu Glu Cys Asp Cys Gly Thr Pro Ala Glu
            420                 425                 430

Cys Val Leu Glu Gly Ala Glu Cys Cys Lys Lys Cys Thr Leu Thr Gln
        435                 440                 445

Asp Ser Gln Cys Ser Asp Gly Leu Cys Cys Lys Lys Cys Lys Phe Gln
    450                 455                 460

Pro Met Gly Thr Val Cys Arg Glu Ala Val Asn Asp Cys Asp Ile Arg
465                 470                 475                 480

Glu Thr Cys Ser Gly Asn Ser Ser Gln Cys Ala Pro Asn Ile His Lys
                485                 490                 495

Met Asp Gly Tyr Ser Cys Asp Gly Val Gln Gly Ile Cys Phe Gly Gly
            500                 505                 510

Arg Cys Lys Thr Arg Asp Arg Gln Cys Lys Tyr Ile Trp Gly Gln Lys
        515                 520                 525

Val Thr Ala Ser Asp Lys Tyr Cys Tyr Glu Lys Leu Asn Ile Glu Gly
    530                 535                 540
```

```
Thr Glu Lys Gly Asn Cys Gly Lys Asp Lys Asp Thr Trp Ile Gln Cys
545                 550                 555                 560

Asn Lys Arg Asp Val Leu Cys Gly Tyr Leu Leu Cys Thr Asn Ile Gly
                565                 570                 575

Asn Ile Pro Arg Leu Gly Glu Leu Asp Gly Glu Ile Thr Ser Thr Leu
            580                 585                 590

Val Val Gln Gln Gly Arg Thr Leu Asn Cys Ser Gly Gly His Val Lys
        595                 600                 605

Leu Glu Glu Asp Val Asp Leu Gly Tyr Val Glu Asp Gly Thr Pro Cys
    610                 615                 620

Gly Pro Gln Met Met Cys Leu Glu His Arg Cys Leu Pro Val Ala Ser
625                 630                 635                 640

Phe Asn Phe Ser Thr Cys Leu Ser Ser Lys Glu Gly Thr Ile Cys Ser
                645                 650                 655

Gly Asn Gly Val Cys Ser Asn Glu Leu Lys Cys Val Cys Asn Arg His
            660                 665                 670

Trp Ile Gly Ser Asp Cys Asn Thr Tyr Phe Pro His Asn Asp Asp Ala
        675                 680                 685

Lys Thr Gly Ile Thr Leu Ser Gly Asn Gly Val Ala Gly Thr Asn Ile
    690                 695                 700

Ile Ile Gly Ile Ile Ala Gly Thr Ile Leu Val Leu Ala Leu Ile Leu
705                 710                 715                 720

Gly Ile Thr Ala Trp Gly Tyr Lys Asn Tyr Arg Glu Gln Arg Gln Leu
                725                 730                 735

Pro Gln Gly Asp Tyr Val Lys Lys Pro Gly Asp Gly Asp Ser Phe Tyr
            740                 745                 750

Ser Asp Ile Pro Pro Gly Val Ser Thr Asn Ser Ala Ser Ser Ser Lys
        755                 760                 765
```

Lys Arg Ser Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile Pro Asp
    770   775   780

Thr Lys His Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg Ser Asn
785   790   795   800

Ser Trp Gln Gly

<210> 2188
<211> 870
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 546; "

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      ADAM metallopeptidase domain 22; "

<220>
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<223> /note="Uniprot ID: Q9P0K1; "

<220>
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<223> /note="ENSP ID: ENSP00000381262"

<400> 2188
Met Gln Ala Ala Val Ala Val Ser Val Pro Phe Leu Leu Leu Cys Val
1   5   10   15

Leu Gly Thr Cys Pro Pro Ala Arg Cys Gly Gln Ala Gly Asp Ala Ser
            20   25   30

Leu Met Glu Leu Glu Lys Arg Lys Glu Asn Arg Phe Val Glu Arg Gln
        35   40   45

Ser Ile Val Pro Leu Arg Leu Ile Tyr Arg Ser Gly Gly Glu Asp Glu
    50   55   60

Ser Arg His Asp Ala Leu Asp Thr Arg Val Arg Gly Asp Leu Gly Gly

65 70 75 80

Pro Gln Leu Thr His Val Asp Gln Ala Ser Phe Gln Val Asp Ala Phe
85 90 95

Gly Thr Ser Phe Ile Leu Asp Val Val Leu Asn His Asp Leu Leu Ser
100 105 110

Ser Glu Tyr Ile Glu Arg His Ile Glu His Gly Gly Lys Thr Val Glu
115 120 125

Val Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly Asn
130 135 140

Pro Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly Met
145 150 155 160

Phe Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn Asp
165 170 175

Thr Thr Gln Glu Asp Phe His Phe His Ser Val Tyr Lys Ser Arg Leu
180 185 190

Phe Glu Phe Ser Leu Asp Asp Leu Pro Ser Glu Phe Gln Gln Val Asn
195 200 205

Ile Thr Pro Ser Lys Phe Ile Leu Lys Pro Arg Pro Lys Arg Ser Lys
210 215 220

Arg Gln Leu Arg Arg Tyr Pro Arg Asn Val Glu Glu Glu Thr Lys Tyr
225 230 235 240

Ile Glu Leu Met Ile Val Asn Asp His Leu Met Phe Lys Lys His Arg
245 250 255

Leu Ser Val Val His Thr Asn Thr Tyr Ala Lys Ser Val Val Asn Met
260 265 270

Ala Asp Leu Ile Tyr Lys Asp Gln Leu Lys Thr Arg Ile Val Leu Val
275 280 285

Ala Met Glu Thr Trp Ala Thr Asp Asn Lys Phe Ala Ile Ser Glu Asn
290 295 300

```
Pro Leu Ile Thr Leu Arg Glu Phe Met Lys Tyr Arg Arg Asp Phe Ile
305                 310                 315                 320

Lys Glu Lys Ser Asp Ala Val His Leu Phe Ser Gly Ser Gln Phe Glu
                325                 330                 335

Ser Ser Arg Ser Gly Ala Ala Tyr Ile Gly Gly Ile Cys Ser Leu Leu
            340                 345                 350

Lys Gly Gly Gly Val Asn Glu Phe Gly Lys Thr Asp Leu Met Ala Val
        355                 360                 365

Thr Leu Ala Gln Ser Leu Ala His Asn Ile Gly Ile Ile Ser Asp Lys
    370                 375                 380

Arg Lys Leu Ala Ser Gly Glu Cys Lys Cys Glu Asp Thr Trp Ser Gly
385                 390                 395                 400

Cys Ile Met Gly Asp Thr Gly Tyr Tyr Leu Pro Lys Lys Phe Thr Gln
                405                 410                 415

Cys Asn Ile Glu Glu Tyr His Asp Phe Leu Asn Ser Gly Gly Gly Ala
            420                 425                 430

Cys Leu Phe Asn Lys Pro Ser Lys Leu Leu Asp Pro Pro Glu Cys Gly
        435                 440                 445

Asn Gly Phe Ile Glu Thr Gly Glu Glu Cys Asp Cys Gly Thr Pro Ala
    450                 455                 460

Glu Cys Val Leu Glu Gly Ala Glu Cys Cys Lys Lys Cys Thr Leu Thr
465                 470                 475                 480

Gln Asp Ser Gln Cys Ser Asp Gly Leu Cys Cys Lys Lys Cys Lys Phe
                485                 490                 495

Gln Pro Met Gly Thr Val Cys Arg Glu Ala Val Asn Asp Cys Asp Ile
            500                 505                 510

Arg Glu Thr Cys Ser Gly Asn Ser Ser Gln Cys Ala Pro Asn Ile His
        515                 520                 525
```

```
Lys Met Asp Gly Tyr Ser Cys Asp Gly Val Gln Gly Ile Cys Phe Gly
    530                 535                 540

Gly Arg Cys Lys Thr Arg Asp Arg Gln Cys Lys Tyr Ile Trp Gly Gln
545                 550                 555                 560

Lys Val Thr Ala Ser Asp Lys Tyr Cys Tyr Glu Lys Leu Asn Ile Glu
                565                 570                 575

Gly Thr Glu Lys Gly Asn Cys Gly Lys Asp Lys Asp Thr Trp Ile Gln
            580                 585                 590

Cys Asn Lys Arg Asp Val Leu Cys Gly Tyr Leu Leu Cys Thr Asn Ile
        595                 600                 605

Gly Asn Ile Pro Arg Leu Gly Glu Leu Asp Gly Glu Ile Thr Ser Thr
    610                 615                 620

Leu Val Val Gln Gln Gly Arg Thr Leu Asn Cys Ser Gly Gly His Val
625                 630                 635                 640

Lys Leu Glu Glu Asp Val Asp Leu Gly Tyr Val Glu Asp Gly Thr Pro
                645                 650                 655

Cys Gly Pro Gln Met Met Cys Leu Glu His Arg Cys Leu Pro Val Ala
            660                 665                 670

Ser Phe Asn Phe Ser Thr Cys Leu Ser Ser Lys Glu Gly Thr Ile Cys
        675                 680                 685

Ser Gly Asn Gly Val Cys Ser Asn Glu Leu Lys Cys Val Cys Asn Arg
    690                 695                 700

His Trp Ile Gly Ser Asp Cys Asn Thr Tyr Phe Pro His Asn Asp Asp
705                 710                 715                 720

Ala Lys Thr Gly Ile Thr Leu Ser Gly Asn Gly Val Ala Gly Thr Asn
                725                 730                 735

Ile Ile Ile Gly Ile Ile Ala Gly Thr Ile Leu Val Leu Ala Leu Ile
            740                 745                 750
```

```
Leu Gly Ile Thr Ala Trp Gly Tyr Lys Asn Tyr Arg Glu Gln Arg Ser
        755                 760                 765

Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile Pro Asp Thr Lys His
    770                 775                 780

Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg Ser Asn Ser Trp Gln
785                 790                 795                 800

Gly Asn Leu Gly Gly Asn Lys Lys Lys Ile Arg Gly Lys Arg Phe Arg
                805                 810                 815

Pro Arg Ser Asn Ser Thr Glu Thr Leu Ser Pro Ala Lys Ser Pro Ser
            820                 825                 830

Ser Ser Thr Gly Ser Ile Ala Ser Ser Arg Lys Tyr Pro Tyr Pro Met
        835                 840                 845

Pro Pro Leu Pro Asp Glu Asp Lys Lys Val Asn Arg Gln Ser Ala Arg
    850                 855                 860

Leu Trp Glu Thr Ser Ile
865                 870


<210> 2189
<211> 899
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID:  Q9P0K1; "

<220>
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<223> /note="ENSP ID: ENSP00000381267"
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<400> 2189
Met Gln Ala Ala Val Ala Val Ser Val Pro Phe Leu Leu Leu Cys Val
1 5 10 15

Leu Gly Thr Cys Pro Pro Ala Arg Cys Gly Gln Ala Gly Asp Ala Ser
20 25 30

Leu Met Glu Leu Glu Lys Arg Lys Glu Asn Arg Phe Val Glu Arg Gln
35 40 45

Ser Ile Val Pro Leu Arg Leu Ile Tyr Arg Ser Gly Gly Glu Asp Glu
50 55 60

Ser Arg His Asp Ala Leu Asp Thr Arg Val Arg Gly Asp Leu Gly Gly
65 70 75 80

Pro Gln Leu Thr His Val Asp Gln Ala Ser Phe Gln Val Asp Ala Phe
85 90 95

Gly Thr Ser Phe Ile Leu Asp Val Val Leu Asn His Asp Leu Leu Ser
100 105 110

Ser Glu Tyr Ile Glu Arg His Ile Glu His Gly Gly Lys Thr Val Glu
115 120 125

Val Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly Asn
130 135 140

Pro Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly Met
145 150 155 160

Phe Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn Asp
165 170 175

Thr Thr Gln Glu Asp Phe His Phe His Ser Val Tyr Lys Ser Arg Leu
180 185 190

Phe Glu Phe Ser Leu Asp Asp Leu Pro Ser Glu Phe Gln Gln Val Asn
195 200 205

Ile Thr Pro Ser Lys Phe Ile Leu Lys Pro Arg Pro Lys Arg Ser Lys
210 215 220

```
Arg Gln Leu Arg Arg Tyr Pro Arg Asn Val Glu Glu Glu Thr Lys Tyr
225                 230                 235                 240

Ile Glu Leu Met Ile Val Asn Asp His Leu Met Phe Lys Lys His Arg
                245                 250                 255

Leu Ser Val Val His Thr Asn Thr Tyr Ala Lys Ser Val Val Asn Met
            260                 265                 270

Ala Asp Leu Ile Tyr Lys Asp Gln Leu Lys Thr Arg Ile Val Leu Val
        275                 280                 285

Ala Met Glu Thr Trp Ala Thr Asp Asn Lys Phe Ala Ile Ser Glu Asn
    290                 295                 300

Pro Leu Ile Thr Leu Arg Glu Phe Met Lys Tyr Arg Arg Asp Phe Ile
305                 310                 315                 320

Lys Glu Lys Ser Asp Ala Val His Leu Phe Ser Gly Ser Gln Phe Glu
                325                 330                 335

Ser Ser Arg Ser Gly Ala Ala Tyr Ile Gly Gly Ile Cys Ser Leu Leu
            340                 345                 350

Lys Gly Gly Gly Val Asn Glu Phe Gly Lys Thr Asp Leu Met Ala Val
        355                 360                 365

Thr Leu Ala Gln Ser Leu Ala His Asn Ile Gly Ile Ile Ser Asp Lys
    370                 375                 380

Arg Lys Leu Ala Ser Gly Glu Cys Lys Cys Glu Asp Thr Trp Ser Gly
385                 390                 395                 400

Cys Ile Met Gly Asp Thr Gly Tyr Tyr Leu Pro Lys Lys Phe Thr Gln
                405                 410                 415

Cys Asn Ile Glu Glu Tyr His Asp Phe Leu Asn Ser Gly Gly Gly Ala
            420                 425                 430

Cys Leu Phe Asn Lys Pro Ser Lys Leu Leu Asp Pro Pro Glu Cys Gly
        435                 440                 445
```

```
Asn Gly Phe Ile Glu Thr Gly Glu Glu Cys Asp Cys Gly Thr Pro Ala
    450                 455                 460

Glu Cys Val Leu Glu Gly Ala Glu Cys Cys Lys Lys Cys Thr Leu Thr
465                 470                 475                 480

Gln Asp Ser Gln Cys Ser Asp Gly Leu Cys Cys Lys Lys Cys Lys Phe
                485                 490                 495

Gln Pro Met Gly Thr Val Cys Arg Glu Ala Val Asn Asp Cys Asp Ile
            500                 505                 510

Arg Glu Thr Cys Ser Gly Asn Ser Ser Gln Cys Ala Pro Asn Ile His
        515                 520                 525

Lys Met Asp Gly Tyr Ser Cys Asp Gly Val Gln Gly Ile Cys Phe Gly
    530                 535                 540

Gly Arg Cys Lys Thr Arg Asp Arg Gln Cys Lys Tyr Ile Trp Gly Gln
545                 550                 555                 560

Lys Val Thr Ala Ser Asp Lys Tyr Cys Tyr Glu Lys Leu Asn Ile Glu
                565                 570                 575

Gly Thr Glu Lys Gly Asn Cys Gly Lys Asp Lys Asp Thr Trp Ile Gln
            580                 585                 590

Cys Asn Lys Arg Asp Val Leu Cys Gly Tyr Leu Leu Cys Thr Asn Ile
        595                 600                 605

Gly Asn Ile Pro Arg Leu Gly Glu Leu Asp Gly Glu Ile Thr Ser Thr
    610                 615                 620

Leu Val Val Gln Gln Gly Arg Thr Leu Asn Cys Ser Gly Gly His Val
625                 630                 635                 640

Lys Leu Glu Glu Asp Val Asp Leu Gly Tyr Val Glu Asp Gly Thr Pro
                645                 650                 655

Cys Gly Pro Gln Met Met Cys Leu Glu His Arg Cys Leu Pro Val Ala
            660                 665                 670

Ser Phe Asn Phe Ser Thr Cys Leu Ser Ser Lys Glu Gly Thr Ile Cys
```

675 680 685

Ser Gly Asn Gly Val Cys Ser Asn Glu Leu Lys Cys Val Cys Asn Arg
690 695 700

His Trp Ile Gly Ser Asp Cys Asn Thr Tyr Phe Pro His Asn Asp Asp
705 710 715 720

Ala Lys Thr Gly Ile Thr Leu Ser Gly Asn Gly Val Ala Gly Thr Asn
725 730 735

Ile Ile Ile Gly Ile Ile Ala Gly Thr Ile Leu Val Leu Ala Leu Ile
740 745 750

Leu Gly Ile Thr Ala Trp Gly Tyr Lys Asn Tyr Arg Glu Gln Arg Ser
755 760 765

Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile Pro Asp Thr Lys His
770 775 780

Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg Ser Asn Ser Trp Gln
785 790 795 800

Gly Asn Leu Gly Gly Asn Lys Lys Lys Ile Arg Gly Lys Arg Phe Arg
805 810 815

Pro Arg Ser Asn Ser Thr Glu Tyr Leu Asn Pro Trp Phe Lys Arg Asp
820 825 830

Tyr Asn Val Ala Lys Trp Val Glu Asp Val Asn Lys Asn Thr Glu Gly
835 840 845

Pro Tyr Phe Arg Thr Leu Ser Pro Ala Lys Ser Pro Ser Ser Ser Thr
850 855 860

Gly Ser Ile Ala Ser Ser Arg Lys Tyr Pro Tyr Pro Met Pro Pro Leu
865 870 875 880

Pro Asp Glu Asp Lys Lys Val Asn Arg Gln Ser Ala Arg Leu Trp Glu
885 890 895

Thr Ser Ile

<210> 2190
<211> 342
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 546; "

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ADAM metallopeptidase domain 22; "

<220>
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<223> /note="ENSP ID: ENSP00000391334"

<400> 2190
Met Gln Ala Ala Val Ala Val Ser Val Pro Phe Leu Leu Leu Cys Val
1 5 10 15

Leu Gly Thr Cys Pro Pro Ala Arg Cys Gly Gln Ala Gly Asp Ala Ser
20 25 30

Leu Met Glu Leu Glu Lys Arg Lys Glu Asn Arg Phe Val Glu Arg Gln
35 40 45

Ser Ile Val Pro Leu Arg Leu Ile Tyr Arg Ser Gly Gly Glu Asp Glu
50 55 60

Ser Arg His Asp Ala Leu Asp Thr Arg Val Arg Gly Asp Leu Gly Gly
65 70 75 80

Pro Gln Leu Thr His Val Asp Gln Ala Ser Phe Gln Val Asp Ala Phe
85 90 95

Gly Thr Ser Phe Ile Leu Asp Val Val Leu Asn His Asp Leu Leu Ser
100 105 110

Ser Glu Tyr Ile Glu Arg His Ile Glu His Gly Gly Lys Thr Val Glu
115 120 125

```
Val Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly Asn
    130                 135                 140

Pro Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly Met
145                 150                 155                 160

Phe Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn Asp
                165                 170                 175

Thr Thr Gln Glu Asp Phe His Phe His Ser Val Tyr Lys Ser Arg Leu
            180                 185                 190

Phe Glu Phe Ser Leu Asp Asp Leu Pro Ser Glu Phe Gln Gln Val Asn
        195                 200                 205

Ile Thr Pro Ser Lys Phe Ile Leu Lys Pro Arg Pro Lys Arg Ser Lys
    210                 215                 220

Arg Gln Leu Arg Arg Tyr Pro Arg Asn Val Glu Glu Glu Thr Lys Tyr
225                 230                 235                 240

Ile Glu Leu Met Ile Val Asn Asp His Leu Met Phe Lys Lys His Arg
                245                 250                 255

Leu Ser Val Val His Thr Asn Thr Tyr Ala Lys Ser Val Val Asn Met
            260                 265                 270

Ala Asp Leu Ile Tyr Lys Asp Gln Leu Lys Thr Arg Ile Val Leu Val
        275                 280                 285

Ala Met Glu Thr Trp Ala Thr Asp Asn Lys Phe Ala Ile Ser Glu Asn
    290                 295                 300

Pro Leu Ile Thr Leu Arg Glu Phe Met Lys Tyr Arg Arg Asp Phe Ile
305                 310                 315                 320

Lys Glu Lys Ser Asp Ala Val His Leu Phe Ser Tyr Val Thr Ser Val
                325                 330                 335

Met Met Tyr Tyr Phe Phe
            340
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<210> 2191

<211> 330
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 22; "

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<400> 2191

Glu	Glu	Asp	Val	Asp	Leu	Gly	Tyr	Val	Glu	Asp	Gly	Thr	Pro	Cys	Gly
1				5				10					15		
Pro	Gln	Met	Met	Cys	Leu	Glu	His	Arg	Cys	Leu	Pro	Val	Ala	Ser	Phe
			20					25					30		
Asn	Phe	Ser	Thr	Cys	Leu	Ser	Ser	Lys	Glu	Gly	Thr	Ile	Cys	Ser	Gly
		35					40					45			
Asn	Gly	Val	Cys	Ser	Asn	Glu	Leu	Lys	Cys	Val	Cys	Asn	Arg	His	Trp
	50					55					60				
Ile	Gly	Ser	Asp	Cys	Asn	Thr	Tyr	Phe	Pro	His	Asn	Asp	Asp	Ala	Lys
65					70					75					80
Thr	Gly	Ile	Thr	Leu	Ser	Gly	Asn	Gly	Val	Ala	Gly	Thr	Asn	Ile	Ile
				85					90					95	
Ile	Gly	Ile	Ile	Ala	Gly	Thr	Ile	Leu	Val	Leu	Ala	Leu	Ile	Leu	Gly
			100					105					110		
Ile	Thr	Ala	Trp	Gly	Tyr	Lys	Asn	Tyr	Arg	Glu	Gln	Arg	Gln	Leu	Pro
		115					120					125			
Gln	Gly	Asp	Tyr	Val	Lys	Lys	Pro	Gly	Asp	Gly	Asp	Ser	Phe	Tyr	Ser
	130					135					140				

```
Asp Ile Pro Pro Gly Val Ser Thr Asn Ser Ala Ser Ser Ser Lys Lys
145                 150                 155                 160

Arg Ser Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile Pro Asp Thr
                165                 170                 175

Lys His Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg Ser Asn Ser
            180                 185                 190

Trp Gln Gly Asn Leu Gly Gly Asn Lys Lys Lys Ile Arg Gly Lys Arg
        195                 200                 205

Phe Arg Pro Arg Ser Asn Ser Thr Glu Arg Glu Pro Gln Ala Pro Glu
    210                 215                 220

Pro Gly His Ser Leu Ala Gln Thr Val Pro Ser Gln Gly Ile Ser Pro
225                 230                 235                 240

Gly Gly Ser Asp Ser Pro Gln Thr Gly Ser Leu Asp His Arg Tyr Leu
                245                 250                 255

Asn Pro Trp Phe Lys Arg Asp Tyr Asn Val Ala Lys Trp Val Glu Asp
            260                 265                 270

Val Asn Lys Asn Thr Glu Gly Pro Tyr Phe Arg Thr Leu Ser Pro Ala
        275                 280                 285

Lys Ser Pro Ser Ser Ser Thr Gly Ser Ile Ala Ser Ser Arg Lys Tyr
    290                 295                 300

Pro Tyr Pro Met Pro Pro Leu Pro Asp Glu Asp Lys Lys Val Asn Arg
305                 310                 315                 320

Gln Ser Ala Arg Leu Trp Glu Thr Ser Ile
                325                 330
```

<210> 2192
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Gene Name:
ADAM metallopeptidase domain 22; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000412085"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2192
Xaa Cys Asn Arg His Trp Ile Gly Ser Asp Cys Asn Thr Tyr Phe Pro
1 5 10 15

His Asn Asp Asp Ala Lys Thr Gly Ile Thr Leu Ser Gly Asn Gly Val
20 25 30

Ala Gly Thr Asn Ile Ile Ile Gly Ile Ile Ala Gly Thr Ile Leu Val
35 40 45

Leu Ala Leu Ile Leu Gly Ile Thr Ala Trp Gly Tyr Lys Asn Tyr Arg
50 55 60

Glu Gln Arg Gln Leu Pro Gln Gly Asp Tyr Val Lys Lys Pro Gly Asp
65 70 75 80

Gly Asp Ser Phe Tyr Ser Asp Ile Pro Pro Gly Val Ser Thr Asn Ser
85 90 95

Ala Ser Ser Ser Lys Lys Arg Ser Ala Phe Leu Ser His Phe Gln Ile
100 105 110

Ser Thr Cys Ser Ile Thr His Tyr Ser Ile Ser Gln Asn Ile Ser Leu
115 120 125

Phe Cys Ser Arg Ser Asn Gly Leu Ser His Ser Trp Ser Glu Arg Ile
130 135 140

```
Pro Asp Thr Lys His Ile Ser Asp Ile Cys Glu Asn Gly Arg Pro Arg
145                 150                 155                 160

Ser Asn Ser Trp Gln Gly Asn Leu Gly Gly Asn Lys Lys Lys Ile Arg
                165                 170                 175

Gly Lys Arg Phe Arg Pro Arg Ser Asn Ser Thr Glu Tyr Leu Asn Pro
            180                 185                 190

Trp Phe Lys Arg Asp Tyr Asn Val Ala Lys Trp Val Glu Asp Val Asn
        195                 200                 205

Lys Asn Thr Glu Gly Pro Tyr Phe Arg Thr Leu Ser Pro Ala Lys Ser
    210                 215                 220

Pro Ser Ser Ser Thr Gly Ser Ile Ala Ser Ser Arg Lys Tyr Pro Tyr
225                 230                 235                 240

Pro Met Pro Pro Leu Pro Asp Glu Asp Lys Lys Val Asn Arg Gln Ser
                245                 250                 255

Ala Arg Leu Trp Glu Thr Ser Ile
            260


<210> 2193
<211> 196
<212> PRT
<213> Homo sapiens

<220>
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      ADAM metallopeptidase domain 22; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000413899"

<400> 2193
Met Gln Ala Ala Val Ala Val Ser Val Pro Phe Leu Leu Leu Cys Val
1               5                   10                  15
```

```
Leu Gly Thr Cys Pro Pro Ala Arg Cys Gly Gln Ala Gly Asp Ala Ser
            20                  25                  30

Leu Met Glu Leu Glu Lys Arg Lys Glu Asn Arg Phe Val Glu Arg Gln
        35                  40                  45

Ser Ile Val Pro Leu Arg Leu Ile Tyr Arg Ser Gly Gly Glu Asp Glu
    50                  55                  60

Ser Arg His Asp Ala Leu Asp Thr Arg Val Arg Gly Asp Leu Gly Gly
65                  70                  75                  80

Pro Gln Ile Gln Met Phe Leu Lys Ser Glu Ser Gln Lys Thr Ile Tyr
                85                  90                  95

Gln Ile Gln Leu Thr His Val Asp Gln Ala Ser Phe Gln Val Asp Ala
            100                 105                 110

Phe Gly Thr Ser Phe Ile Leu Asp Val Val Leu Asn His Asp Leu Leu
        115                 120                 125

Ser Ser Glu Tyr Ile Glu Arg His Ile Glu His Gly Gly Lys Thr Val
    130                 135                 140

Glu Val Lys Gly Gly Glu His Cys Tyr Tyr Gln Gly His Ile Arg Gly
145                 150                 155                 160

Asn Pro Asp Ser Phe Val Ala Leu Ser Thr Cys His Gly Leu His Gly
                165                 170                 175

Met Phe Tyr Asp Gly Asn His Thr Tyr Leu Ile Glu Pro Glu Glu Asn
            180                 185                 190

Asp Thr Thr Gln
        195


<210> 2194
<211> 832
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 547; "

<220>
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<223> /note="Gene Symbol: ADAM23; "

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<223> /note="Gene Name:
ADAM metallopeptidase domain 23; "

<220>
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<223> /note="Uniprot ID: O75077; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000264377"

<400> 2194

```
Met Lys Pro Pro Gly Ser Ser Ser Arg Gln Pro Pro Leu Ala Gly Cys
1               5                   10                  15

Ser Leu Ala Gly Ala Ser Cys Gly Pro Gln Arg Gly Pro Ala Gly Ser
            20                  25                  30

Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu
        35                  40                  45

Val Leu Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala
    50                  55                  60

Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu
65                  70                  75                  80

Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn
                85                  90                  95

Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr
            100                 105                 110

Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro
        115                 120                 125

Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys
    130                 135                 140

Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser
```

145 150 155 160

Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp
165 170 175

Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly
180 185 190

Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser
195 200 205

Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp
210 215 220

Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu
225 230 235 240

Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln
245 250 255

Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp
260 265 270

Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val
275 280 285

Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met
290 295 300

Ile Val Asn Asp His Lys Thr Tyr Lys Lys His Arg Ser Ser His Ala
305 310 315 320

His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile
325 330 335

Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr
340 345 350

Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met
355 360 365

Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp
370 375 380

```
Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser
385                 390                 395                 400

Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val
                405                 410                 415

Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser
            420                 425                 430

Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro
        435                 440                 445

Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr
    450                 455                 460

Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr
465                 470                 475                 480

Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys Leu Phe Asn Arg Pro
                485                 490                 495

Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala
            500                 505                 510

Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys
        515                 520                 525

Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro
    530                 535                 540

Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys
545                 550                 555                 560

Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp
                565                 570                 575

Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys
            580                 585                 590

Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp
        595                 600                 605
```

```
Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys
    610                 615                 620

Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys
625                 630                 635                 640

Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe
                645                 650                 655

Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly
            660                 665                 670

Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg
        675                 680                 685

Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp
    690                 695                 700

Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys
705                 710                 715                 720

Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys
                725                 730                 735

Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser
            740                 745                 750

Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys
        755                 760                 765

Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly
    770                 775                 780

Pro Lys Gly Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly
785                 790                 795                 800

Ala Ile Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe
                805                 810                 815

Lys Asn Val Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile
            820                 825                 830
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<210> 2195
<211> 832
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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ADAM metallopeptidase domain 23; "

<220>
<221> source
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<400> 2195
Met Lys Pro Pro Gly Ser Ser Ser Arg Gln Pro Pro Leu Ala Gly Cys
1 5 10 15

Ser Leu Ala Gly Ala Ser Cys Gly Pro Gln Arg Gly Pro Ala Gly Ser
20 25 30

Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu
35 40 45

Val Leu Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala
50 55 60

Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu
65 70 75 80

Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn
85 90 95

Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr
100 105 110

Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro
115 120 125

Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys
130 135 140

```
Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser
145                 150                 155                 160

Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp
                165                 170                 175

Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly
            180                 185                 190

Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser
        195                 200                 205

Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp
    210                 215                 220

Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu
225                 230                 235                 240

Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln
                245                 250                 255

Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp
            260                 265                 270

Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val
        275                 280                 285

Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met
    290                 295                 300

Ile Val Asn Asp His Lys Thr Tyr Lys Lys His Arg Ser Ser His Ala
305                 310                 315                 320

His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile
                325                 330                 335

Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr
            340                 345                 350

Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met
        355                 360                 365
```

```
Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp
    370                 375                 380

Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser
385                 390                 395                 400

Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val
                405                 410                 415

Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser
            420                 425                 430

Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro
        435                 440                 445

Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr
    450                 455                 460

Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr
465                 470                 475                 480

Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys Leu Phe Asn Arg Pro
                485                 490                 495

Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala
            500                 505                 510

Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys
        515                 520                 525

Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro
    530                 535                 540

Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys
545                 550                 555                 560

Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp
                565                 570                 575

Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys
            580                 585                 590
```

```
Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp
        595                 600                 605

Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys
    610                 615                 620

Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys
625                 630                 635                 640

Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe
                645                 650                 655

Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly
            660                 665                 670

Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg
        675                 680                 685

Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp
    690                 695                 700

Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys
705                 710                 715                 720

Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys
                725                 730                 735

Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser
            740                 745                 750

Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys
        755                 760                 765

Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly
    770                 775                 780

Pro Lys Val Asn Met Ala Thr Ser Arg Leu Ile Gly Ala Val Ala Gly
785                 790                 795                 800

Thr Ile Leu Ala Leu Gly Val Ile Phe Gly Gly Thr Gly Trp Gly Ile
                805                 810                 815

Glu Asn Val Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile
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820 825 830

<210> 2196
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000406827"

<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 2196
Xaa Gln Ile Gln Ala Leu Asn Met Ser Ser Cys Pro Leu Asp Ser Lys
1 5 10 15

Gly Lys Val Cys Ser Gly His Gly Val Cys Ser Asn Glu Ala Thr Cys
20 25 30

Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys Ser Ile Arg Asp Pro
35 40 45

Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly Pro Lys Glu Met Ser
50 55 60

Arg Arg Glu Gly Ser Ile Leu Leu Ser Lys Ala Pro Ser Glu Ser Ala
65 70 75 80

Ala Leu Asp Gly His Arg Leu Ala Leu Leu Asp Ser Gly Tyr Asp Ile
85 90 95

Leu Ala Ala Val Leu Leu Glu Leu Leu Ser Leu

100 105

<210> 2197
<211> 775
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 548; "

<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 28; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKQ2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000265769"

<400> 2197
Met Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val
1 5 10 15

Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
20 25 30

Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
35 40 45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
50 55 60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
65 70 75 80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
85 90 95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu
100 105 110

```
Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg
        115                 120                 125

Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
    130                 135                 140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro
145                 150                 155                 160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
                165                 170                 175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
            180                 185                 190

Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr
        195                 200                 205

Tyr Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln
    210                 215                 220

Asp Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met
225                 230                 235                 240

Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile
                245                 250                 255

Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr
            260                 265                 270

Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys
        275                 280                 285

Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr
    290                 295                 300

Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val
305                 310                 315                 320

Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr
                325                 330                 335
```

```
Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr
            340                 345                 350

Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser
        355                 360                 365

Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp
    370                 375                 380

Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu
385                 390                 395                 400

Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu
                405                 410                 415

Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile
            420                 425                 430

Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala
        435                 440                 445

Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val
    450                 455                 460

Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly
465                 470                 475                 480

Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro
                485                 490                 495

Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu
            500                 505                 510

Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Thr Glu Val Ala Asp
        515                 520                 525

Lys Ser Cys Tyr Asn Arg Asn Glu Gly Gly Ser Lys Tyr Gly Tyr Cys
    530                 535                 540

Arg Arg Val Asp Asp Thr Leu Ile Pro Cys Lys Ala Asn Asp Thr Met
545                 550                 555                 560

Cys Gly Lys Leu Phe Cys Gln Gly Gly Ser Asp Asn Leu Pro Trp Lys
```

565 570 575

Gly Arg Ile Val Thr Phe Leu Thr Cys Lys Thr Phe Asp Pro Glu Asp
580 585 590

Thr Ser Gln Glu Ile Gly Met Val Ala Asn Gly Thr Lys Cys Gly Asp
595 600 605

Asn Lys Val Cys Ile Asn Ala Glu Cys Val Asp Ile Glu Lys Ala Tyr
610 615 620

Lys Ser Thr Asn Cys Ser Ser Lys Cys Lys Gly His Ala Val Cys Asp
625 630 635 640

His Glu Leu Gln Cys Gln Cys Glu Glu Gly Trp Ile Pro Pro Asp Cys
645 650 655

Asp Asp Ser Ser Val Val Phe His Phe Ser Ile Val Val Gly Val Leu
660 665 670

Phe Pro Met Ala Val Ile Phe Val Val Val Ala Met Val Ile Arg His
675 680 685

Gln Ser Ser Arg Glu Lys Gln Lys Lys Asp Gln Arg Pro Leu Ser Thr
690 695 700

Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val Lys
705 710 715 720

Ala Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr Asp
725 730 735

Leu Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Phe His Lys Asp Thr
740 745 750

Asn Ala Leu Pro Pro Thr Val Phe Lys Asp Asn Pro Val Ser Thr Pro
755 760 765

Lys Asp Ser Asn Pro Lys Ala
770 775

<210> 2198
<211> 540

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 548; "

<220>
<221> source
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 28; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKQ2; "

<220>
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<223> /note="ENSP ID: ENSP00000393699"

<400> 2198

Met	Leu	Gln	Gly	Leu	Leu	Pro	Val	Ser	Leu	Leu	Leu	Ser	Val	Ala	Val
1				5				10					15		
Ser	Ala	Ile	Lys	Glu	Leu	Pro	Gly	Val	Lys	Lys	Tyr	Glu	Val	Val	Tyr
			20					25				30			
Pro	Ile	Arg	Leu	His	Pro	Leu	His	Lys	Arg	Glu	Ala	Lys	Glu	Pro	Glu
		35					40					45			
Gln	Gln	Glu	Gln	Phe	Glu	Thr	Glu	Leu	Lys	Tyr	Lys	Met	Thr	Ile	Asn
	50					55					60				
Gly	Lys	Ile	Ala	Val	Leu	Tyr	Leu	Lys	Lys	Asn	Lys	Asn	Leu	Leu	Ala
65					70					75					80
Pro	Gly	Tyr	Thr	Glu	Thr	Tyr	Tyr	Asn	Ser	Thr	Gly	Lys	Glu	Ile	Thr
				85					90					95	
Thr	Ser	Pro	Gln	Ile	Met	Asp	Asp	Cys	Tyr	Tyr	Gln	Gly	His	Ile	Leu
			100					105					110		
Asn	Glu	Lys	Val	Ser	Asp	Ala	Ser	Ile	Ser	Thr	Cys	Arg	Gly	Leu	Arg
		115					120					125			

```
Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
    130                 135                 140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro
145                 150                 155                 160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
                165                 170                 175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
            180                 185                 190

Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr
        195                 200                 205

Tyr Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln
    210                 215                 220

Asp Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met
225                 230                 235                 240

Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile
                245                 250                 255

Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr
            260                 265                 270

Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys
        275                 280                 285

Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr
    290                 295                 300

Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val
305                 310                 315                 320

Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr
                325                 330                 335

Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr
            340                 345                 350

Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser
```

355 360 365

Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp
370 375 380

Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu
385 390 395 400

Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu
405 410 415

Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile
420 425 430

Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala
435 440 445

Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val
450 455 460

Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly
465 470 475 480

Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro
485 490 495

Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu
500 505 510

Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro
515 520 525

Phe Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg
530 535 540

<210> 2199
<211> 387
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 28; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429484"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2199

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Xaa Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr
1               5                  10                  15

Asp Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro
            20                  25                  30

Leu Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val
        35                  40                  45

Glu Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn
    50                  55                  60

Ile Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys
65                  70                  75                  80

Ala Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met
                85                  90                  95

Val Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn
            100                 105                 110

Gly Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe
        115                 120                 125

Pro Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr
    130                 135                 140

Leu Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Thr Glu Val Ala
145                 150                 155                 160
```

```
Asp Lys Ser Cys Tyr Asn Arg Asn Glu Gly Gly Ser Lys Tyr Gly Tyr
                 165                 170                 175

Cys Arg Arg Val Asp Asp Thr Leu Ile Pro Cys Lys Ala Asn Asp Thr
             180                 185                 190

Met Cys Gly Lys Leu Phe Cys Gln Gly Gly Ser Asp Asn Leu Pro Trp
         195                 200                 205

Lys Gly Arg Ile Val Thr Phe Leu Thr Cys Lys Thr Phe Asp Pro Glu
     210                 215                 220

Asp Thr Ser Gln Glu Ile Gly Met Val Ala Asn Gly Thr Lys Cys Gly
225                 230                 235                 240

Asp Asn Lys Val Cys Ile Asn Ala Glu Cys Val Asp Ile Glu Lys Ala
                 245                 250                 255

Tyr Lys Ser Thr Asn Cys Ser Ser Lys Cys Lys Gly His Ala Val Cys
             260                 265                 270

Asp His Glu Leu Gln Cys Gln Cys Glu Glu Gly Trp Ile Pro Pro Asp
         275                 280                 285

Cys Asp Asp Ser Ser Val Val Phe His Phe Ser Ile Val Val Gly Val
     290                 295                 300

Leu Phe Pro Met Ala Val Ile Phe Val Val Val Ala Met Val Ile Arg
305                 310                 315                 320

His Gln Ser Ser Arg Glu Lys Gln Lys Lys Asp Gln Arg Pro Leu Ser
                 325                 330                 335

Thr Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val
             340                 345                 350

Lys Ala Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr
         355                 360                 365

Asp Leu Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Phe Asp Ser Asn
     370                 375                 380
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Pro Lys Ala
385

<210> 2200
<211> 217
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ADAM28; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 28; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430085"

<400> 2200
Met Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val
1 5 10 15

Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
20 25 30

Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
35 40 45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
50 55 60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
65 70 75 80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
85 90 95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu
100 105 110

Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg

```
        115                 120                 125

Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
    130                 135                 140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro
145                 150                 155                 160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
                165                 170                 175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
            180                 185                 190

Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr
        195                 200                 205

Tyr Leu Val Leu Asp Asn Gly Glu Phe
    210                 215


<210> 2201
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 548; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM28; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 28; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430094"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2201
Xaa Lys Gly Arg Ile Val Thr Phe Leu Thr Cys Lys Thr Phe Asp Pro
```

```
1               5                   10                  15

Glu Asp Thr Ser Gln Glu Ile Gly Met Val Ala Asn Gly Thr Lys Cys
            20                  25                  30

Gly Asp Asn Lys Val Cys Ile Asn Ala Glu Cys Val Asp Ile Glu Lys
        35                  40                  45

Ala Tyr Lys Ser Thr Asn Cys Ser Ser Lys Cys Lys Gly His Ala Val
    50                  55                  60

Cys Asp His Glu Leu Gln Cys Gln Cys Glu Glu Gly Trp Ile Pro Pro
65                  70                  75                  80

Asp Cys Asp Asp Ser Ser Val Val Phe His Phe Ser Ile Val Val Gly
                85                  90                  95

Val Leu Phe Pro Met Ala Val Ile Phe Val Val Val Ala Met Val Ile
            100                 105                 110

Arg His Gln Ser Ser Arg Glu Lys Gln Lys Lys Asp Gln Arg Pro Leu
        115                 120                 125

Ser Thr Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met
    130                 135                 140

Val Lys Ala Val Gln Pro Gln Glu Val Asn Tyr Ile Val Trp Ala Val
145                 150                 155                 160

Ile Thr Met Ala Pro Leu Cys Val Ser Leu Thr Leu Leu Ser
                165                 170
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<210> 2202
<211> 58
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ADAM28; "

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<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 28; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431108"

<400> 2202
Met Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val
1 5 10 15

Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
20 25 30

Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
35 40 45

Gln Gln Phe Leu Ser Ser Met Lys Ile Ser
50 55

<210> 2203
<211> 820
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 549; "

<220>
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<223> /note="Gene Symbol: ADAM29; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 29; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKF5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000352177"

<400> 2203
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp

```
            20                  25                  30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
        35                  40                  45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
    50                  55                  60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65                  70                  75                  80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
                85                  90                  95

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
            100                 105                 110

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
        115                 120                 125

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
    130                 135                 140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145                 150                 155                 160

Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
                165                 170                 175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
            180                 185                 190

Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
        195                 200                 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
    210                 215                 220

Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225                 230                 235                 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
                245                 250                 255
```

```
Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
            260                 265                 270

Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
        275                 280                 285

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
    290                 295                 300

Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
305                 310                 315                 320

Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
                325                 330                 335

Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
            340                 345                 350

Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
        355                 360                 365

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
    370                 375                 380

Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
385                 390                 395                 400

Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
                405                 410                 415

Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
            420                 425                 430

Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
        435                 440                 445

Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
    450                 455                 460

Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
465                 470                 475                 480
```

```
Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
                485                 490                 495

Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
            500                 505                 510

Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
        515                 520                 525

Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
    530                 535                 540

Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
545                 550                 555                 560

Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
                565                 570                 575

Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
            580                 585                 590

Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
        595                 600                 605

Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
    610                 615                 620

Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
625                 630                 635                 640

His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
                645                 650                 655

Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
            660                 665                 670

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
        675                 680                 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
    690                 695                 700
```

```
Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
705                 710                 715                 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
                725                 730                 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
            740                 745                 750

Gln Val Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser
        755                 760                 765

Gln Pro Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
    770                 775                 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785                 790                 795                 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
                805                 810                 815

Val Thr Pro Ser
            820
```

<210> 2204
<211> 820
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 549; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM29; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 29; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKF5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000384229"

<400> 2204
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
20 25 30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
35 40 45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
50 55 60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65 70 75 80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
85 90 95

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
100 105 110

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
115 120 125

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
130 135 140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145 150 155 160

Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
165 170 175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
180 185 190

Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
195 200 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
210 215 220

```
Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225                 230                 235                 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
                245                 250                 255

Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
            260                 265                 270

Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
        275                 280                 285

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
    290                 295                 300

Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
305                 310                 315                 320

Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
                325                 330                 335

Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
            340                 345                 350

Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
        355                 360                 365

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
    370                 375                 380

Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
385                 390                 395                 400

Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
                405                 410                 415

Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
            420                 425                 430

Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
        435                 440                 445
```

```
Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
    450                 455                 460

Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
465                 470                 475                 480

Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
                485                 490                 495

Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
            500                 505                 510

Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
        515                 520                 525

Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
    530                 535                 540

Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
545                 550                 555                 560

Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
                565                 570                 575

Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
            580                 585                 590

Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
        595                 600                 605

Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
    610                 615                 620

Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
625                 630                 635                 640

His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
                645                 650                 655

Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
            660                 665                 670

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
```

675 680 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
690 695 700

Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
705 710 715 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
725 730 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
740 745 750

Gln Val Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser
755 760 765

Gln Pro Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
770 775 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785 790 795 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
805 810 815

Val Thr Pro Ser
820

<210> 2205
<211> 820
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 549; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM29; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 29; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKF5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000414544"

<400> 2205
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1   5   10   15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
            20   25   30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
        35   40   45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
    50   55   60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65   70   75   80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
                85   90   95

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
            100   105   110

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
        115   120   125

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
    130   135   140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145   150   155   160

Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
                165   170   175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
            180   185   190

```
Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
        195                 200                 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
    210                 215                 220

Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225                 230                 235                 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
                245                 250                 255

Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
            260                 265                 270

Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
        275                 280                 285

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
    290                 295                 300

Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
305                 310                 315                 320

Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
                325                 330                 335

Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
            340                 345                 350

Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
        355                 360                 365

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
    370                 375                 380

Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
385                 390                 395                 400

Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
                405                 410                 415

Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
```

```
            420                 425                 430

Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
        435                 440                 445

Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
    450                 455                 460

Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
465                 470                 475                 480

Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
                485                 490                 495

Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
            500                 505                 510

Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
        515                 520                 525

Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
    530                 535                 540

Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
545                 550                 555                 560

Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
                565                 570                 575

Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
            580                 585                 590

Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
        595                 600                 605

Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
    610                 615                 620

Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
625                 630                 635                 640

His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
                645                 650                 655
```

```
Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
            660                 665                 670

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
        675                 680                 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
    690                 695                 700

Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
705                 710                 715                 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
                725                 730                 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
            740                 745                 750

Gln Val Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser
        755                 760                 765

Gln Pro Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
    770                 775                 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785                 790                 795                 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
                805                 810                 815

Val Thr Pro Ser
            820
```

<210> 2206
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 549; "

<220>
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<223> /note="Gene Symbol: ADAM29; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 29; "

<220>
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<223> /note="ENSP ID: ENSP00000422537"

<400> 2206
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
20 25 30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg
35 40

<210> 2207
<211> 820
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 549; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM29; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 29; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKF5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000423517"

<400> 2207
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
20 25 30

```
Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
        35                  40                  45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
    50                  55                  60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65                  70                  75                  80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
                85                  90                  95

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
            100                 105                 110

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
        115                 120                 125

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
    130                 135                 140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145                 150                 155                 160

Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
                165                 170                 175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
            180                 185                 190

Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
        195                 200                 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
    210                 215                 220

Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225                 230                 235                 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
                245                 250                 255
```

```
Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
            260                 265                 270

Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
        275                 280                 285

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
    290                 295                 300

Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
305                 310                 315                 320

Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
                325                 330                 335

Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
            340                 345                 350

Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
        355                 360                 365

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
    370                 375                 380

Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
385                 390                 395                 400

Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
                405                 410                 415

Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
            420                 425                 430

Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
        435                 440                 445

Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
    450                 455                 460

Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
465                 470                 475                 480
```

```
Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
                485                 490                 495

Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
            500                 505                 510

Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
        515                 520                 525

Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
    530                 535                 540

Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
545                 550                 555                 560

Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
                565                 570                 575

Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
            580                 585                 590

Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
        595                 600                 605

Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
    610                 615                 620

Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
625                 630                 635                 640

His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
                645                 650                 655

Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
            660                 665                 670

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
        675                 680                 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
    690                 695                 700

Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
```

705 710 715 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
725 730 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
740 745 750

Gln Val Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser
755 760 765

Gln Pro Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
770 775 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785 790 795 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
805 810 815

Val Thr Pro Ser
820

<210> 2208
<211> 14
<212> PRT
<213> Homo sapiens

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<400> 2208
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu
1 5 10

<210> 2209
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<400> 2209
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
20 25 30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
35 40 45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
50 55 60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65 70 75 80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile
85

<210> 2210
<211> 820
<212> PRT
<213> Homo sapiens

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<400> 2210
Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
20 25 30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
35 40 45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
50 55 60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65 70 75 80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
85 90 95

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
100 105 110

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
115 120 125

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
130 135 140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145 150 155 160

```
Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
                165                 170                 175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
            180                 185                 190

Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
        195                 200                 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
    210                 215                 220

Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225                 230                 235                 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
                245                 250                 255

Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
            260                 265                 270

Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
        275                 280                 285

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
    290                 295                 300

Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
305                 310                 315                 320

Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
                325                 330                 335

Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
            340                 345                 350

Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
        355                 360                 365

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
    370                 375                 380
```

```
Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
385                 390                 395                 400

Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
                405                 410                 415

Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
            420                 425                 430

Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
        435                 440                 445

Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
    450                 455                 460

Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
465                 470                 475                 480

Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
                485                 490                 495

Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
            500                 505                 510

Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
        515                 520                 525

Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
    530                 535                 540

Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
545                 550                 555                 560

Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
                565                 570                 575

Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
            580                 585                 590

Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
        595                 600                 605

Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
```

610 615 620

Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
625 630 635 640

His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
645 650 655

Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
660 665 670

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
675 680 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
690 695 700

Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
705 710 715 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
725 730 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
740 745 750

Gln Val Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser
755 760 765

Gln Pro Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
770 775 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785 790 795 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
805 810 815

Val Thr Pro Ser
820

<210> 2211
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<212> PRT
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<400> 2211

Met	Lys	Met	Leu	Leu	Leu	Leu	His	Cys	Leu	Gly	Val	Phe	Leu	Ser	Cys
1				5				10						15	

Ser	Gly	His	Ile	Gln	Asp	Glu	His	Pro	Gln	Tyr	His	Ser	Pro	Pro	Asp
			20					25					30		

Val	Val	Ile	Pro	Val	Arg	Ile	Thr	Gly	Thr	Thr	Arg	Gly	Met	Thr	Pro
		35					40					45			

Pro	Gly	Trp	Leu	Ser	Tyr	Ile	Leu	Pro	Phe	Gly	Gly	Gln	Lys	His	Ile
	50					55					60				

Ile	His	Ile	Lys	Val	Lys	Lys	Leu	Leu	Phe	Ser	Lys	His	Leu	Pro	Val
65					70					75					80

Phe	Thr	Tyr	Thr	Asp	Gln	Gly	Ala	Ile	Leu	Glu	Asp	Gln	Pro	Phe	Val
				85					90					95	

Gln	Asn	Asn	Cys	Tyr	Tyr	His	Gly	Tyr	Val	Glu	Gly	Asp	Pro	Glu	Ser
			100					105					110		

Leu	Val	Ser	Leu	Ser	Thr	Cys	Phe	Gly	Gly	Phe	Gln	Gly	Ile	Leu	Gln
		115					120					125			

```
Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
    130                 135                 140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145                 150                 155                 160

Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
                165                 170                 175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
            180                 185                 190

Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
        195                 200                 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
    210                 215                 220

Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225                 230                 235                 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
                245                 250                 255

Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
            260                 265                 270

Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
        275                 280                 285

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
    290                 295                 300

Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
305                 310                 315                 320

Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
                325                 330                 335

Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
            340                 345                 350

Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
```

```
        355                 360                 365

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
    370                 375                 380

Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
385                 390                 395                 400

Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
                405                 410                 415

Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
            420                 425                 430

Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
        435                 440                 445

Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
    450                 455                 460

Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
465                 470                 475                 480

Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
                485                 490                 495

Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
            500                 505                 510

Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
        515                 520                 525

Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
    530                 535                 540

Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
545                 550                 555                 560

Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
                565                 570                 575

Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
            580                 585                 590
```

```
Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
        595                 600                 605

Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
    610                 615                 620

Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
625                 630                 635                 640

His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
                645                 650                 655

Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
            660                 665                 670

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
        675                 680                 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
    690                 695                 700

Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
705                 710                 715                 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
                725                 730                 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
            740                 745                 750

Gln Val Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser
        755                 760                 765

Gln Pro Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
    770                 775                 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785                 790                 795                 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
                805                 810                 815
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Val Thr Pro Ser
820

<210> 2212
<211> 790
<212> PRT
<213> Homo sapiens

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<223> /note="Uniprot ID: Q9UKF2; "

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Met Arg Ser Val Gln Ile Phe Leu Ser Gln Cys Arg Leu Leu Leu Leu
1 5 10 15

Leu Val Pro Thr Met Leu Leu Lys Ser Leu Gly Glu Asp Val Ile Phe
20 25 30

His Pro Glu Gly Glu Phe Asp Ser Tyr Glu Val Thr Ile Pro Glu Lys
35 40 45

Leu Ser Phe Arg Gly Glu Val Gln Gly Val Val Ser Pro Val Ser Tyr
50 55 60

Leu Leu Gln Leu Lys Gly Lys Lys His Val Leu His Leu Trp Pro Lys
65 70 75 80

Arg Leu Leu Leu Pro Arg His Leu Arg Val Phe Ser Phe Thr Glu His
85 90 95

Gly Glu Leu Leu Glu Asp His Pro Tyr Ile Pro Lys Asp Cys Asn Tyr

```
            100                 105                 110

Met Gly Ser Val Lys Glu Ser Leu Asp Ser Lys Ala Thr Ile Ser Thr
        115                 120                 125

Cys Met Gly Gly Leu Arg Gly Val Phe Asn Ile Asp Ala Lys His Tyr
    130                 135                 140

Gln Ile Glu Pro Leu Lys Ala Ser Pro Ser Phe Glu His Val Val Tyr
145                 150                 155                 160

Leu Leu Lys Lys Glu Gln Phe Gly Asn Gln Val Cys Gly Leu Ser Asp
                165                 170                 175

Asp Glu Ile Glu Trp Gln Met Ala Pro Tyr Glu Asn Lys Ala Arg Leu
            180                 185                 190

Arg Asp Phe Pro Gly Ser Tyr Lys His Pro Lys Tyr Leu Glu Leu Ile
        195                 200                 205

Leu Leu Phe Asp Gln Ser Arg Tyr Arg Phe Val Asn Asn Asn Leu Ser
    210                 215                 220

Gln Val Ile His Asp Ala Ile Leu Leu Thr Gly Ile Met Asp Thr Tyr
225                 230                 235                 240

Phe Gln Asp Val Arg Met Arg Ile His Leu Lys Ala Leu Glu Val Trp
                245                 250                 255

Thr Asp Phe Asn Lys Ile Arg Val Gly Tyr Pro Glu Leu Ala Glu Val
            260                 265                 270

Leu Gly Arg Phe Val Ile Tyr Lys Lys Ser Val Leu Asn Ala Arg Leu
        275                 280                 285

Ser Ser Asp Trp Ala His Leu Tyr Leu Gln Arg Lys Tyr Asn Asp Ala
    290                 295                 300

Leu Ala Trp Ser Phe Gly Lys Val Cys Ser Leu Glu Tyr Ala Gly Ser
305                 310                 315                 320

Val Ser Thr Leu Leu Asp Thr Asn Ile Leu Ala Pro Ala Thr Trp Ser
                325                 330                 335
```

```
Ala His Glu Leu Gly His Ala Val Gly Met Ser His Asp Glu Gln Tyr
            340                 345                 350

Cys Gln Cys Arg Gly Arg Leu Asn Cys Ile Met Gly Ser Gly Arg Thr
        355                 360                 365

Gly Phe Ser Asn Cys Ser Tyr Ile Ser Phe Phe Lys His Ile Ser Ser
    370                 375                 380

Gly Ala Thr Cys Leu Asn Asn Ile Pro Gly Leu Gly Tyr Val Leu Lys
385                 390                 395                 400

Arg Cys Gly Asn Lys Ile Val Glu Asp Asn Glu Glu Cys Asp Cys Gly
                405                 410                 415

Ser Thr Glu Glu Cys Gln Lys Asp Arg Cys Cys Gln Ser Asn Cys Lys
            420                 425                 430

Leu Gln Pro Gly Ala Asn Cys Ser Ile Gly Leu Cys Cys His Asp Cys
        435                 440                 445

Arg Phe Arg Pro Ser Gly Tyr Val Cys Arg Gln Glu Gly Asn Glu Cys
    450                 455                 460

Asp Leu Ala Glu Tyr Cys Asp Gly Asn Ser Ser Ser Cys Pro Asn Asp
465                 470                 475                 480

Val Tyr Lys Gln Asp Gly Thr Pro Cys Lys Tyr Glu Gly Arg Cys Phe
                485                 490                 495

Arg Lys Gly Cys Arg Ser Arg Tyr Met Gln Cys Gln Ser Ile Phe Gly
            500                 505                 510

Pro Asp Ala Met Glu Ala Pro Ser Glu Cys Tyr Asp Ala Val Asn Leu
        515                 520                 525

Ile Gly Asp Gln Phe Gly Asn Cys Glu Ile Thr Gly Ile Arg Asn Phe
    530                 535                 540

Lys Lys Cys Glu Ser Ala Asn Ser Ile Cys Gly Arg Leu Gln Cys Ile
545                 550                 555                 560
```

```
Asn Val Glu Thr Ile Pro Asp Leu Pro Glu His Thr Thr Ile Ile Ser
                565                 570                 575

Thr His Leu Gln Ala Glu Asn Leu Met Cys Trp Gly Thr Gly Tyr His
            580                 585                 590

Leu Ser Met Lys Pro Met Gly Ile Pro Asp Leu Gly Met Ile Asn Asp
        595                 600                 605

Gly Thr Ser Cys Gly Glu Gly Arg Val Cys Phe Lys Lys Asn Cys Val
    610                 615                 620

Asn Ser Ser Val Leu Gln Phe Asp Cys Leu Pro Glu Lys Cys Asn Thr
625                 630                 635                 640

Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys Met Tyr Gly Trp
                645                 650                 655

Ala Pro Pro Phe Cys Glu Glu Val Gly Tyr Gly Gly Ser Ile Asp Ser
            660                 665                 670

Gly Pro Pro Gly Leu Leu Arg Gly Ala Ile Pro Ser Ser Ile Trp Val
        675                 680                 685

Val Ser Ile Ile Met Phe Arg Leu Ile Leu Leu Ile Leu Ser Val Val
    690                 695                 700

Phe Val Phe Phe Arg Gln Val Ile Gly Asn His Leu Lys Pro Lys Gln
705                 710                 715                 720

Glu Lys Met Pro Leu Ser Lys Ala Lys Thr Glu Gln Glu Glu Ser Lys
                725                 730                 735

Thr Lys Thr Val Gln Glu Glu Ser Lys Thr Lys Thr Gly Gln Glu Glu
            740                 745                 750

Ser Glu Ala Lys Thr Gly Gln Glu Glu Ser Lys Ala Lys Thr Gly Gln
        755                 760                 765

Glu Glu Ser Lys Ala Asn Ile Glu Ser Lys Arg Pro Lys Ala Lys Ser
    770                 775                 780
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Val Lys Lys Gln Lys Lys
785 790

<210> 2213
<211> 787
<212> PRT
<213> Homo sapiens

<220>
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<220>
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Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1 5 10 15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
20 25 30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
35 40 45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
50 55 60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65 70 75 80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
85 90 95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
100 105 110

```
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
        115                 120                 125

Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu Tyr
    130                 135                 140

Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
145                 150                 155                 160

Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
                165                 170                 175

Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
            180                 185                 190

Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
        195                 200                 205

Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
    210                 215                 220

Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
225                 230                 235                 240

Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
                245                 250                 255

Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
            260                 265                 270

Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
        275                 280                 285

Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
    290                 295                 300

Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr
305                 310                 315                 320

Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys
                325                 330                 335
```

```
Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln
            340                 345                 350

Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln
        355                 360                 365

Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln
    370                 375                 380

Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu
385                 390                 395                 400

Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala
                405                 410                 415

Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys
            420                 425                 430

Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val
        435                 440                 445

Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys
    450                 455                 460

Asn Gly Thr Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly
465                 470                 475                 480

Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His
                485                 490                 495

Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn
            500                 505                 510

Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe
        515                 520                 525

Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp
    530                 535                 540

Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys
545                 550                 555                 560
```

```
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp
                565                 570                 575

Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp
            580                 585                 590

Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys
        595                 600                 605

Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His
    610                 615                 620

Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn
625                 630                 635                 640

Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg
                645                 650                 655

Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met
            660                 665                 670

Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu
        675                 680                 685

Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg
    690                 695                 700

Lys Gln Leu Lys Lys Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser
705                 710                 715                 720

Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
                725                 730                 735

Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Thr Arg Ser Glu Ser
            740                 745                 750

Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu
        755                 760                 765

Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
    770                 775                 780

Ser Ser Asn
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785

<210> 2214
<211> 155
<212> PRT
<213> Homo sapiens

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<220>
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Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1 5 10 15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
20 25 30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
35 40 45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
50 55 60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65 70 75 80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
85 90 95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
100 105 110

Thr Cys Ser Gly Leu Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn
115 120 125

Ile Phe Ile Ser Glu Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro
    130   135   140

Leu Tyr Leu Glu Met His Ile Val Val Asp Lys
145   150   155

<210> 2215
<211> 688
<212> PRT
<213> Homo sapiens

<220>
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<400> 2215
Met Asn Val Arg Gly Ala Ala Pro Gly Val Arg Ala Ser Pro Arg Pro
1   5   10   15

Trp Gln Phe Pro Thr Ser Gln Arg Leu Pro Ala Gly Ser Pro Glu Ala
            20   25   30

Ala Pro Cys Ser Ala Ser Gly Cys Cys Trp Pro Gly Ser Ala Ala Ser
        35   40   45

Trp Arg Gln Asp Pro Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu
    50   55   60

Lys Leu Tyr Thr Val His Leu Lys Gln Arg Tyr Phe Leu Ala Asp Asn
65   70   75   80

Phe Met Ile Tyr Leu Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser
                85   90   95

Asp Ile Gln Thr Gln Cys Tyr Tyr Gln Gly Asn Ile Glu Gly Tyr Pro

```
            100                 105                 110

Asp Ser Met Val Thr Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu
        115                 120                 125

Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val
    130                 135                 140

Glu Phe Gln His Val Leu Tyr Lys Leu Lys Asn Glu Asp Asn Asp Ile
145                 150                 155                 160

Ala Ile Phe Ile Asp Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn
                165                 170                 175

Ile Phe Ile Ser Glu Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro
            180                 185                 190

Leu Tyr Leu Glu Met His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr
        195                 200                 205

Trp Gly Ser Asp Ser Met Ile Val Thr Asn Lys Val Ile Glu Ile Val
    210                 215                 220

Gly Leu Ala Asn Ser Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu
225                 230                 235                 240

Ser Ser Leu Glu Leu Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly
                245                 250                 255

Glu Ala Asp Glu Leu Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr
            260                 265                 270

Leu Asn Leu Arg Pro His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp
        275                 280                 285

Tyr Pro Arg Tyr Leu Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr
    290                 295                 300

Arg Tyr Ser Ala Gly Val Ala Leu Gln Cys Gly Pro Ala Ser Cys Cys
305                 310                 315                 320

Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys Tyr Lys Gly
                325                 330                 335
```

```
Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val Glu Cys Arg
            340                 345                 350

Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys Asn Gly Thr
        355                 360                 365

Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly Leu Ser Cys
    370                 375                 380

Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His Asp Leu Asp
385                 390                 395                 400

Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn Ala Pro Phe
                405                 410                 415

Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe Gly Asn Cys
            420                 425                 430

Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp Arg Asn Leu
        435                 440                 445

Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys Pro Phe His
    450                 455                 460

Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp Ser Val Cys
465                 470                 475                 480

Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp Pro Leu Ala
                485                 490                 495

Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys Val Asn Arg
            500                 505                 510

Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His Val Cys Ser
        515                 520                 525

Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn Lys Cys His
    530                 535                 540

Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg Ser Lys Gly
545                 550                 555                 560
```

```
Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met Glu Arg Ala
                565                 570                 575

Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu Ile Ala Leu
            580                 585                 590

Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg Lys Gln Leu
        595                 600                 605

Lys Lys Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser Glu Ser Lys
    610                 615                 620

Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser Ser Glu Gly
625                 630                 635                 640

Ser Thr Gln Thr Tyr Ala Ser Gln Thr Arg Ser Glu Ser Ser Ser Gln
                645                 650                 655

Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu Ala Tyr Thr
            660                 665                 670

Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser Ser Ser Asn
        675                 680                 685


<210> 2216
<211> 172
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<400> 2216
Met Gln Leu Ala Leu Phe Lys Asn Met Lys Ser Trp His Phe Ile Leu
```

```
1               5                   10                  15

Lys Ser Gly Ser Leu Phe Pro Ser Leu Glu Cys Ser His Ile Trp Leu
            20                  25                  30

Asn Ser Phe Glu Lys Ile Leu Glu Thr Gly Leu Ala Asn Met Asn Ile
        35                  40                  45

Tyr Leu Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu Lys
    50                  55                  60

Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln Ile
65                  70                  75                  80

Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu Lys
                85                  90                  95

Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn Gln
            100                 105                 110

Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr Tyr
        115                 120                 125

Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser Thr
    130                 135                 140

Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr Gly
145                 150                 155                 160

Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His
                165                 170
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<210> 2217
<211> 184
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="ENSP ID: ENSP00000429066"

<400> 2217

```
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1               5                  10                  15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
            20                  25                  30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
        35                  40                  45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
    50                  55                  60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65                  70                  75                  80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
                85                  90                  95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
            100                 105                 110

Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
        115                 120                 125

Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu Tyr
    130                 135                 140

Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
145                 150                 155                 160

Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Tyr
                165                 170                 175

Asp Tyr Trp Gly Ser Asp Ser Met
            180
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<210> 2218
<211> 629
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000429422"

<400> 2218

```
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1               5                  10                  15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
            20                  25                  30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
        35                  40                  45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
    50                  55                  60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65                  70                  75                  80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
                85                  90                  95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
            100                 105                 110

Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
        115                 120                 125

Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu Tyr
    130                 135                 140
```

```
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
145                 150                 155                 160

Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
                165                 170                 175

Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
            180                 185                 190

Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
        195                 200                 205

Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
    210                 215                 220

Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
225                 230                 235                 240

Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
                245                 250                 255

Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
            260                 265                 270

Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
        275                 280                 285

Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
    290                 295                 300

Leu Gln Cys Gly Pro Ala Ser Cys Cys Asp Phe Arg Thr Cys Val Leu
305                 310                 315                 320

Lys Asp Gly Ala Lys Cys Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln
                325                 330                 335

Ile Leu Gln Ser Gly Val Glu Cys Arg Pro Lys Ala His Pro Glu Cys
            340                 345                 350

Asp Ile Ala Glu Asn Cys Asn Gly Thr Ser Pro Glu Cys Gly Pro Asp
        355                 360                 365
```

```
Ile Thr Leu Ile Asn Gly Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys
    370                 375                 380

Tyr Asp Gly Asp Cys His Asp Leu Asp Ala Arg Cys Glu Ser Val Phe
385                 390                 395                 400

Gly Lys Gly Ser Arg Asn Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln
                405                 410                 415

Ser Gln Ser Asp Arg Phe Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys
            420                 425                 430

Tyr Val Phe Cys Gly Trp Arg Asn Leu Ile Cys Gly Arg Leu Val Cys
        435                 440                 445

Thr Tyr Pro Thr Arg Lys Pro Phe His Gln Glu Asn Gly Asp Val Ile
    450                 455                 460

Tyr Ala Phe Val Arg Asp Ser Val Cys Ile Thr Val Asp Tyr Lys Leu
465                 470                 475                 480

Pro Arg Thr Val Pro Asp Pro Leu Ala Val Lys Asn Gly Ser Gln Cys
                485                 490                 495

Asp Ile Gly Arg Val Cys Val Asn Arg Glu Cys Val Glu Ser Arg Ile
            500                 505                 510

Ile Lys Ala Ser Ala His Val Cys Ser Gln Gln Cys Ser Gly His Gly
        515                 520                 525

Val Cys Asp Ser Arg Asn Lys Cys His Cys Ser Pro Gly Tyr Lys Pro
    530                 535                 540

Pro Asn Cys Gln Ile Arg Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu
545                 550                 555                 560

Asp Met Gly Ser Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr
                565                 570                 575

Trp Leu Leu Gly Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr
            580                 585                 590
```

Ala Ile Val Leu Ala Arg Lys Gln Leu Lys Lys Trp Phe Ala Lys Glu
595 600 605

Glu Glu Phe Pro Ser Ser Glu Ser Lys Ser Gln Asp Ser Thr Gln Thr
610 615 620

Gln Ser Ser Ser Asn
625

<210> 2219
<211> 53
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000431050"

<400> 2219
Met Ile Tyr Leu Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp
1 5 10 15

Ile Gln Thr Gln Cys Tyr Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp
20 25 30

Ser Met Val Thr Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln
35 40 45

Phe Glu Asn Val Ser
50

<210> 2220
<211> 629
<212> PRT
<213> Homo sapiens

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<223> /note="ENSP ID: ENSP00000483377"

<400> 2220
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1 5 10 15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
20 25 30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
35 40 45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
50 55 60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65 70 75 80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
85 90 95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
100 105 110

Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
115 120 125

Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu Tyr
130 135 140

Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
145 150 155 160

```
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
                165                 170                 175

Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
            180                 185                 190

Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
        195                 200                 205

Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
    210                 215                 220

Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
225                 230                 235                 240

Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
                245                 250                 255

Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
            260                 265                 270

Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
        275                 280                 285

Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
    290                 295                 300

Leu Gln Cys Gly Pro Ala Ser Cys Cys Asp Phe Arg Thr Cys Val Leu
305                 310                 315                 320

Lys Asp Gly Ala Lys Cys Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln
                325                 330                 335

Ile Leu Gln Ser Gly Val Glu Cys Arg Pro Lys Ala His Pro Glu Cys
            340                 345                 350

Asp Ile Ala Glu Asn Cys Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp
        355                 360                 365

Ile Thr Leu Ile Asn Gly Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys
    370                 375                 380

Tyr Asp Gly Asp Cys His Asp Leu Asp Ala Arg Cys Glu Ser Val Phe
```

385 390 395 400

Gly Lys Gly Ser Arg Asn Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln
405 410 415

Ser Gln Ser Asp Arg Phe Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys
420 425 430

Tyr Val Phe Cys Gly Trp Arg Asn Leu Ile Cys Gly Arg Leu Val Cys
435 440 445

Thr Tyr Pro Thr Arg Lys Pro Phe His Gln Glu Asn Gly Asp Val Ile
450 455 460

Tyr Ala Phe Val Arg Asp Ser Val Cys Ile Thr Val Asp Tyr Lys Leu
465 470 475 480

Pro Arg Thr Val Pro Asp Pro Leu Ala Val Lys Asn Gly Ser Gln Cys
485 490 495

Asp Ile Gly Arg Val Cys Val Asn Arg Glu Cys Val Glu Ser Arg Ile
500 505 510

Ile Lys Ala Ser Ala His Val Cys Ser Gln Gln Cys Ser Gly His Gly
515 520 525

Val Cys Asp Ser Arg Asn Lys Cys His Cys Ser Pro Gly Tyr Lys Pro
530 535 540

Pro Asn Cys Gln Ile Arg Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu
545 550 555 560

Asp Met Gly Ser Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr
565 570 575

Trp Leu Leu Gly Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr
580 585 590

Ala Ile Val Leu Ala Arg Lys Gln Leu Lys Lys Trp Phe Ala Lys Glu
595 600 605

Glu Glu Phe Pro Ser Ser Glu Ser Lys Ser Gln Asp Ser Thr Gln Thr
610 615 620

Gln Ser Ser Ser Asn
625

<210> 2221
<211> 787
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Uniprot ID: Q8TC27; "

<220>
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<223> /note="ENSP ID: ENSP00000484817"

<400> 2221
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1 5 10 15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
20 25 30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
35 40 45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
50 55 60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65 70 75 80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
85 90 95

```
Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
            100                 105                 110

Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
        115                 120                 125

Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu Tyr
    130                 135                 140

Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
145                 150                 155                 160

Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
                165                 170                 175

Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
            180                 185                 190

Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
        195                 200                 205

Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
    210                 215                 220

Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
225                 230                 235                 240

Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
                245                 250                 255

Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
            260                 265                 270

Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
        275                 280                 285

Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
    290                 295                 300

Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr
305                 310                 315                 320

Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys
```

```
                325                 330                 335

Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln
            340                 345                 350

Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln
        355                 360                 365

Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln
    370                 375                 380

Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu
385                 390                 395                 400

Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala
                405                 410                 415

Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys
            420                 425                 430

Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val
        435                 440                 445

Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys
    450                 455                 460

Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly
465                 470                 475                 480

Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His
                485                 490                 495

Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn
            500                 505                 510

Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe
        515                 520                 525

Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp
    530                 535                 540

Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys
545                 550                 555                 560
```

```
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp
                565                 570                 575

Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp
            580                 585                 590

Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys
        595                 600                 605

Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His
    610                 615                 620

Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn
625                 630                 635                 640

Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg
                645                 650                 655

Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met
            660                 665                 670

Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu
        675                 680                 685

Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg
    690                 695                 700

Lys Gln Leu Lys Lys Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser
705                 710                 715                 720

Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
                725                 730                 735

Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Thr Arg Ser Glu Ser
            740                 745                 750

Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu
        755                 760                 765

Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
    770                 775                 780
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Ser Ser Asn
785

<210> 2222
<211> 155
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 551; "

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<220>
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<223> /note="ENSP ID: ENSP00000487692"

<400> 2222
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1 5 10 15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
20 25 30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
35 40 45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
50 55 60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65 70 75 80

Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
85 90 95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
100 105 110

Thr Cys Ser Gly Leu Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn

```
        115                 120                 125

Ile Phe Ile Ser Glu Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro
    130                 135                 140

Leu Tyr Leu Glu Met His Ile Val Val Asp Lys
145                 150                 155


<210> 2223
<211> 53
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      ADAM metallopeptidase domain 32; "

<220>
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<223> /note="ENSP ID: ENSP00000487983"

<400> 2223
Met Ile Tyr Leu Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp
1               5                   10                  15

Ile Gln Thr Gln Cys Tyr Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp
            20                  25                  30

Ser Met Val Thr Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln
        35                  40                  45

Phe Glu Asn Val Ser
    50


<210> 2224
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 551; "

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<223> /note="Gene Name:
ADAM metallopeptidase domain 32; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488048"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2224
Xaa Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
1 5 10 15

Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Thr Arg Ser Glu Ser
20 25 30

Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Gln Asp Ser Thr Gln
35 40 45

Thr Gln Ser Ser Ser Asn
50

<210> 2225
<211> 688
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 32; "

<220>

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<400> 2225
Met Asn Val Arg Gly Ala Ala Pro Gly Val Arg Ala Ser Pro Arg Pro
1 5 10 15

Trp Gln Phe Pro Thr Ser Gln Arg Leu Pro Ala Gly Ser Pro Glu Ala
20 25 30

Ala Pro Cys Ser Ala Ser Gly Cys Cys Trp Pro Gly Ser Ala Ala Ser
35 40 45

Trp Arg Gln Asp Pro Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu
50 55 60

Lys Leu Tyr Thr Val His Leu Lys Gln Arg Tyr Phe Leu Ala Asp Asn
65 70 75 80

Phe Met Ile Tyr Leu Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser
85 90 95

Asp Ile Gln Thr Gln Cys Tyr Tyr Gln Gly Asn Ile Glu Gly Tyr Pro
100 105 110

Asp Ser Met Val Thr Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu
115 120 125

Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val
130 135 140

Glu Phe Gln His Val Leu Tyr Lys Leu Lys Asn Glu Asp Asn Asp Ile
145 150 155 160

Ala Ile Phe Ile Asp Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn
165 170 175

Ile Phe Ile Ser Glu Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro
180 185 190

Leu Tyr Leu Glu Met His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr
195 200 205

Trp Gly Ser Asp Ser Met Ile Val Thr Asn Lys Val Ile Glu Ile Val

```
    210                 215                 220

Gly Leu Ala Asn Ser Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu
225                 230                 235                 240

Ser Ser Leu Glu Leu Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly
                245                 250                 255

Glu Ala Asp Glu Leu Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr
            260                 265                 270

Leu Asn Leu Arg Pro His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp
        275                 280                 285

Tyr Pro Arg Tyr Leu Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr
    290                 295                 300

Arg Tyr Ser Ala Gly Val Ala Leu Gln Cys Gly Pro Ala Ser Cys Cys
305                 310                 315                 320

Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys Tyr Lys Gly
                325                 330                 335

Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val Glu Cys Arg
            340                 345                 350

Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys Asn Gly Ser
        355                 360                 365

Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly Leu Ser Cys
    370                 375                 380

Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His Asp Leu Asp
385                 390                 395                 400

Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn Ala Pro Phe
                405                 410                 415

Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe Gly Asn Cys
            420                 425                 430

Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp Arg Asn Leu
        435                 440                 445
```

```
Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys Pro Phe His
    450                 455                 460

Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp Ser Val Cys
465                 470                 475                 480

Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp Pro Leu Ala
                485                 490                 495

Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys Val Asn Arg
            500                 505                 510

Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His Val Cys Ser
        515                 520                 525

Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn Lys Cys His
    530                 535                 540

Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg Ser Lys Gly
545                 550                 555                 560

Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met Glu Arg Ala
                565                 570                 575

Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu Ile Ala Leu
            580                 585                 590

Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg Lys Gln Leu
        595                 600                 605

Lys Lys Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser Glu Ser Lys
    610                 615                 620

Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser Ser Glu Gly
625                 630                 635                 640

Ser Thr Gln Thr Tyr Ala Ser Gln Thr Arg Ser Glu Ser Ser Ser Gln
                645                 650                 655

Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu Ala Tyr Thr
            660                 665                 670
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Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser Ser Ser Asn
675 680 685

<210> 2226
<211> 172
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 551; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM32; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 32; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488605"

<400> 2226
Met Gln Leu Ala Leu Phe Lys Asn Met Lys Ser Trp His Phe Ile Leu
1 5 10 15

Lys Ser Gly Ser Leu Phe Pro Ser Leu Glu Cys Ser His Ile Trp Leu
20 25 30

Asn Ser Phe Glu Lys Ile Leu Glu Thr Gly Leu Ala Asn Met Asn Ile
35 40 45

Tyr Leu Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu Lys
50 55 60

Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln Ile
65 70 75 80

Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu Lys
85 90 95

Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn Gln
100 105 110

Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr Tyr

```
        115                 120                 125

Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser Thr
    130                 135                 140

Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr Gly
145                 150                 155                 160

Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His
                165                 170


<210> 2227
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 551; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM32; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 32; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488698"

<400> 2227
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
1               5                   10                  15

Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
            20                  25                  30

Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
        35                  40                  45

Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
    50                  55                  60

Lys Gln Arg Tyr Phe Leu Ala Asp Asn Phe Met Ile Tyr Leu Tyr Asn
65                  70                  75                  80
```

```
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
                85                  90                  95

Tyr Gln Gly Asn Ile Glu Gly Tyr Pro Asp Ser Met Val Thr Leu Ser
            100                 105                 110

Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
        115                 120                 125

Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu Tyr
    130                 135                 140

Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
145                 150                 155                 160

Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Tyr
                165                 170                 175

Asp Tyr Trp Gly Ser Asp Ser Met
            180


<210> 2228
<211> 787
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 552; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM33; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 33; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9BZ11; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000322550"

<400> 2228
Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
```

```
1               5                   10                  15

Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
            20                  25                  30

Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
        35                  40                  45

Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
    50                  55                  60

Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
65                  70                  75                  80

Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
                85                  90                  95

Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp
            100                 105                 110

His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val
        115                 120                 125

Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg
    130                 135                 140

Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp
145                 150                 155                 160

Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys
                165                 170                 175

Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser
            180                 185                 190

Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr
        195                 200                 205

Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu
    210                 215                 220

Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val
225                 230                 235                 240
```

```
Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala
                245                 250                 255

Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr
            260                 265                 270

Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly
        275                 280                 285

Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg
    290                 295                 300

Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys
305                 310                 315                 320

Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro
                325                 330                 335

Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly
            340                 345                 350

Leu Ser His Asp Pro Asp Gly Cys Cys Val Glu Ala Ala Ala Glu Ser
        355                 360                 365

Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val
    370                 375                 380

Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly
385                 390                 395                 400

Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro
                405                 410                 415

Pro Ala Leu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Glu Cys Asp
            420                 425                 430

Cys Gly Pro Gly Gln Glu Cys Arg Asp Leu Cys Cys Phe Ala His Asn
        435                 440                 445

Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala His Gly Asp Cys Cys Val
    450                 455                 460
```

```
Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu Cys Arg Gln Ala Met Gly
465                 470                 475                 480

Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly Thr Ser Ser His Cys Pro
                485                 490                 495

Pro Asp Val Tyr Leu Leu Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly
            500                 505                 510

Tyr Cys Trp Asp Gly Ala Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln
        515                 520                 525

Leu Trp Gly Pro Gly Ser His Pro Ala Pro Glu Ala Cys Phe Gln Val
    530                 535                 540

Val Asn Ser Ala Gly Asp Ala His Gly Asn Cys Gly Gln Asp Ser Glu
545                 550                 555                 560

Gly His Phe Leu Pro Cys Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu
                565                 570                 575

Gln Cys Gln Gly Gly Lys Pro Ser Leu Leu Ala Pro His Met Val Pro
            580                 585                 590

Val Asp Ser Thr Val His Leu Asp Gly Gln Glu Val Thr Cys Arg Gly
        595                 600                 605

Ala Leu Ala Leu Pro Ser Ala Gln Leu Asp Leu Leu Gly Leu Gly Leu
    610                 615                 620

Val Glu Pro Gly Thr Gln Cys Gly Pro Arg Met Val Cys Asn Ser Asn
625                 630                 635                 640

His Asn Cys His Cys Ala Pro Gly Trp Ala Pro Pro Phe Cys Asp Lys
                645                 650                 655

Pro Gly Phe Gly Gly Ser Met Asp Ser Gly Pro Val Gln Ala Glu Asn
            660                 665                 670

His Asp Thr Phe Leu Leu Ala Met Leu Leu Ser Val Leu Leu Pro Leu
        675                 680                 685
```

```
Leu Pro Gly Ala Gly Leu Ala Trp Cys Cys Tyr Arg Leu Pro Gly Ala
    690                 695                 700

His Leu Gln Arg Cys Ser Trp Gly Cys Arg Arg Asp Pro Ala Cys Ser
705                 710                 715                 720

Gly Pro Lys Asp Gly Pro His Arg Asp His Pro Leu Gly Gly Val His
                725                 730                 735

Pro Met Glu Leu Gly Pro Thr Ala Thr Gly Gln Pro Trp Pro Leu Asp
            740                 745                 750

Pro Glu Asn Ser His Glu Pro Ser Ser His Pro Glu Lys Pro Leu Pro
        755                 760                 765

Ala Val Ser Pro Asp Pro Gln Ala Asp Gln Val Gln Met Pro Arg Ser
    770                 775                 780

Cys Leu Trp
785
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<210> 2229
<211> 813
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 552; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM33; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 33; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BZ11; "

<220>
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<223> /note="ENSP ID: ENSP00000348912"

<400> 2229
```
Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
1               5                   10                  15
```

```
Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
            20                  25                  30

Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
        35                  40                  45

Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
    50                  55                  60

Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
65                  70                  75                  80

Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
                85                  90                  95

Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp
            100                 105                 110

His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val
        115                 120                 125

Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg
    130                 135                 140

Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp
145                 150                 155                 160

Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys
                165                 170                 175

Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser
            180                 185                 190

Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr
        195                 200                 205

Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu
    210                 215                 220

Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val
225                 230                 235                 240
```

```
Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala
                245                 250                 255

Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr
            260                 265                 270

Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly
        275                 280                 285

Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg
    290                 295                 300

Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys
305                 310                 315                 320

Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro
                325                 330                 335

Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly
            340                 345                 350

Leu Ser His Asp Pro Asp Gly Cys Cys Val Glu Ala Ala Ala Glu Ser
        355                 360                 365

Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val
    370                 375                 380

Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly
385                 390                 395                 400

Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro
                405                 410                 415

Pro Ala Leu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Glu Cys Asp
            420                 425                 430

Cys Gly Pro Gly Gln Glu Cys Arg Asp Leu Cys Cys Phe Ala His Asn
        435                 440                 445

Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala His Gly Asp Cys Cys Val
    450                 455                 460
```

```
Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu Cys Arg Gln Ala Met Gly
465                 470                 475                 480

Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly Thr Ser Ser His Cys Pro
                485                 490                 495

Pro Asp Val Tyr Leu Leu Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly
            500                 505                 510

Tyr Cys Trp Asp Gly Ala Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln
        515                 520                 525

Leu Trp Gly Pro Gly Ser His Pro Ala Pro Glu Ala Cys Phe Gln Val
    530                 535                 540

Val Asn Ser Ala Gly Asp Ala His Gly Asn Cys Gly Gln Asp Ser Glu
545                 550                 555                 560

Gly His Phe Leu Pro Cys Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu
                565                 570                 575

Gln Cys Gln Gly Gly Lys Pro Ser Leu Leu Ala Pro His Met Val Pro
            580                 585                 590

Val Asp Ser Thr Val His Leu Asp Gly Gln Glu Val Thr Cys Arg Gly
        595                 600                 605

Ala Leu Ala Leu Pro Ser Ala Gln Leu Asp Leu Leu Gly Leu Gly Leu
    610                 615                 620

Val Glu Pro Gly Thr Gln Cys Gly Pro Arg Met Val Cys Gln Ser Arg
625                 630                 635                 640

Arg Cys Arg Lys Asn Ala Phe Gln Glu Leu Gln Arg Cys Leu Thr Ala
                645                 650                 655

Cys His Ser His Gly Val Cys Asn Ser Asn His Asn Cys His Cys Ala
            660                 665                 670

Pro Gly Trp Ala Pro Pro Phe Cys Asp Lys Pro Gly Phe Gly Gly Ser
        675                 680                 685

Met Asp Ser Gly Pro Val Gln Ala Glu Asn His Asp Thr Phe Leu Leu
```

```
    690                 695                 700

Ala Met Leu Leu Ser Val Leu Leu Pro Leu Leu Pro Gly Ala Gly Leu
705                 710                 715                 720

Ala Trp Cys Cys Tyr Arg Leu Pro Gly Ala His Leu Gln Arg Cys Ser
                725                 730                 735

Trp Gly Cys Arg Arg Asp Pro Ala Cys Ser Gly Pro Lys Asp Gly Pro
            740                 745                 750

His Arg Asp His Pro Leu Gly Gly Val His Pro Met Glu Leu Gly Pro
        755                 760                 765

Thr Ala Thr Gly Gln Pro Trp Pro Leu Asp Pro Glu Asn Ser His Glu
    770                 775                 780

Pro Ser Ser His Pro Glu Lys Pro Leu Pro Ala Val Ser Pro Asp Pro
785                 790                 795                 800

Gln Ala Asp Gln Val Gln Met Pro Arg Ser Cys Leu Trp
                805                 810


<210> 2230
<211> 812
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 552; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM33; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 33; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369190"

<400> 2230
Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
1               5                   10                  15
```

```
Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
            20                  25                  30

Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
        35                  40                  45

Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
    50                  55                  60

Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
65                  70                  75                  80

Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
                85                  90                  95

Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp
            100                 105                 110

His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val
        115                 120                 125

Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg
    130                 135                 140

Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp
145                 150                 155                 160

Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys
                165                 170                 175

Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser
            180                 185                 190

Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr
        195                 200                 205

Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu
    210                 215                 220

Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val
225                 230                 235                 240
```

```
Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala
                245                 250                 255

Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr
            260                 265                 270

Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly
        275                 280                 285

Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg
    290                 295                 300

Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys
305                 310                 315                 320

Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro
                325                 330                 335

Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly
            340                 345                 350

Leu Ser His Asp Pro Asp Gly Cys Cys Val Glu Ala Ala Ala Glu Ser
        355                 360                 365

Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val
    370                 375                 380

Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly
385                 390                 395                 400

Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro
                405                 410                 415

Pro Ala Leu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Glu Cys Asp
            420                 425                 430

Cys Gly Pro Gly Gln Glu Cys Arg Asp Leu Cys Cys Phe Ala His Asn
        435                 440                 445

Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala His Gly Asp Cys Cys Val
    450                 455                 460

Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu Cys Arg Gln Ala Met Gly
```

```
465                 470                 475                 480

Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly Thr Ser Ser His Cys Pro
                485                 490                 495

Pro Asp Val Tyr Leu Leu Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly
            500                 505                 510

Tyr Cys Trp Asp Gly Ala Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln
        515                 520                 525

Leu Trp Gly Pro Gly Ser His Pro Ala Pro Glu Ala Cys Phe Gln Val
    530                 535                 540

Val Asn Ser Ala Gly Asp Ala His Gly Asn Cys Gly Gln Asp Ser Glu
545                 550                 555                 560

Gly His Phe Leu Pro Cys Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu
                565                 570                 575

Gln Cys Gln Gly Gly Lys Pro Ser Leu Leu Ala Pro His Met Val Pro
            580                 585                 590

Val Asp Ser Thr Val His Leu Asp Gly Gln Glu Val Thr Cys Arg Gly
        595                 600                 605

Ala Leu Ala Leu Pro Ser Ala Gln Leu Asp Leu Leu Gly Leu Gly Leu
    610                 615                 620

Val Glu Pro Gly Thr Gln Cys Gly Pro Arg Met Val Cys Gln Ser Arg
625                 630                 635                 640

Arg Cys Arg Lys Asn Ala Phe Gln Glu Leu Gln Arg Cys Leu Thr Ala
                645                 650                 655

Cys His Ser His Gly Val Cys Asn Ser Asn His Asn Cys His Cys Ala
            660                 665                 670

Pro Gly Trp Ala Pro Pro Phe Cys Asp Lys Pro Gly Phe Gly Gly Ser
        675                 680                 685

Met Asp Ser Gly Pro Val Gln Ala Glu Asn His Asp Thr Phe Leu Leu
    690                 695                 700
```

```
Ala Met Leu Leu Ser Val Leu Leu Pro Leu Leu Pro Gly Ala Gly Leu
705                 710                 715                 720

Ala Trp Cys Cys Tyr Arg Leu Pro Gly Ala His Leu Gln Arg Cys Ser
                725                 730                 735

Trp Gly Cys Arg Arg Asp Pro Ala Cys Ser Gly Pro Lys Asp Gly Pro
            740                 745                 750

His Arg Asp His Pro Leu Gly Gly Val His Pro Met Glu Leu Gly Pro
        755                 760                 765

Thr Ala Thr Gly Gln Pro Trp Pro Leu Asp Pro Glu Asn Ser His Glu
    770                 775                 780

Pro Ser Ser His Pro Glu Lys Pro Leu Pro Ala Val Ser Pro Asp Pro
785                 790                 795                 800

Gln Asp Gln Val Gln Met Pro Arg Ser Cys Leu Trp
                805                 810
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<210> 2231
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 552; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM33; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 33; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000483343"

<400> 2231

```
Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
1               5                   10                  15
```

```
Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
            20                  25                  30

Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
        35                  40                  45

Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
    50                  55                  60

Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
65                  70                  75                  80

Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
                85                  90                  95

Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Val
            100                 105                 110

Arg Cys Phe His Gly Leu Trp Asp Ala Pro Pro Glu Val Pro Pro His
        115                 120                 125

His Ser Tyr Pro Tyr Ser Ser Leu His Ser
    130                 135


<210> 2232
<211> 692
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 552; "

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<221> source
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<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase domain 33; "

<220>
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<223> /note="ENSP ID: ENSP00000484600"

<400> 2232
Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
1               5                   10                  15
```

```
Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
            20                  25                  30

Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
        35                  40                  45

Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
    50                  55                  60

Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
65                  70                  75                  80

Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
                85                  90                  95

Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp
            100                 105                 110

His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val
        115                 120                 125

Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg
    130                 135                 140

Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp
145                 150                 155                 160

Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys
                165                 170                 175

Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser
            180                 185                 190

Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr
        195                 200                 205

Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu
    210                 215                 220

Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val
225                 230                 235                 240
```

```
Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala
                245                 250                 255

Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Arg Gln
            260                 265                 270

Leu Arg Ala Phe Phe Arg Lys Gly Gly Gly Ala Cys Leu Ser Asn Ala
        275                 280                 285

Pro Asp Pro Gly Leu Pro Val Pro Pro Ala Leu Cys Gly Asn Gly Phe
    290                 295                 300

Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Pro Gly Gln Glu Cys Arg
305                 310                 315                 320

Asp Leu Cys Cys Phe Ala His Asn Cys Ser Leu Arg Pro Gly Ala Gln
                325                 330                 335

Cys Ala His Gly Asp Cys Cys Val Arg Cys Leu Leu Lys Pro Ala Gly
            340                 345                 350

Ala Leu Cys Arg Gln Ala Met Gly Asp Cys Asp Leu Pro Glu Phe Cys
        355                 360                 365

Thr Gly Thr Ser Ser His Cys Pro Pro Asp Val Tyr Leu Leu Asp Gly
    370                 375                 380

Ser Pro Cys Ala Arg Gly Ser Gly Tyr Cys Trp Asp Gly Ala Cys Pro
385                 390                 395                 400

Thr Leu Glu Gln Gln Cys Gln Gln Leu Trp Gly Pro Gly Ser His Pro
                405                 410                 415

Ala Pro Glu Ala Cys Phe Gln Val Val Asn Ser Ala Gly Asp Ala His
            420                 425                 430

Gly Asn Cys Gly Gln Asp Ser Glu Gly His Phe Leu Pro Cys Ala Gly
        435                 440                 445

Arg Asp Ala Leu Cys Gly Lys Leu Gln Cys Gln Gly Gly Lys Pro Ser
    450                 455                 460
```

```
Leu Leu Ala Pro His Met Val Pro Val Asp Ser Thr Val His Leu Asp
465                 470                 475                 480

Gly Gln Glu Val Thr Cys Arg Gly Ala Leu Ala Leu Pro Ser Ala Gln
                485                 490                 495

Leu Asp Leu Leu Gly Leu Gly Leu Val Glu Pro Gly Thr Gln Cys Gly
            500                 505                 510

Pro Arg Met Val Cys Gln Ser Arg Arg Cys Arg Lys Asn Ala Phe Gln
        515                 520                 525

Glu Leu Gln Arg Cys Leu Thr Ala Cys His Ser His Gly Val Cys Asn
    530                 535                 540

Ser Asn His Asn Cys His Cys Ala Pro Gly Trp Ala Pro Pro Phe Cys
545                 550                 555                 560

Asp Lys Pro Gly Phe Gly Gly Ser Met Asp Ser Gly Pro Val Gln Ala
                565                 570                 575

Glu Asn His Asp Thr Phe Leu Leu Ala Met Leu Leu Ser Val Leu Leu
            580                 585                 590

Pro Leu Leu Pro Gly Ala Gly Leu Ala Trp Cys Cys Tyr Arg Leu Pro
        595                 600                 605

Gly Ala His Leu Gln Arg Cys Ser Trp Gly Cys Arg Arg Asp Pro Ala
    610                 615                 620

Cys Ser Gly Pro Lys Asp Gly Pro His Arg Asp His Pro Leu Gly Gly
625                 630                 635                 640

Val His Pro Met Glu Leu Gly Pro Thr Ala Thr Gly Gln Pro Trp Pro
                645                 650                 655

Leu Asp Pro Glu Asn Ser His Glu Pro Ser Ser His Pro Glu Lys Pro
            660                 665                 670

Leu Pro Ala Val Ser Pro Asp Pro Gln Asp Gln Val Gln Met Pro Arg
        675                 680                 685

Ser Cys Leu Trp
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690

<210> 2233
<211> 754
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 553; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM7; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 7; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H2U9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000175238"

<400> 2233
Met Leu Pro Gly Cys Ile Phe Leu Met Ile Leu Leu Ile Pro Gln Val
1   5   10   15

Lys Glu Lys Phe Ile Leu Gly Val Glu Gly Gln Gln Leu Val Arg Pro
            20   25   30

Lys Lys Leu Pro Leu Ile Gln Lys Arg Asp Thr Gly His Thr His Asp
        35   40   45

Asp Asp Ile Leu Lys Thr Tyr Glu Glu Glu Leu Leu Tyr Glu Ile Lys
    50   55   60

Leu Asn Arg Lys Thr Leu Val Leu His Leu Leu Arg Ser Arg Glu Phe
65   70   75   80

Leu Gly Ser Asn Tyr Ser Glu Thr Phe Tyr Ser Met Lys Gly Glu Ala
                85   90   95

Phe Thr Arg His Pro Gln Ile Met Asp His Cys Phe Tyr Gln Gly Ser
            100   105   110

```
Ile Val His Glu Tyr Asp Ser Ala Ala Ser Ile Ser Thr Cys Asn Gly
        115                 120                 125

Leu Arg Gly Phe Phe Arg Ile Asn Asp Gln Arg Tyr Leu Ile Glu Pro
    130                 135                 140

Val Lys Tyr Ser Asp Glu Gly Glu His Leu Val Phe Lys Tyr Asn Leu
145                 150                 155                 160

Arg Val Pro Tyr Gly Ala Asn Tyr Ser Cys Thr Glu Leu Asn Phe Thr
                165                 170                 175

Arg Lys Thr Val Pro Gly Asp Asn Glu Ser Glu Glu Asp Ser Lys Ile
            180                 185                 190

Lys Gly Ile His Asp Glu Lys Tyr Val Glu Leu Phe Ile Val Ala Asp
        195                 200                 205

Asp Thr Val Tyr Arg Arg Asn Gly His Pro His Asn Lys Leu Arg Asn
    210                 215                 220

Arg Ile Trp Gly Met Val Asn Phe Val Asn Met Ile Tyr Lys Thr Leu
225                 230                 235                 240

Asn Ile His Val Thr Leu Val Gly Ile Glu Ile Trp Thr His Glu Asp
                245                 250                 255

Lys Ile Glu Leu Tyr Ser Asn Ile Glu Thr Thr Leu Leu Arg Phe Ser
            260                 265                 270

Phe Trp Gln Glu Lys Ile Leu Lys Thr Arg Lys Asp Phe Asp His Val
        275                 280                 285

Val Leu Leu Ser Gly Lys Trp Leu Tyr Ser His Val Gln Gly Ile Ser
    290                 295                 300

Tyr Pro Gly Gly Met Cys Leu Pro Tyr Tyr Ser Thr Ser Ile Ile Lys
305                 310                 315                 320

Asp Leu Leu Pro Asp Thr Asn Ile Ile Ala Asn Arg Met Ala His Gln
                325                 330                 335
```

```
Leu Gly His Asn Leu Gly Met Gln His Asp Glu Phe Pro Cys Thr Cys
            340                 345                 350

Pro Ser Gly Lys Cys Val Met Asp Ser Asp Gly Ser Ile Pro Ala Leu
        355                 360                 365

Lys Phe Ser Lys Cys Ser Gln Asn Gln Tyr His Gln Tyr Leu Lys Asp
    370                 375                 380

Tyr Lys Pro Thr Cys Met Leu Asn Ile Pro Phe Pro Tyr Asn Phe His
385                 390                 395                 400

Asp Phe Gln Phe Cys Gly Asn Lys Lys Leu Asp Glu Gly Glu Glu Cys
                405                 410                 415

Asp Cys Gly Pro Ala Gln Glu Cys Thr Asn Pro Cys Cys Asp Ala His
            420                 425                 430

Thr Cys Val Leu Lys Pro Gly Phe Thr Cys Ala Glu Gly Glu Cys Cys
        435                 440                 445

Glu Ser Cys Gln Ile Lys Lys Ala Gly Ser Ile Cys Arg Pro Ala Lys
    450                 455                 460

Asp Glu Cys Asp Phe Pro Glu Met Cys Thr Gly His Ser Pro Ala Cys
465                 470                 475                 480

Pro Lys Asp Gln Phe Arg Val Asn Gly Phe Pro Cys Lys Asn Ser Glu
                485                 490                 495

Gly Tyr Cys Phe Met Gly Lys Cys Pro Thr Arg Glu Asp Gln Cys Ser
            500                 505                 510

Glu Leu Phe Asp Asp Glu Ala Ile Glu Ser His Asp Ile Cys Tyr Lys
        515                 520                 525

Met Asn Thr Lys Gly Asn Lys Phe Gly Tyr Cys Lys Asn Lys Glu Asn
    530                 535                 540

Arg Phe Leu Pro Cys Glu Glu Lys Asp Val Arg Cys Gly Lys Ile Tyr
545                 550                 555                 560

Cys Thr Gly Gly Glu Leu Ser Ser Leu Leu Gly Glu Asp Lys Thr Tyr
```

565 570 575

His Leu Lys Asp Pro Gln Lys Asn Ala Thr Val Lys Cys Lys Thr Ile
580 585 590

Phe Leu Tyr His Asp Ser Thr Asp Ile Gly Leu Val Ala Ser Gly Thr
595 600 605

Lys Cys Gly Glu Gly Met Val Cys Asn Asn Gly Glu Cys Leu Asn Met
610 615 620

Glu Lys Val Tyr Ile Ser Thr Asn Cys Pro Ser Gln Cys Asn Glu Asn
625 630 635 640

Pro Val Asp Gly His Gly Leu Gln Cys His Cys Glu Glu Gly Gln Ala
645 650 655

Pro Val Ala Cys Glu Glu Thr Leu His Val Thr Asn Ile Thr Ile Leu
660 665 670

Val Val Val Leu Val Leu Val Ile Val Gly Ile Gly Val Leu Ile Leu
675 680 685

Leu Val Arg Tyr Arg Lys Cys Ile Lys Leu Lys Gln Val Gln Ser Pro
690 695 700

Pro Thr Glu Thr Leu Gly Val Glu Asn Lys Gly Tyr Phe Gly Asp Glu
705 710 715 720

Gln Gln Ile Arg Thr Glu Pro Ile Leu Pro Glu Ile His Phe Leu Asn
725 730 735

Lys Pro Ala Ser Lys Asp Ser Arg Gly Ile Ala Asp Pro Asn Gln Ser
740 745 750

Ala Lys

<210> 2234
<211> 776
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 553; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM7; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370166"

<400> 2234

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Met Leu Pro Gly Cys Ile Phe Leu Met Ile Leu Leu Ile Pro Gln Val
1               5                  10                  15

Lys Glu Lys Phe Ile Leu Gly Val Glu Gly Gln Gln Leu Val Arg Pro
            20                  25                  30

Lys Lys Leu Pro Leu Ile Gln Lys Arg Asp Thr Gly His Thr His Asp
        35                  40                  45

Asp Asp Ile Leu Lys Thr Tyr Glu Glu Glu Leu Leu Tyr Glu Ile Lys
    50                  55                  60

Leu Asn Arg Lys Thr Leu Val Leu His Leu Leu Arg Ser Arg Glu Phe
65                  70                  75                  80

Leu Gly Ser Asn Tyr Ser Glu Thr Phe Tyr Ser Met Lys Gly Glu Ala
                85                  90                  95

Phe Thr Arg His Pro Gln Ile Met Asp His Cys Phe Tyr Gln Gly Ser
            100                 105                 110

Ile Val His Glu Tyr Asp Ser Ala Ala Ser Ile Ser Thr Cys Asn Gly
        115                 120                 125

Leu Arg Gly Phe Phe Arg Ile Asn Asp Gln Arg Tyr Leu Ile Glu Pro
    130                 135                 140

Val Lys Tyr Ser Asp Glu Gly Glu His Leu Val Phe Lys Tyr Asn Leu
145                 150                 155                 160
```

```
Arg Val Pro Tyr Gly Ala Asn Tyr Ser Cys Thr Glu Leu Asn Phe Thr
                165                 170                 175

Arg Lys Thr Val Pro Gly Asp Asn Glu Ser Glu Glu Asp Ser Lys Ile
            180                 185                 190

Lys Gly Ile His Asp Glu Lys Tyr Val Glu Leu Phe Ile Val Ala Asp
        195                 200                 205

Asp Thr Val Tyr Arg Arg Asn Gly His Pro His Asn Lys Leu Arg Asn
    210                 215                 220

Arg Ile Trp Gly Met Val Asn Phe Val Asn Met Ile Tyr Lys Thr Leu
225                 230                 235                 240

Asn Ile His Val Thr Leu Val Gly Ile Glu Ile Trp Thr His Glu Asp
                245                 250                 255

Lys Ile Glu Leu Tyr Ser Asn Ile Glu Thr Thr Leu Leu Arg Phe Ser
            260                 265                 270

Phe Trp Gln Glu Lys Ile Leu Lys Thr Arg Lys Asp Phe Asp His Val
        275                 280                 285

Val Leu Leu Ser Gly Lys Trp Leu Tyr Ser His Val Gln Gly Ile Ser
    290                 295                 300

Tyr Pro Gly Gly Met Cys Leu Pro Tyr Tyr Ser Thr Ser Ile Ile Lys
305                 310                 315                 320

Asp Leu Leu Pro Asp Thr Asn Ile Ile Ala Asn Arg Met Ala His Gln
                325                 330                 335

Leu Gly His Asn Leu Gly Met Gln His Asp Glu Phe Pro Cys Thr Cys
            340                 345                 350

Pro Ser Gly Lys Cys Val Met Asp Ser Asp Gly Ser Ile Pro Ala Leu
        355                 360                 365

Lys Phe Ser Lys Cys Ser Gln Asn Gln Tyr His Gln Tyr Leu Lys Asp
    370                 375                 380

Tyr Lys Pro Thr Cys Met Leu Asn Ile Pro Phe Pro Tyr Asn Phe His
```

385 390 395 400

Asp Phe Gln Phe Cys Gly Asn Lys Lys Leu Asp Glu Gly Glu Glu Cys
405 410 415

Asp Cys Gly Pro Ala Gln Glu Cys Thr Asn Pro Cys Cys Asp Ala His
420 425 430

Thr Cys Val Leu Lys Pro Gly Phe Thr Cys Ala Glu Gly Glu Cys Cys
435 440 445

Glu Ser Cys Gln Ile Lys Lys Ala Gly Ser Ile Cys Arg Pro Ala Lys
450 455 460

Asp Glu Cys Asp Phe Pro Glu Met Cys Thr Gly His Ser Pro Ala Cys
465 470 475 480

Pro Lys Asp Gln Phe Arg Val Asn Gly Phe Pro Cys Lys Asn Ser Glu
485 490 495

Gly Tyr Cys Phe Met Gly Lys Cys Pro Thr Arg Glu Asp Gln Cys Ser
500 505 510

Glu Leu Phe Asp Asp Glu Ala Ile Glu Ser His Asp Ile Cys Tyr Lys
515 520 525

Met Asn Thr Lys Gly Asn Lys Phe Gly Tyr Cys Lys Asn Lys Glu Asn
530 535 540

Arg Phe Leu Pro Cys Glu Glu Lys Asp Val Arg Cys Gly Lys Ile Tyr
545 550 555 560

Cys Thr Gly Gly Glu Leu Ser Ser Leu Leu Gly Glu Asp Lys Thr Tyr
565 570 575

His Leu Lys Asp Pro Gln Lys Asn Ala Thr Val Lys Cys Lys Thr Ile
580 585 590

Phe Leu Tyr His Asp Ser Thr Asp Ile Gly Leu Val Ala Ser Gly Thr
595 600 605

Lys Cys Gly Glu Gly Met Val Cys Asn Asn Gly Glu Cys Leu Asn Met
610 615 620

```
Glu Lys Val Tyr Ile Ser Thr Asn Cys Pro Ser Gln Cys Asn Glu Asn
625                 630                 635                 640

Pro Val Asp Gly His Gly Leu Gln Cys His Cys Glu Glu Gly Gln Ala
                645                 650                 655

Pro Val Ala Cys Glu Glu Thr Leu His Val Thr Asn Ile Thr Ile Leu
            660                 665                 670

Val Val Val Leu Val Leu Val Ile Val Gly Ile Gly Val Leu Ile Leu
        675                 680                 685

Leu Val Arg Tyr Arg Lys Cys Ile Lys Leu Lys Gln Val Gln Ser Pro
    690                 695                 700

Pro Thr Glu Thr Leu Gly Val Glu Asn Lys Gly Tyr Phe Gly Asp Glu
705                 710                 715                 720

Gln Gln Ile Arg Thr Glu Pro Ile Leu Pro Glu Ile His Phe Leu Asn
                725                 730                 735

Gln Arg Thr Pro Glu Ser Leu Glu Ser Leu Pro Thr Ser Phe Ser Ser
            740                 745                 750

Pro His Tyr Ile Thr Leu Lys Pro Ala Ser Lys Asp Ser Arg Gly Ile
        755                 760                 765

Ala Asp Pro Asn Gln Ser Ala Lys
    770                 775


<210> 2235
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 553; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM7; "

<220>
<221> source
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<223> /note="Gene Name:
ADAM metallopeptidase domain 7; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H2U9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000393073"

<400> 2235

```
Met Leu Pro Gly Cys Ile Phe Leu Met Ile Leu Leu Ile Pro Gln Val
1               5                  10                  15

Lys Glu Lys Phe Ile Leu Gly Val Glu Gly Gln Gln Leu Val Arg Pro
            20                  25                  30

Lys Lys Leu Pro Leu Ile Gln Lys Arg Asp Thr Gly His Thr His Asp
        35                  40                  45

Asp Asp Ile Leu Lys Thr Tyr Glu Glu Glu Leu Leu Tyr Glu Ile Lys
    50                  55                  60

Leu Asn Arg Lys Thr Leu Val Leu His Leu Leu Arg Ser Arg Glu Phe
65                  70                  75                  80

Leu Gly Ser Asn Tyr Ser Glu Thr Phe Tyr Ser Met Lys Gly Glu Ala
                85                  90                  95

Phe Thr Arg His Pro Gln Ile Met Asp His Cys Phe Tyr Gln Gly Ser
            100                 105                 110

Ile Val His Glu Tyr Asp Ser Ala Ala Ser Ile Ser Thr Cys Asn Gly
        115                 120                 125

Leu Arg Gly Phe Phe Arg Ile Asn Asp Gln Arg Tyr Leu Ile Glu Pro
    130                 135                 140

Val Lys Tyr Ser Asp Glu Gly Glu His Leu Val Phe Lys Tyr Asn Leu
145                 150                 155                 160

Arg Val Pro Tyr Gly Ala Asn Tyr Ser Cys Thr Glu Leu Asn Phe Thr
                165                 170                 175

Arg Lys Thr Val Pro Gly Asp Asn Glu Ser Glu Glu Asp Ser Lys Ile
```

180 185 190

Lys Val Ser Thr Leu Leu Leu Ser Leu Pro Gln Met Lys His Leu Leu
195 200 205

Phe Ser
210

<210> 2236
<211> 516
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 553; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM7; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 7; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000430400"

<400> 2236
Met Val Asn Phe Val Asn Met Ile Tyr Lys Thr Leu Asn Ile His Val
1 5 10 15

Thr Leu Val Gly Ile Glu Ile Trp Thr His Glu Asp Lys Ile Glu Leu
20 25 30

Tyr Ser Asn Ile Glu Thr Thr Leu Leu Arg Phe Ser Phe Trp Gln Glu
35 40 45

Lys Ile Leu Lys Thr Arg Lys Asp Phe Asp His Val Val Leu Leu Ser
50 55 60

Gly Lys Trp Leu Tyr Ser His Val Gln Gly Ile Ser Tyr Pro Gly Gly
65 70 75 80

Met Cys Leu Pro Tyr Tyr Ser Thr Ser Ile Ile Lys Asp Leu Leu Pro
85 90 95

```
Asp Thr Asn Ile Ile Ala Asn Arg Met Ala His Gln Leu Gly His Asn
            100                 105                 110

Leu Gly Met Gln His Asp Glu Phe Pro Cys Thr Cys Pro Ser Gly Lys
        115                 120                 125

Cys Val Met Asp Ser Asp Gly Ser Ile Pro Ala Leu Lys Phe Ser Lys
    130                 135                 140

Cys Ser Gln Asn Gln Tyr His Gln Tyr Leu Lys Asp Tyr Lys Pro Thr
145                 150                 155                 160

Cys Met Leu Asn Ile Pro Phe Pro Tyr Asn Phe His Asp Phe Gln Phe
                165                 170                 175

Cys Gly Asn Lys Lys Leu Asp Glu Gly Glu Glu Cys Asp Cys Gly Pro
            180                 185                 190

Ala Gln Glu Cys Thr Asn Pro Cys Cys Asp Ala His Thr Cys Val Leu
        195                 200                 205

Lys Pro Gly Phe Thr Cys Ala Glu Gly Glu Cys Cys Glu Ser Cys Gln
    210                 215                 220

Ile Lys Lys Ala Gly Ser Ile Cys Arg Pro Ala Lys Asp Glu Cys Asp
225                 230                 235                 240

Phe Pro Glu Met Cys Thr Gly His Ser Pro Ala Cys Pro Lys Asp Gln
                245                 250                 255

Phe Arg Val Asn Gly Phe Pro Cys Lys Asn Ser Glu Gly Tyr Cys Phe
            260                 265                 270

Met Gly Lys Cys Pro Thr Arg Glu Asp Gln Cys Ser Glu Leu Phe Asp
        275                 280                 285

Asp Glu Ala Ile Glu Ser His Asp Ile Cys Tyr Lys Met Asn Thr Lys
    290                 295                 300

Gly Asn Lys Phe Gly Tyr Cys Lys Asn Lys Glu Asn Arg Phe Leu Pro
305                 310                 315                 320
```

Cys Glu Glu Lys Asp Val Arg Cys Gly Lys Ile Tyr Cys Thr Gly Gly
325 330 335

Glu Leu Ser Ser Leu Leu Gly Glu Asp Lys Thr Tyr His Leu Lys Asp
340 345 350

Pro Gln Lys Asn Ala Thr Val Lys Cys Lys Thr Ile Phe Leu Tyr His
355 360 365

Asp Ser Thr Asp Ile Gly Leu Val Ala Ser Gly Thr Lys Cys Gly Glu
370 375 380

Gly Met Val Cys Asn Asn Gly Glu Cys Leu Asn Met Glu Lys Val Tyr
385 390 395 400

Ile Ser Thr Asn Cys Pro Ser Gln Cys Asn Glu Asn Pro Val Asp Gly
405 410 415

His Gly Leu Gln Cys His Cys Glu Glu Gly Gln Ala Pro Val Ala Cys
420 425 430

Glu Glu Thr Leu His Val Thr Asn Ile Thr Ile Leu Val Val Val Leu
435 440 445

Val Leu Val Ile Val Gly Ile Gly Val Leu Ile Leu Leu Val Arg Tyr
450 455 460

Arg Lys Cys Ile Lys Leu Lys Gln Val Gln Ser Pro Pro Thr Glu Thr
465 470 475 480

Leu Gly Val Glu Asn Lys Gly Tyr Phe Gly Asp Glu Gln Gln Ile Arg
485 490 495

Thr Glu Pro Ile Leu Pro Glu Ile His Phe Leu Asn His Leu Leu Tyr
500 505 510

Gly Arg His Gln
515

<210> 2237
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 554; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM8; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452994"

<400> 2237
Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Gly
1 5 10 15

Pro Ala Pro Arg Glu Gly Glu Leu Arg Pro Trp Gly His Arg Ala Gln
20 25 30

Leu His Pro Pro Pro Ala Glu Glu Gln Gly Pro Ala Gly Leu Arg Leu
35 40 45

His Arg Asp Leu Tyr Gly Cys Gln Trp Leu Arg Gly Asp Gly Ala Ala
50 55 60

Ser Arg Ala Gly Pro Leu Leu Leu Pro Gly Pro Arg Arg Gly Val Pro
65 70 75 80

Gly Leu Ser Arg Gln Pro Gln His Leu Cys Arg Pro Gln Gly Phe Leu
85 90 95

Pro Gly Gly Val Arg Pro Ala Pro Asp Arg Ala Pro Gly
100 105

<210> 2238
<211> 733
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 554; "

<220>
<221> source

<223> /note="Gene Symbol: ADAM8; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 8; "

<220>
<221> source
<223> /note="Uniprot ID: P78325; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453043"

<400> 2238

```
Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Gly
1               5                  10                  15

Pro Ala Pro Arg Glu Gly Glu Leu Arg Pro Trp Gly His Arg Ala Gln
            20                  25                  30

Leu His Pro Pro Pro Ala Glu Glu Gln Gly Pro Ala Gly Leu Arg Leu
        35                  40                  45

His Arg Asp Leu Tyr Gly Cys Gln Trp Leu Arg Gly Asp Gly Ala Ala
    50                  55                  60

Ser Arg Ala Gly Pro Leu Leu Leu Pro Gly Pro Arg Arg Gly Val Pro
65                  70                  75                  80

Gly Leu Ser Arg Gln Pro Gln His Leu Cys Arg Pro Gln Val Gly Ser
                85                  90                  95

Asp Leu His Leu Ile Glu Pro Leu Asp Glu Gly Gly Glu Gly Gly Arg
            100                 105                 110

His Ala Val Tyr Gln Ala Glu His Leu Leu Gln Thr Ala Gly Thr Cys
        115                 120                 125

Gly Val Ser Asp Asp Ser Leu Gly Ser Leu Leu Gly Pro Arg Thr Ala
    130                 135                 140

Ala Val Phe Arg Pro Arg Pro Gly Asp Ser Leu Pro Ser Arg Glu Thr
145                 150                 155                 160

Arg Tyr Val Glu Leu Tyr Val Val Val Asp Asn Ala Glu Phe Gln Met
```

```
                165                 170                 175

Leu Gly Ser Glu Ala Ala Val Arg His Arg Val Leu Glu Val Val Asn
            180                 185                 190

His Val Asp Lys Leu Tyr Gln Lys Leu Asn Phe Arg Val Val Leu Val
        195                 200                 205

Gly Leu Glu Ile Trp Asn Ser Gln Asp Arg Phe His Val Ser Pro Asp
    210                 215                 220

Pro Ser Val Thr Leu Glu Asn Leu Leu Thr Trp Gln Ala Arg Gln Arg
225                 230                 235                 240

Thr Arg Arg His Leu His Asp Asn Val Gln Leu Ile Thr Gly Val Asp
                245                 250                 255

Phe Thr Gly Thr Thr Val Gly Phe Ala Arg Val Ser Ala Met Cys Ser
            260                 265                 270

His Ser Ser Gly Ala Val Asn Gln Asp His Ser Lys Asn Pro Val Gly
        275                 280                 285

Val Ala Cys Thr Met Ala His Glu Met Gly His Asn Leu Gly Met Asp
    290                 295                 300

His Asp Glu Asn Val Gln Gly Cys Arg Cys Gln Glu Arg Phe Glu Ala
305                 310                 315                 320

Gly Arg Cys Ile Met Ala Gly Ser Ile Gly Ser Ser Phe Pro Arg Met
                325                 330                 335

Phe Ser Asp Cys Ser Gln Ala Tyr Leu Glu Ser Phe Leu Glu Arg Pro
            340                 345                 350

Gln Ser Val Cys Leu Ala Asn Ala Pro Asp Leu Ser His Leu Val Gly
        355                 360                 365

Gly Pro Val Cys Gly Asn Leu Phe Val Glu Arg Gly Glu Gln Cys Asp
    370                 375                 380

Cys Gly Pro Pro Glu Asp Cys Arg Asn Arg Cys Cys Asn Ser Thr Thr
385                 390                 395                 400
```

```
Cys Gln Leu Ala Glu Gly Ala Gln Cys Ala His Gly Thr Cys Cys Gln
                405                 410                 415

Glu Cys Lys Val Lys Pro Ala Gly Glu Leu Cys Arg Pro Lys Lys Asp
            420                 425                 430

Met Cys Asp Leu Glu Glu Phe Cys Asp Gly Arg His Pro Glu Cys Pro
        435                 440                 445

Glu Asp Ala Phe Gln Glu Asn Gly Thr Pro Cys Ser Gly Gly Tyr Cys
    450                 455                 460

Tyr Asn Gly Ala Cys Pro Thr Leu Ala Gln Gln Cys Gln Ala Phe Trp
465                 470                 475                 480

Gly Pro Gly Gly Gln Ala Ala Glu Glu Ser Cys Phe Ser Tyr Asp Ile
                485                 490                 495

Leu Pro Gly Cys Lys Ala Ser Arg Tyr Arg Ala Asp Met Cys Gly Val
            500                 505                 510

Leu Gln Cys Lys Gly Gly Gln Gln Pro Leu Gly Arg Ala Ile Cys Ile
        515                 520                 525

Val Asp Val Cys His Ala Leu Thr Thr Glu Asp Gly Thr Ala Tyr Glu
    530                 535                 540

Pro Val Pro Glu Gly Thr Arg Cys Gly Pro Glu Lys Val Cys Asn His
545                 550                 555                 560

Lys Gln Glu Cys His Cys His Ala Gly Trp Ala Pro Pro His Cys Ala
                565                 570                 575

Lys Leu Leu Thr Glu Val His Ala Ala Ser Gly Ser Leu Pro Val Phe
            580                 585                 590

Val Val Val Val Leu Val Leu Leu Ala Val Val Leu Val Thr Leu Ala
        595                 600                 605

Gly Ile Ile Val Tyr Arg Lys Ala Arg Ser Arg Ile Leu Ser Arg Asn
    610                 615                 620
```

```
Val Ala Pro Lys Thr Thr Met Gly Arg Ser Asn Pro Leu Phe His Gln
625                 630                 635                 640

Ala Ala Ser Arg Val Pro Ala Lys Gly Gly Ala Pro Ala Pro Ser Arg
                645                 650                 655

Gly Pro Gln Glu Leu Val Pro Thr Thr His Pro Gly Gln Pro Ala Arg
            660                 665                 670

His Pro Ala Ser Ser Val Ala Leu Lys Arg Pro Pro Pro Ala Pro Pro
        675                 680                 685

Val Thr Val Ser Ser Pro Pro Phe Pro Val Pro Val Tyr Thr Arg Gln
    690                 695                 700

Ala Pro Lys Gln Gly Ala Val Gly Pro Lys Val Ala Leu Lys Pro Pro
705                 710                 715                 720

Ile Gln Arg Lys Gln Gly Ala Gly Ala Pro Thr Ala Pro
                725                 730
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<210> 2239
<211> 824
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 554; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM8; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 8; "

<220>
<221> source
<223> /note="Uniprot ID: P78325; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453302"

<400> 2239

```
Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Ala
```

1 5 10 15

Ile Ala Pro Ser Arg Pro Trp Ala Leu Met Glu Gln Tyr Glu Val Val
20 25 30

Leu Pro Trp Arg Leu Pro Gly Pro Arg Val Arg Arg Ala Leu Pro Ser
35 40 45

His Leu Gly Leu His Pro Glu Arg Val Ser Tyr Val Leu Gly Ala Thr
50 55 60

Gly His Asn Phe Thr Leu His Leu Arg Lys Asn Arg Asp Leu Leu Gly
65 70 75 80

Ser Gly Tyr Thr Glu Thr Tyr Thr Ala Ala Asn Gly Ser Glu Val Thr
85 90 95

Glu Gln Pro Arg Gly Gln Asp His Cys Phe Tyr Gln Gly His Val Glu
100 105 110

Gly Tyr Pro Asp Ser Ala Ala Ser Leu Ser Thr Cys Ala Gly Leu Arg
115 120 125

Gly Phe Phe Gln Val Gly Ser Asp Leu His Leu Ile Glu Pro Leu Asp
130 135 140

Glu Gly Gly Glu Gly Gly Arg His Ala Val Tyr Gln Ala Glu His Leu
145 150 155 160

Leu Gln Thr Ala Gly Thr Cys Gly Val Ser Asp Asp Ser Leu Gly Ser
165 170 175

Leu Leu Gly Pro Arg Thr Ala Ala Val Phe Arg Pro Arg Pro Gly Asp
180 185 190

Ser Leu Pro Ser Arg Glu Thr Arg Tyr Val Glu Leu Tyr Val Val Val
195 200 205

Asp Asn Ala Glu Phe Gln Met Leu Gly Ser Glu Ala Ala Val Arg His
210 215 220

Arg Val Leu Glu Val Val Asn His Val Asp Lys Leu Tyr Gln Lys Leu
225 230 235 240

```
Asn Phe Arg Val Val Leu Val Gly Leu Glu Ile Trp Asn Ser Gln Asp
                245                 250                 255

Arg Phe His Val Ser Pro Asp Pro Ser Val Thr Leu Glu Asn Leu Leu
            260                 265                 270

Thr Trp Gln Ala Arg Gln Arg Thr Arg Arg His Leu His Asp Asn Val
        275                 280                 285

Gln Leu Ile Thr Gly Val Asp Phe Thr Gly Thr Thr Val Gly Phe Ala
    290                 295                 300

Arg Val Ser Ala Met Cys Ser His Ser Ser Gly Ala Val Asn Gln Asp
305                 310                 315                 320

His Ser Lys Asn Pro Val Gly Val Ala Cys Thr Met Ala His Glu Met
                325                 330                 335

Gly His Asn Leu Gly Met Asp His Asp Glu Asn Val Gln Gly Cys Arg
            340                 345                 350

Cys Gln Glu Arg Phe Glu Ala Gly Arg Cys Ile Met Ala Gly Ser Ile
        355                 360                 365

Gly Ser Ser Phe Pro Arg Met Phe Ser Asp Cys Ser Gln Ala Tyr Leu
    370                 375                 380

Glu Ser Phe Leu Glu Arg Pro Gln Ser Val Cys Leu Ala Asn Ala Pro
385                 390                 395                 400

Asp Leu Ser His Leu Val Gly Gly Pro Val Cys Gly Asn Leu Phe Val
                405                 410                 415

Glu Arg Gly Glu Gln Cys Asp Cys Gly Pro Pro Glu Asp Cys Arg Asn
            420                 425                 430

Arg Cys Cys Asn Ser Thr Thr Cys Gln Leu Ala Glu Gly Ala Gln Cys
        435                 440                 445

Ala His Gly Thr Cys Cys Gln Glu Cys Lys Val Lys Pro Ala Gly Glu
    450                 455                 460
```

```
Leu Cys Arg Pro Lys Lys Asp Met Cys Asp Leu Glu Glu Phe Cys Asp
465                 470                 475                 480

Gly Arg His Pro Glu Cys Pro Glu Asp Ala Phe Gln Glu Asn Gly Thr
                485                 490                 495

Pro Cys Ser Gly Gly Tyr Cys Tyr Asn Gly Ala Cys Pro Thr Leu Ala
            500                 505                 510

Gln Gln Cys Gln Ala Phe Trp Gly Pro Gly Gly Gln Ala Ala Glu Glu
        515                 520                 525

Ser Cys Phe Ser Tyr Asp Ile Leu Pro Gly Cys Lys Ala Ser Arg Tyr
    530                 535                 540

Arg Ala Asp Met Cys Gly Val Leu Gln Cys Lys Gly Gly Gln Gln Pro
545                 550                 555                 560

Leu Gly Arg Ala Ile Cys Ile Val Asp Val Cys His Ala Leu Thr Thr
                565                 570                 575

Glu Asp Gly Thr Ala Tyr Glu Pro Val Pro Glu Gly Thr Arg Cys Gly
            580                 585                 590

Pro Glu Lys Val Cys Trp Lys Gly Arg Cys Gln Asp Leu His Val Tyr
        595                 600                 605

Arg Ser Ser Asn Cys Ser Ala Gln Cys His Asn His Gly Val Cys Asn
    610                 615                 620

His Lys Gln Glu Cys His Cys His Ala Gly Trp Ala Pro Pro His Cys
625                 630                 635                 640

Ala Lys Leu Leu Thr Glu Val His Ala Ala Ser Gly Ser Leu Pro Val
                645                 650                 655

Phe Val Val Val Val Leu Val Leu Leu Ala Val Val Leu Val Thr Leu
            660                 665                 670

Ala Gly Ile Ile Val Tyr Arg Lys Ala Arg Ser Arg Ile Leu Ser Arg
        675                 680                 685
```

```
Asn Val Ala Pro Lys Thr Thr Met Gly Arg Ser Asn Pro Leu Phe His
    690                 695                 700

Gln Ala Ala Ser Arg Val Pro Ala Lys Gly Gly Ala Pro Ala Pro Ser
705                 710                 715                 720

Arg Gly Pro Gln Glu Leu Val Pro Thr Thr His Pro Gly Gln Pro Ala
                725                 730                 735

Arg His Pro Ala Ser Ser Val Ala Leu Lys Arg Pro Pro Pro Ala Pro
            740                 745                 750

Pro Val Thr Val Ser Ser Pro Pro Phe Pro Val Pro Val Tyr Thr Arg
        755                 760                 765

Gln Ala Pro Lys Gln Val Ile Lys Pro Thr Phe Ala Pro Pro Val Pro
    770                 775                 780

Pro Val Lys Pro Gly Ala Gly Ala Ala Asn Pro Gly Pro Ala Glu Gly
785                 790                 795                 800

Ala Val Gly Pro Lys Val Ala Leu Lys Pro Pro Ile Gln Arg Lys Gln
                805                 810                 815

Gly Ala Gly Ala Pro Thr Ala Pro
            820


<210> 2240
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 554; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM8; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453735"
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<400> 2240
Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Ala
1 5 10 15

Ile Ala Pro Ser Arg Pro Trp Ala Leu Met Glu Gln Tyr Glu Val Val
20 25 30

Leu Pro Trp Arg Leu Pro Gly Pro Arg Val Arg Arg Ala Leu Pro Ser
35 40 45

His Leu Gly Gly Gln Phe Arg Pro Gln Pro Cys Pro Tyr Leu Ser Ile
50 55 60

Arg Gly Thr Tyr Tyr Arg Pro Ala Arg Cys Pro Gly Leu Ile Gln Pro
65 70 75 80

Val Ala Gln Leu Arg Leu Ser Gln Ser Ser Ala Gly Arg Ala Pro Ala
85 90 95

Cys Thr Trp Gly Leu Glu Met Gln Trp Ser Ser Arg Arg Leu Cys Arg
100 105 110

His His Gln Gly Leu His Pro Glu Arg Val Ser Tyr Val Leu Gly Ala
115 120 125

Thr Gly His Asn Phe Thr Leu His Leu Arg Lys Asn Arg Asp Leu Leu
130 135 140

Gly Ser Gly Tyr Thr Glu Thr Tyr Thr Ala Ala Asn Gly Ser Glu Val
145 150 155 160

Thr Glu Gln Pro Arg Gly Gln Asp His Cys Phe Tyr Gln Gly His Val
165 170 175

Glu Gly Tyr Pro Asp Ser Ala Ala Ser Leu Ser Thr Cys Ala Gly Leu
180 185 190

Arg Gly Phe Phe Gln Val Gly Ser Asp Leu His Leu Ile Glu Pro Leu
195 200 205

Asp Glu Gly Gly Glu Gly Gly Arg His Ala Val Tyr Gln Ala Glu His
210 215 220

Leu Leu Gln Thr Ala Gly Thr Cys Gly Val Ser Asp Asp Ser Leu Gly
225 230 235 240

Ser Leu Leu Gly Pro
245

<210> 2241
<211> 742
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ADAM8; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 8; "

<220>
<221> source
<223> /note="Uniprot ID: P78325; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453855"

<400> 2241
Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Ala
1 5 10 15

Ile Ala Pro Ser Arg Pro Trp Ala Leu Met Glu Gln Tyr Glu Val Val
20 25 30

Leu Pro Trp Arg Leu Pro Gly Pro Arg Val Arg Arg Ala Leu Pro Ser
35 40 45

His Leu Gly Leu His Pro Glu Arg Val Ser Tyr Val Leu Gly Ala Thr
50 55 60

Gly His Asn Phe Thr Leu His Leu Arg Lys Asn Arg Asp Leu Leu Gly
65 70 75 80

Ser Gly Tyr Thr Glu Thr Tyr Thr Ala Ala Asn Gly Ser Glu Val Thr

```
                85                  90                  95

Glu Gln Pro Arg Gly Gln Asp His Cys Phe Tyr Gln Gly His Val Glu
            100                 105                 110

Gly Tyr Pro Asp Ser Ala Ala Ser Leu Ser Thr Cys Ala Gly Leu Arg
        115                 120                 125

Gly Phe Phe Gln Val Gly Ser Asp Leu His Leu Ile Glu Pro Leu Asp
    130                 135                 140

Glu Gly Gly Glu Gly Gly Arg His Ala Val Tyr Gln Ala Glu His Leu
145                 150                 155                 160

Leu Gln Thr Ala Gly Thr Cys Gly Val Ser Asp Asp Ser Leu Gly Ser
                165                 170                 175

Leu Leu Gly Pro Arg Thr Ala Ala Val Phe Arg Pro Arg Pro Gly Asp
            180                 185                 190

Ser Leu Pro Ser Arg Glu Thr Arg Tyr Val Glu Leu Tyr Val Val Val
        195                 200                 205

Asp Asn Ala Glu Phe Gln Met Leu Gly Ser Glu Ala Ala Val Arg His
    210                 215                 220

Arg Val Leu Glu Val Val Asn His Val Asp Lys Leu Tyr Gln Lys Leu
225                 230                 235                 240

Asn Phe Arg Val Val Leu Val Gly Leu Glu Ile Trp Asn Ser Gln Asp
                245                 250                 255

Arg Phe His Val Ser Pro Asp Pro Ser Val Thr Leu Glu Asn Leu Leu
            260                 265                 270

Thr Trp Gln Ala Arg Gln Arg Thr Arg Arg His Leu His Asp Asn Val
        275                 280                 285

Gln Leu Ile Thr Gly Val Asp Phe Thr Gly Thr Thr Val Gly Phe Ala
    290                 295                 300

Arg Val Ser Ala Met Cys Ser His Ser Ser Gly Ala Val Asn Gln Asp
305                 310                 315                 320
```

```
His Ser Lys Asn Pro Val Gly Val Ala Cys Thr Met Ala His Glu Met
                325                 330                 335

Gly His Asn Leu Gly Met Asp His Asp Glu Asn Val Gln Gly Cys Arg
            340                 345                 350

Cys Gln Glu Arg Phe Glu Ala Gly Arg Cys Ile Met Ala Gly Ser Ile
        355                 360                 365

Gly Ser Ser Phe Pro Arg Met Phe Ser Asp Cys Ser Gln Ala Tyr Leu
    370                 375                 380

Glu Ser Phe Leu Glu Arg Pro Gln Ser Val Cys Leu Ala Asn Ala Pro
385                 390                 395                 400

Asp Leu Ser His Leu Val Gly Gly Pro Val Cys Gly Asn Leu Phe Val
                405                 410                 415

Glu Arg Gly Glu Gln Cys Asp Cys Gly Pro Pro Glu Asp Cys Arg Asn
            420                 425                 430

Arg Cys Cys Asn Ser Thr Thr Cys Gln Leu Ala Glu Gly Ala Gln Cys
        435                 440                 445

Ala His Gly Thr Cys Cys Gln Glu Cys Lys Val Lys Pro Ala Gly Glu
    450                 455                 460

Leu Cys Arg Pro Lys Lys Asp Met Cys Asp Leu Glu Glu Phe Cys Asp
465                 470                 475                 480

Gly Arg His Pro Glu Cys Pro Glu Asp Ala Phe Gln Glu Asn Gly Thr
                485                 490                 495

Pro Cys Ser Gly Gly Tyr Cys Tyr Asn Gly Ala Cys Pro Thr Leu Ala
            500                 505                 510

Gln Gln Cys Gln Ala Phe Trp Gly Pro Gly Gly Gln Ala Ala Glu Glu
        515                 520                 525

Ser Cys Phe Ser Tyr Asp Ile Leu Pro Gly Cys Lys Ala Ser Arg Tyr
    530                 535                 540
```

```
Arg Ala Asp Met Cys Gly Val Leu Gln Cys Lys Gly Gly Gln Gln Pro
545                 550                 555                 560

Leu Gly Arg Ala Ile Cys Ile Val Asp Val Cys His Ala Leu Thr Thr
                565                 570                 575

Glu Asp Gly Thr Ala Tyr Glu Pro Val Pro Glu Gly Thr Arg Cys Gly
            580                 585                 590

Pro Glu Lys Val Cys Trp Lys Gly Arg Cys Gln Asp Leu His Val Tyr
        595                 600                 605

Arg Ser Ser Asn Cys Ser Ala Gln Cys His Asn His Gly Val Cys Asn
    610                 615                 620

His Lys Gln Glu Cys His Cys His Ala Gly Trp Ala Pro Pro His Cys
625                 630                 635                 640

Ala Lys Leu Leu Thr Glu Val His Ala Gly Cys Gln Pro Arg Ala Gly
                645                 650                 655

Gln Gly Arg Gly Ser Ser Pro Ile Gln Gly Pro Pro Arg Ala Gly Pro
            660                 665                 670

His His Pro Pro Gly Pro Ala Arg Pro Thr Pro Gly Leu Leu Gly Gly
        675                 680                 685

Ser Glu Glu Ala Ala Pro Cys Ser Ser Gly His Cys Val Gln Pro Thr
    690                 695                 700

Leu Pro Ser Ser Cys Leu His Pro Ala Gly Thr Lys Ala Gly His Gln
705                 710                 715                 720

Ala Asn Val Arg Thr Pro Ser Ala Pro Ser Gln Thr Arg Gly Trp Cys
                725                 730                 735

Gly Gln Pro Trp Ser Ser
            740
```

<210> 2242
<211> 655
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM9; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="Uniprot ID: Q13443; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369249"

<400> 2242
Met Gly Ser Gly Ala Arg Phe Pro Ser Gly Thr Leu Arg Val Arg Trp
1   5   10   15

Leu Leu Leu Leu Gly Leu Val Gly Pro Val Leu Gly Ala Ala Arg Pro
            20   25   30

Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
        35   40   45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
    50   55   60

Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
65   70   75   80

Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
                85   90   95

Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Asn
            100   105   110

His Cys His Tyr Arg Gly Tyr Val Glu Gly Val His Asn Ser Ser Ile
        115   120   125

Ala Leu Ser Asp Cys Phe Gly Leu Arg Gly Leu Leu His Leu Glu Asn
    130   135   140

```
Ala Ser Tyr Gly Ile Glu Pro Leu Gln Asn Ser Ser His Phe Glu His
145                 150                 155                 160

Ile Ile Tyr Arg Met Asp Asp Val Tyr Lys Glu Pro Leu Lys Cys Gly
                165                 170                 175

Val Ser Asn Lys Asp Ile Glu Lys Glu Thr Ala Lys Asp Glu Glu Glu
            180                 185                 190

Glu Pro Pro Ser Met Thr Gln Leu Leu Arg Arg Arg Arg Ala Val Leu
        195                 200                 205

Pro Gln Thr Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg
    210                 215                 220

Tyr Asp Met Met Gly Arg Asn Gln Thr Ala Val Arg Glu Glu Met Ile
225                 230                 235                 240

Leu Leu Ala Asn Tyr Leu Asp Ser Met Tyr Ile Met Leu Asn Ile Arg
                245                 250                 255

Ile Val Leu Val Gly Leu Glu Ile Trp Thr Asn Gly Asn Leu Ile Asn
            260                 265                 270

Ile Val Gly Gly Ala Gly Asp Val Leu Gly Asn Phe Val Gln Trp Arg
        275                 280                 285

Glu Lys Phe Leu Ile Thr Arg Arg Arg His Asp Ser Ala Gln Leu Val
    290                 295                 300

Leu Lys Lys Gly Phe Gly Gly Thr Ala Gly Met Ala Phe Val Gly Thr
305                 310                 315                 320

Val Cys Ser Arg Ser His Ala Gly Gly Ile Asn Val Phe Gly Gln Ile
                325                 330                 335

Thr Val Glu Thr Phe Ala Ser Ile Val Ala His Glu Leu Gly His Asn
            340                 345                 350

Leu Gly Met Asn His Asp Asp Gly Arg Asp Cys Ser Cys Gly Ala Lys
        355                 360                 365
```

```
Ser Cys Ile Met Asn Ser Gly Ala Ser Gly Ser Arg Asn Phe Ser Ser
    370                 375                 380

Cys Ser Ala Glu Asp Phe Glu Lys Leu Thr Leu Asn Lys Gly Gly Asn
385                 390                 395                 400

Cys Leu Leu Asn Ile Pro Lys Pro Asp Glu Ala Tyr Ser Ala Pro Ser
                405                 410                 415

Cys Gly Asn Lys Leu Val Asp Ala Gly Glu Glu Cys Asp Cys Gly Thr
            420                 425                 430

Pro Lys Glu Cys Glu Leu Asp Pro Cys Cys Glu Gly Ser Thr Cys Lys
        435                 440                 445

Leu Lys Ser Phe Ala Glu Cys Ala Tyr Gly Asp Cys Cys Lys Asp Cys
    450                 455                 460

Arg Phe Leu Pro Gly Gly Thr Leu Cys Arg Gly Lys Thr Ser Glu Cys
465                 470                 475                 480

Asp Val Pro Glu Tyr Cys Asn Gly Ser Ser Gln Phe Cys Gln Pro Asp
                485                 490                 495

Val Phe Ile Gln Asn Gly Tyr Pro Cys Gln Asn Asn Lys Ala Tyr Cys
            500                 505                 510

Tyr Asn Gly Met Cys Gln Tyr Tyr Asp Ala Gln Cys Gln Val Ile Phe
        515                 520                 525

Gly Ser Lys Ala Lys Ala Ala Pro Lys Asp Cys Phe Ile Glu Val Asn
    530                 535                 540

Ser Lys Gly Asp Arg Phe Gly Asn Cys Gly Phe Ser Gly Asn Glu Tyr
545                 550                 555                 560

Lys Lys Cys Ala Thr Gly Asn Ala Leu Cys Gly Lys Leu Gln Cys Glu
                565                 570                 575

Asn Val Gln Glu Ile Pro Val Phe Gly Ile Val Pro Ala Ile Ile Gln
            580                 585                 590
```

```
Thr Pro Ser Arg Gly Thr Lys Cys Trp Gly Val Asp Phe Gln Leu Gly
        595                 600                 605

Ser Asp Val Pro Asp Pro Gly Met Val Asn Glu Gly Thr Lys Cys Gly
    610                 615                 620

Ala Gly Lys Ile Cys Arg Asn Phe Gln Cys Val Asp Ala Ser Val Leu
625                 630                 635                 640

Asn Tyr Asp Cys Asp Val Gln Lys Lys Cys His Gly His Gly Lys
                645                 650                 655
```

<210> 2243
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM9; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000417066"

<400> 2243

```
Met Gly Ser Gly Ala Arg Phe Pro Ser Gly Thr Leu Arg Val Arg Trp
1               5                   10                  15

Leu Leu Leu Leu Gly Leu Val Gly Pro Val Leu Gly Ala Ala Arg Pro
            20                  25                  30

Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
        35                  40                  45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
    50                  55                  60

Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
65                  70                  75                  80
```

```
Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
                85                  90                  95

Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Val
            100                 105                 110

Met Tyr Phe Ser Leu Asp Pro Ile Ala Asn Phe Lys Thr Ile Ile Ile
        115                 120                 125


<210> 2244
<211> 712
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM9; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418437"

<400> 2244
Met Gly Ser Gly Ala Arg Phe Pro Ser Gly Thr Leu Arg Val Arg Trp
1               5                   10                  15

Leu Leu Leu Leu Gly Leu Val Gly Pro Val Leu Gly Ala Ala Arg Pro
            20                  25                  30

Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
        35                  40                  45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
    50                  55                  60

Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
65                  70                  75                  80
```

```
Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
                85                  90                  95

Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Asn
            100                 105                 110

His Cys His Tyr Arg Gly Tyr Val Glu Gly Val His Asn Ser Ser Ile
        115                 120                 125

Ala Leu Ser Asp Cys Phe Gly Leu Arg Gly Leu Leu His Leu Glu Asn
    130                 135                 140

Ala Ser Tyr Gly Ile Glu Pro Leu Gln Asn Ser Ser His Phe Glu His
145                 150                 155                 160

Ile Ile Tyr Arg Met Asp Asp Val Tyr Lys Glu Pro Leu Lys Cys Gly
                165                 170                 175

Val Ser Asn Lys Asp Ile Glu Lys Glu Thr Ala Lys Asp Glu Glu Glu
            180                 185                 190

Glu Pro Pro Ser Met Thr Gln Leu Leu Arg Arg Arg Arg Ala Val Leu
        195                 200                 205

Pro Gln Thr Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg
    210                 215                 220

Tyr Asp Met Met Gly Arg Asn Gln Thr Ala Val Arg Glu Glu Met Ile
225                 230                 235                 240

Leu Leu Ala Asn Tyr Leu Asp Ser Met Tyr Ile Met Leu Asn Ile Arg
                245                 250                 255

Ile Val Leu Val Gly Leu Glu Ile Trp Thr Asn Gly Asn Leu Ile Asn
            260                 265                 270

Ile Val Gly Gly Ala Gly Asp Val Leu Gly Asn Phe Val Gln Trp Arg
        275                 280                 285

Glu Lys Phe Leu Ile Thr Arg Arg Arg His Asp Ser Ala Gln Leu Val
    290                 295                 300

Leu Lys Lys Gly Phe Gly Gly Thr Ala Gly Met Ala Phe Val Gly Thr
```

305 310 315 320

Val Cys Ser Arg Ser His Ala Gly Gly Ile Asn Val Phe Gly Gln Ile
325 330 335

Thr Val Glu Thr Phe Ala Ser Ile Val Ala His Glu Leu Gly His Asn
340 345 350

Leu Gly Met Asn His Asp Asp Gly Arg Asp Cys Ser Cys Gly Ala Lys
355 360 365

Ser Cys Ile Met Asn Ser Gly Ala Ser Gly Ser Arg Asn Phe Ser Ser
370 375 380

Cys Ser Ala Glu Asp Phe Glu Lys Leu Thr Leu Asn Lys Gly Gly Asn
385 390 395 400

Cys Leu Leu Asn Ile Pro Lys Pro Asp Glu Ala Tyr Ser Ala Pro Ser
405 410 415

Cys Gly Asn Lys Leu Val Asp Ala Gly Glu Glu Cys Asp Cys Gly Thr
420 425 430

Pro Lys Glu Cys Glu Leu Asp Pro Cys Cys Glu Gly Ser Thr Cys Lys
435 440 445

Leu Lys Ser Phe Ala Glu Cys Ala Tyr Gly Asp Cys Cys Lys Asp Cys
450 455 460

Arg Phe Leu Pro Gly Gly Thr Leu Cys Arg Gly Lys Thr Ser Glu Cys
465 470 475 480

Asp Val Pro Glu Tyr Cys Asn Gly Ser Ser Gln Phe Cys Gln Pro Asp
485 490 495

Val Phe Ile Gln Asn Gly Tyr Pro Cys Gln Asn Asn Lys Ala Tyr Cys
500 505 510

Tyr Asn Gly Met Cys Gln Tyr Tyr Asp Ala Gln Cys Gln Val Ile Phe
515 520 525

Gly Ser Lys Ala Lys Ala Ala Pro Lys Asp Cys Phe Ile Glu Val Asn
530 535 540

```
Ser Lys Gly Asp Arg Phe Gly Asn Cys Gly Phe Ser Gly Asn Glu Tyr
545                 550                 555                 560

Lys Lys Cys Ala Thr Gly Asn Ala Leu Cys Gly Lys Leu Gln Cys Glu
                565                 570                 575

Asn Val Gln Glu Ile Pro Val Phe Gly Ile Val Pro Ala Ile Ile Gln
            580                 585                 590

Thr Pro Ser Arg Gly Thr Lys Cys Trp Gly Val Asp Phe Gln Leu Gly
        595                 600                 605

Ser Asp Val Pro Asp Pro Gly Met Val Asn Glu Gly Thr Lys Cys Gly
    610                 615                 620

Ala Gly Lys Ile Cys Arg Asn Phe Gln Cys Val Asp Ala Ser Val Leu
625                 630                 635                 640

Asn Tyr Asp Cys Asp Val Gln Lys Lys Cys His Gly His Gly Val Cys
                645                 650                 655

Asn Ser Asn Lys Asn Cys His Cys Glu Asn Gly Trp Ala Pro Pro Asn
            660                 665                 670

Cys Glu Thr Lys Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Thr Tyr
        675                 680                 685

Asn Gly Gln Met Ala Lys Ile Lys Gln Thr Leu Leu Asp Ser Arg Gly
    690                 695                 700

Val Phe Leu Asp Met Phe Leu Gln
705                 710


<210> 2245
<211> 628
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
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<223> /note="Gene Symbol: ADAM9; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000418737"

<400> 2245

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Met Gly Ser Gly Ala Arg Phe Pro Ser Gly Thr Leu Arg Val Arg Trp
1               5                  10                  15

Leu Leu Leu Leu Gly Leu Val Gly Pro Val Leu Gly Ala Ala Arg Pro
            20                  25                  30

Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
        35                  40                  45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
    50                  55                  60

Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
65                  70                  75                  80

Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
                85                  90                  95

Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Asn
            100                 105                 110

His Cys His Tyr Arg Gly Tyr Val Glu Gly Val His Asn Ser Ser Ile
        115                 120                 125

Ala Leu Ser Asp Cys Phe Gly Leu Arg Gly Leu Leu His Leu Glu Asn
    130                 135                 140

Ala Ser Tyr Gly Ile Glu Pro Leu Gln Asn Ser Ser His Phe Glu His
145                 150                 155                 160

Ile Ile Tyr Arg Met Asp Asp Val Tyr Lys Glu Pro Leu Lys Cys Gly
                165                 170                 175

Val Ser Asn Lys Asp Ile Glu Lys Glu Thr Ala Lys Asp Glu Glu Glu
```

```
            180                 185                 190

Glu Pro Pro Ser Met Thr Gln Leu Leu Arg Arg Arg Ala Val Leu
        195                 200                 205

Pro Gln Thr Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg
    210                 215                 220

Tyr Asp Met Met Gly Arg Asn Gln Thr Ala Val Arg Glu Glu Met Ile
225                 230                 235                 240

Leu Leu Ala Asn Tyr Leu Asp Ser Met Tyr Ile Met Leu Asn Ile Arg
                245                 250                 255

Ile Val Leu Val Gly Leu Glu Ile Trp Thr Asn Gly Asn Leu Ile Asn
            260                 265                 270

Ile Val Gly Gly Ala Gly Asp Val Leu Gly Asn Phe Val Gln Trp Arg
        275                 280                 285

Glu Lys Phe Leu Ile Thr Arg Arg Arg His Asp Ser Ala Gln Leu Val
    290                 295                 300

Leu Lys Lys Gly Phe Gly Gly Thr Ala Gly Met Ala Phe Val Gly Thr
305                 310                 315                 320

Val Cys Ser Arg Ser His Ala Gly Gly Ile Asn Val Phe Gly Gln Ile
                325                 330                 335

Thr Val Glu Thr Phe Ala Ser Ile Val Ala His Glu Leu Gly His Asn
            340                 345                 350

Leu Gly Met Asn His Asp Asp Gly Arg Asp Cys Ser Cys Gly Ala Lys
        355                 360                 365

Ser Cys Ile Met Asn Ser Gly Ala Ser Gly Ser Arg Asn Phe Ser Ser
    370                 375                 380

Cys Ser Ala Glu Asp Phe Glu Lys Leu Thr Leu Asn Lys Gly Gly Asn
385                 390                 395                 400

Cys Leu Leu Asn Ile Pro Lys Pro Asp Glu Ala Tyr Ser Ala Pro Ser
                405                 410                 415
```

Cys Gly Asn Lys Leu Val Asp Ala Gly Glu Glu Cys Asp Cys Gly Thr
420 425 430

Pro Lys Glu Cys Glu Leu Asp Pro Cys Cys Glu Gly Ser Thr Cys Lys
435 440 445

Leu Lys Ser Phe Ala Glu Cys Ala Tyr Gly Asp Cys Cys Lys Asp Cys
450 455 460

Arg Phe Leu Pro Gly Gly Thr Leu Cys Arg Gly Lys Thr Ser Glu Cys
465 470 475 480

Asp Val Pro Glu Tyr Cys Asn Gly Ser Ser Gln Phe Cys Gln Pro Asp
485 490 495

Val Phe Ile Gln Asn Gly Tyr Pro Cys Gln Asn Asn Lys Ala Tyr Cys
500 505 510

Tyr Asn Gly Met Cys Gln Tyr Tyr Asp Ala Gln Cys Gln Val Ile Phe
515 520 525

Gly Ser Lys Ala Lys Ala Ala Pro Lys Asp Cys Phe Ile Glu Val Asn
530 535 540

Ser Lys Gly Asp Arg Phe Gly Asn Cys Gly Phe Ser Gly Asn Glu Tyr
545 550 555 560

Lys Lys Cys Ala Thr Gly Asn Ala Leu Cys Gly Lys Leu Gln Cys Glu
565 570 575

Asn Val Gln Glu Ile Pro Val Phe Gly Ile Val Pro Ala Ile Ile Gln
580 585 590

Thr Pro Ser Arg Gly Thr Lys Cys Trp Gly Val Asp Phe Gln Leu Gly
595 600 605

Ser Asp Val Pro Asp Pro Gly Met Val Asn Glu Gly Thr Lys Cys Gly
610 615 620

Ala Gly Lys Lys
625

<210> 2246
<211> 819
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM9; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="Uniprot ID: Q13443; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419446"

<400> 2246
Met Gly Ser Gly Ala Arg Phe Pro Ser Gly Thr Leu Arg Val Arg Trp
1   5   10   15

Leu Leu Leu Leu Gly Leu Val Gly Pro Val Leu Gly Ala Ala Arg Pro
            20   25   30

Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
        35   40   45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
    50   55   60

Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
65   70   75   80

Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
                85   90   95

Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Asn
            100   105   110

His Cys His Tyr Arg Gly Tyr Val Glu Gly Val His Asn Ser Ser Ile

```
        115                 120                 125

Ala Leu Ser Asp Cys Phe Gly Leu Arg Gly Leu Leu His Leu Glu Asn
    130                 135                 140

Ala Ser Tyr Gly Ile Glu Pro Leu Gln Asn Ser Ser His Phe Glu His
145                 150                 155                 160

Ile Ile Tyr Arg Met Asp Asp Val Tyr Lys Glu Pro Leu Lys Cys Gly
                165                 170                 175

Val Ser Asn Lys Asp Ile Glu Lys Glu Thr Ala Lys Asp Glu Glu Glu
            180                 185                 190

Glu Pro Pro Ser Met Thr Gln Leu Leu Arg Arg Arg Arg Ala Val Leu
        195                 200                 205

Pro Gln Thr Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg
    210                 215                 220

Tyr Asp Met Met Gly Arg Asn Gln Thr Ala Val Arg Glu Glu Met Ile
225                 230                 235                 240

Leu Leu Ala Asn Tyr Leu Asp Ser Met Tyr Ile Met Leu Asn Ile Arg
                245                 250                 255

Ile Val Leu Val Gly Leu Glu Ile Trp Thr Asn Gly Asn Leu Ile Asn
            260                 265                 270

Ile Val Gly Gly Ala Gly Asp Val Leu Gly Asn Phe Val Gln Trp Arg
        275                 280                 285

Glu Lys Phe Leu Ile Thr Arg Arg Arg His Asp Ser Ala Gln Leu Val
    290                 295                 300

Leu Lys Lys Gly Phe Gly Gly Thr Ala Gly Met Ala Phe Val Gly Thr
305                 310                 315                 320

Val Cys Ser Arg Ser His Ala Gly Gly Ile Asn Val Phe Gly Gln Ile
                325                 330                 335

Thr Val Glu Thr Phe Ala Ser Ile Val Ala His Glu Leu Gly His Asn
            340                 345                 350
```

```
Leu Gly Met Asn His Asp Asp Gly Arg Asp Cys Ser Cys Gly Ala Lys
        355                 360                 365

Ser Cys Ile Met Asn Ser Gly Ala Ser Gly Ser Arg Asn Phe Ser Ser
    370                 375                 380

Cys Ser Ala Glu Asp Phe Glu Lys Leu Thr Leu Asn Lys Gly Gly Asn
385                 390                 395                 400

Cys Leu Leu Asn Ile Pro Lys Pro Asp Glu Ala Tyr Ser Ala Pro Ser
                405                 410                 415

Cys Gly Asn Lys Leu Val Asp Ala Gly Glu Glu Cys Asp Cys Gly Thr
            420                 425                 430

Pro Lys Glu Cys Glu Leu Asp Pro Cys Cys Glu Gly Ser Thr Cys Lys
        435                 440                 445

Leu Lys Ser Phe Ala Glu Cys Ala Tyr Gly Asp Cys Cys Lys Asp Cys
    450                 455                 460

Arg Phe Leu Pro Gly Gly Thr Leu Cys Arg Gly Lys Thr Ser Glu Cys
465                 470                 475                 480

Asp Val Pro Glu Tyr Cys Asn Gly Ser Ser Gln Phe Cys Gln Pro Asp
                485                 490                 495

Val Phe Ile Gln Asn Gly Tyr Pro Cys Gln Asn Asn Lys Ala Tyr Cys
            500                 505                 510

Tyr Asn Gly Met Cys Gln Tyr Tyr Asp Ala Gln Cys Gln Val Ile Phe
        515                 520                 525

Gly Ser Lys Ala Lys Ala Ala Pro Lys Asp Cys Phe Ile Glu Val Asn
    530                 535                 540

Ser Lys Gly Asp Arg Phe Gly Asn Cys Gly Phe Ser Gly Asn Glu Tyr
545                 550                 555                 560

Lys Lys Cys Ala Thr Gly Asn Ala Leu Cys Gly Lys Leu Gln Cys Glu
                565                 570                 575
```

```
Asn Val Gln Glu Ile Pro Val Phe Gly Ile Val Pro Ala Ile Ile Gln
            580                 585                 590

Thr Pro Ser Arg Gly Thr Lys Cys Trp Gly Val Asp Phe Gln Leu Gly
        595                 600                 605

Ser Asp Val Pro Asp Pro Gly Met Val Asn Glu Gly Thr Lys Cys Gly
    610                 615                 620

Ala Gly Lys Ile Cys Arg Asn Phe Gln Cys Val Asp Ala Ser Val Leu
625                 630                 635                 640

Asn Tyr Asp Cys Asp Val Gln Lys Lys Cys His Gly His Gly Val Cys
                645                 650                 655

Asn Ser Asn Lys Asn Cys His Cys Glu Asn Gly Trp Ala Pro Pro Asn
            660                 665                 670

Cys Glu Thr Lys Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Thr Tyr
        675                 680                 685

Asn Glu Met Asn Thr Ala Leu Arg Asp Gly Leu Leu Val Phe Phe Phe
    690                 695                 700

Leu Ile Val Pro Leu Ile Val Cys Ala Ile Phe Ile Phe Ile Lys Arg
705                 710                 715                 720

Asp Gln Leu Trp Arg Ser Tyr Phe Arg Lys Lys Arg Ser Gln Thr Tyr
                725                 730                 735

Glu Ser Asp Gly Lys Asn Gln Ala Asn Pro Ser Arg Gln Pro Gly Ser
            740                 745                 750

Val Pro Arg His Val Ser Pro Val Thr Pro Pro Arg Glu Val Pro Ile
        755                 760                 765

Tyr Ala Asn Arg Phe Ala Val Pro Thr Tyr Ala Ala Lys Gln Pro Gln
    770                 775                 780

Gln Phe Pro Ser Arg Pro Pro Pro Pro Gln Pro Lys Val Ser Ser Gln
785                 790                 795                 800
```

Gly Asn Leu Ile Pro Ala Arg Pro Ala Pro Ala Pro Pro Leu Tyr Ser
805 810 815

Ser Leu Thr

<210> 2247
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM9; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000420257"

<400> 2247
Met Gly Ser Gly Ala Arg Phe Pro Ser Gly Thr Leu Arg Val Arg Trp
1 5 10 15

Leu Leu Leu Leu Gly Leu Val Gly Pro Val Leu Gly Ala Ala Arg Pro
20 25 30

Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
35 40 45

Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
50 55 60

Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
65 70 75 80

Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
85 90 95

Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Arg
100 105 110

Cys Gly Pro Leu Cys Ile Arg Glu Gln Ser Thr Pro Gly Asp Arg Ala
115 120 125

Gly Gln Asn Thr Gln Asn Asn Trp Gln Met Ser Asn Leu Ala Phe Cys
130 135 140

Val Tyr Tyr
145

<210> 2248
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 555; "

<220>
<221> source
<223> /note="Gene Symbol: ADAM9; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase domain 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000488700"

<400> 2248
Pro Ile Tyr Ala Asn Arg Phe Ala Val Pro Thr Tyr Ala Ala Lys Gln
1 5 10 15

Pro Gln Gln Phe Pro Ser Arg Pro Pro Pro Pro Gln Pro Lys Val Ser
20 25 30

Ser Gln Gly Asn Leu Ile Pro Ala Arg Pro Ala Pro Ala Pro Pro Leu
35 40 45

Tyr Ser Ser Leu Thr
50

<210> 2249
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485845"

<400> 2249

```
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                   10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
```

145 150 155 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
165 170 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
180 185 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
195 200 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
210 215 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225 230 235 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
245 250 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
260 265 270

Leu Leu Arg Pro Val Pro Pro Ser Pro Leu Pro Leu Leu Ala Thr His
275 280 285

Leu Cys Ala Gly Arg Ser Leu Ser Leu Gly Pro Ser Gln Glu Pro Ala
290 295 300

Pro Gly Gly Gly Arg Gly Pro Arg Thr Pro Val Pro Thr His Lys Arg
305 310 315 320

Pro Arg Phe Gln Thr Leu Pro Ser Ser Cys Pro Leu Leu Arg Pro Ala
325 330 335

Ser Ser Arg Cys Thr Pro Arg Asp
340

<210> 2250
<211> 1340
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 556; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485989"

<400> 2250

```
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                   10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160
```

```
Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala
        275                 280                 285

Val Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu
    290                 295                 300

Ser Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu
305                 310                 315                 320

Val Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser
                325                 330                 335

Lys Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val
            340                 345                 350

His Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser
        355                 360                 365

Cys Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg
    370                 375                 380
```

```
Pro Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu
385                 390                 395                 400

Met Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser
                405                 410                 415

Gln Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly
            420                 425                 430

Gly Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly
        435                 440                 445

Asp Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile
    450                 455                 460

Met Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser
465                 470                 475                 480

Gly Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys
                485                 490                 495

Arg Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp
            500                 505                 510

Arg Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys
        515                 520                 525

Gly Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr
    530                 535                 540

Val Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu
545                 550                 555                 560

Phe Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly
                565                 570                 575

Lys Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp
            580                 585                 590

Gly Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg
        595                 600                 605

Leu Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile
```

610 615 620

Gln Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro
625 630 635 640

Asp Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val
645 650 655

Trp Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu
660 665 670

Arg Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val
675 680 685

Glu Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu
690 695 700

Ala Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe
705 710 715 720

Gly Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val
725 730 735

Arg Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala
740 745 750

Arg Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys
755 760 765

Asn Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser
770 775 780

Cys Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys
785 790 795 800

Val Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly
805 810 815

Ser Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser
820 825 830

Cys Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys
835 840 845

```
Ala Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His
    850                 855                 860

Val Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly
865                 870                 875                 880

Leu Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro
                885                 890                 895

Val Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg
            900                 905                 910

Glu Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu
        915                 920                 925

Ala Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu
    930                 935                 940

Tyr Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu
945                 950                 955                 960

Asp Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys
                965                 970                 975

Ser Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser Leu Gly Pro
            980                 985                 990

Cys Ser Ala Ser Cys Gly Leu Gly  Thr Ala Arg Arg Ser  Val Ala
Cys
        995                 1000                1005

Val Gln  Leu Asp Gln Gly Gln  Asp Val Glu Val Asp  Glu Ala Ala
    1010                1015                1020

Cys Ala  Ala Leu Val Arg Pro  Glu Ala Ser Val Pro  Cys Leu Ile
    1025                1030                1035

Ala Asp  Cys Thr Tyr Arg Trp  His Val Gly Thr Trp  Met Glu Cys
    1040                1045                1050

Ser Val  Ser Cys Gly Asp Gly  Ile Gln Arg Arg Arg  Asp Thr Cys
    1055                1060                1065
```

```
Leu Gly  Pro Gln Ala Gln Ala  Pro Val Pro Ala Asp  Phe Cys Gln
    1070                1075                1080

His Leu  Pro Lys Pro Val Thr  Val Arg Gly Cys Trp  Ala Gly Pro
    1085                1090                1095

Cys Val  Gly Gln Gly Ala Cys  Gly Arg Gln His Leu  Glu Pro Thr
    1100                1105                1110

Gly Thr  Ile Asp Met Arg Gly  Pro Gly Gln Ala Asp  Cys Ala Val
    1115                1120                1125

Ala Ile  Gly Arg Pro Leu Gly  Glu Val Val Thr Leu  Arg Val Leu
    1130                1135                1140

Glu Ser  Ser Leu Asn Cys Ser  Ala Gly Asp Met Leu  Leu Leu Trp
    1145                1150                1155

Gly Arg  Leu Thr Trp Arg Lys  Met Cys Arg Lys Leu  Leu Asp Met
    1160                1165                1170

Thr Phe  Ser Ser Lys Thr Asn  Thr Leu Val Val Arg  Gln Arg Cys
    1175                1180                1185

Gly Arg  Pro Gly Gly Gly Val  Leu Leu Arg Tyr Gly  Ser Gln Leu
    1190                1195                1200

Ala Pro  Glu Thr Phe Tyr Arg  Glu Cys Asp Met Gln  Leu Phe Gly
    1205                1210                1215

Pro Trp  Gly Glu Ile Val Ser  Pro Ser Leu Ser Pro  Ala Thr Ser
    1220                1225                1230

Asn Ala  Gly Gly Cys Arg Leu  Phe Ile Asn Val Ala  Pro His Ala
    1235                1240                1245

Arg Ile  Ala Ile His Ala Leu  Ala Thr Asn Met Gly  Ala Gly Thr
    1250                1255                1260

Glu Gly  Ala Asn Ala Ser Tyr  Ile Leu Ile Arg Asp  Thr His Ser
    1265                1270                1275
```

```
Leu Arg  Thr Thr Ala Phe His  Gly Gln Gln Val Leu  Tyr Trp Glu
    1280                1285                1290

Ser Glu  Ser Ser Gln Ala Glu  Met Glu Phe Ser Glu  Gly Phe Leu
    1295                1300                1305

Lys Ala  Gln Ala Ser Leu Arg  Gly Gln Tyr Trp Thr  Leu Gln Ser
    1310                1315                1320

Trp Val  Pro Glu Met Gln Asp  Pro Gln Ser Trp Lys  Gly Lys Glu
    1325                1330                1335

Gly Thr
    1340
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<210> 2251
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486060"

<400> 2251

```
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                  10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45
```

```
Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Arg Pro Val Pro Pro Ser Pro Leu Pro Leu Leu Ala Thr His
```

275 280 285

Leu Cys Ala Gly Arg Ser Leu Ser Leu Gly Pro Ser Gln Glu Pro Ala
290 295 300

Pro Gly Gly Gly Arg Gly Pro Arg Thr Pro Val Pro Thr His Lys Arg
305 310 315 320

Pro Arg Phe Gln Thr Leu Pro Ser Ser Cys Pro Leu Leu Arg Pro Ala
325 330 335

Ser Ser Arg Cys Thr Pro Arg Asp
340

<210> 2252
<211> 1427
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486201"

<400> 2252
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1 5 10 15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
20 25 30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
35 40 45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
50 55 60

```
Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
        275                 280                 285
```

```
Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290                 295                 300

Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305                 310                 315                 320

Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325                 330                 335

Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
            340                 345                 350

Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
        355                 360                 365

Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
    370                 375                 380

Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385                 390                 395                 400

Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
                405                 410                 415

Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
            420                 425                 430

Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
        435                 440                 445

Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
    450                 455                 460

Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465                 470                 475                 480

Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
                485                 490                 495

Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
            500                 505                 510
```

```
Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
        515                 520                 525

Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
    530                 535                 540

Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545                 550                 555                 560

Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
                565                 570                 575

Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
            580                 585                 590

Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
        595                 600                 605

Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
    610                 615                 620

Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625                 630                 635                 640

Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
                645                 650                 655

Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
            660                 665                 670

Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
        675                 680                 685

Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
    690                 695                 700

Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705                 710                 715                 720

Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
                725                 730                 735

Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
```

740 745 750

Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
755 760 765

Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
770 775 780

Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785 790 795 800

Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
805 810 815

Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
820 825 830

Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
835 840 845

Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
850 855 860

Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865 870 875 880

Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
885 890 895

Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
900 905 910

Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
915 920 925

Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
930 935 940

Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945 950 955 960

Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
965 970 975

```
Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
            980                 985                 990

Thr Gln Cys Gln Gly Leu Pro Arg  Pro Glu Pro Gln Glu  Ala Cys
Ser
        995                 1000                1005

Leu Glu  Pro Cys Pro Pro Arg  Trp Lys Val Met Ser  Leu Gly Pro
    1010                1015                1020

Cys Ser  Ala Ser Cys Gly Leu  Gly Thr Ala Arg Arg  Ser Val Ala
    1025                1030                1035

Cys Val  Gln Leu Asp Gln Gly  Gln Asp Val Glu Val  Asp Glu Ala
    1040                1045                1050

Ala Cys  Ala Ala Leu Val Arg  Pro Glu Ala Ser Val  Pro Cys Leu
    1055                1060                1065

Ile Ala  Asp Cys Thr Tyr Arg  Trp His Val Gly Thr  Trp Met Glu
    1070                1075                1080

Cys Ser  Val Ser Cys Gly Asp  Gly Ile Gln Arg Arg  Arg Asp Thr
    1085                1090                1095

Cys Leu  Gly Pro Gln Ala Gln  Ala Pro Val Pro Ala  Asp Phe Cys
    1100                1105                1110

Gln His  Leu Pro Lys Pro Val  Thr Val Arg Gly Cys  Trp Ala Gly
    1115                1120                1125

Pro Cys  Val Gly Gln Gly Thr  Pro Ser Leu Val Pro  His Glu Glu
    1130                1135                1140

Ala Ala  Ala Pro Gly Arg Thr  Thr Ala Thr Pro Ala  Gly Ala Ser
    1145                1150                1155

Leu Glu  Trp Ser Gln Ala Arg  Gly Leu Leu Phe Ser  Pro Ala Pro
    1160                1165                1170

Gln Pro  Arg Arg Leu Leu Pro  Gly Pro Gln Glu Asn  Ser Val Gln
    1175                1180                1185
```

```
Ser Ser  Ala Cys Gly Arg Gln  His Leu Glu Pro Thr  Gly Thr Ile
    1190                 1195                 1200

Asp Met  Arg Gly Pro Gly Gln  Ala Asp Cys Ala Val  Ala Ile Gly
    1205                 1210                 1215

Arg Pro  Leu Gly Glu Val Val  Thr Leu Arg Val Leu  Glu Ser Ser
    1220                 1225                 1230

Leu Asn  Cys Ser Ala Gly Asp  Met Leu Leu Leu Trp  Gly Arg Leu
    1235                 1240                 1245

Thr Trp  Arg Lys Met Cys Arg  Lys Leu Leu Asp Met  Thr Phe Ser
    1250                 1255                 1260

Ser Lys  Thr Asn Thr Leu Val  Val Arg Gln Arg Cys  Gly Arg Pro
    1265                 1270                 1275

Gly Gly  Gly Val Leu Leu Arg  Tyr Gly Ser Gln Leu  Ala Pro Glu
    1280                 1285                 1290

Thr Phe  Tyr Arg Glu Cys Asp  Met Gln Leu Phe Gly  Pro Trp Gly
    1295                 1300                 1305

Glu Ile  Val Ser Pro Ser Leu  Ser Pro Ala Thr Ser  Asn Ala Gly
    1310                 1315                 1320

Gly Cys  Arg Leu Phe Ile Asn  Val Ala Pro His Ala  Arg Ile Ala
    1325                 1330                 1335

Ile His  Ala Leu Ala Thr Asn  Met Gly Ala Gly Thr  Glu Gly Ala
    1340                 1345                 1350

Asn Ala  Ser Tyr Ile Leu Ile  Arg Asp Thr His Ser  Leu Arg Thr
    1355                 1360                 1365

Thr Ala  Phe His Gly Gln Gln  Val Leu Tyr Trp Glu  Ser Glu Ser
    1370                 1375                 1380

Ser Gln  Ala Glu Met Glu Phe  Ser Glu Gly Phe Leu  Lys Ala Gln
    1385                 1390                 1395
```

Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val Pro
1400 1405 1410

Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
1415 1420 1425

<210> 2253
<211> 276
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486371"

<400> 2253
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1 5 10 15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
20 25 30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
35 40 45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
50 55 60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65 70 75 80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
85 90 95

```
Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Arg Ile Cys Ala Arg Pro Ser Pro Ala Thr Gln Thr
225                 230                 235                 240

Arg Trp Thr Lys Ala Ala Ala Ala Ala Ser Ser Phe Leu Ser Trp Met
                245                 250                 255

Gly Gln Asn Val Ala Trp Arg Ser Gly Ala Pro Arg Val Ala Ala Ala
            260                 265                 270

Pro Trp Trp Ser
        275


<210> 2254
<211> 1371
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "
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<220>
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<220>
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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486734"

<400> 2254

```
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                  10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175
```

```
Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
        275                 280                 285

Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290                 295                 300

Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305                 310                 315                 320

Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325                 330                 335

Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
            340                 345                 350

Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
        355                 360                 365

Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
    370                 375                 380

Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385                 390                 395                 400
```

```
Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
                405                 410                 415

Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
            420                 425                 430

Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
        435                 440                 445

Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
    450                 455                 460

Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465                 470                 475                 480

Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
                485                 490                 495

Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
            500                 505                 510

Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
        515                 520                 525

Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
    530                 535                 540

Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545                 550                 555                 560

Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
                565                 570                 575

Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
            580                 585                 590

Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
        595                 600                 605

Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
    610                 615                 620
```

```
Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625                 630                 635                 640

Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
                645                 650                 655

Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
            660                 665                 670

Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
        675                 680                 685

Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
    690                 695                 700

Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705                 710                 715                 720

Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
                725                 730                 735

Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
            740                 745                 750

Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
        755                 760                 765

Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
    770                 775                 780

Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785                 790                 795                 800

Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
                805                 810                 815

Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
            820                 825                 830

Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
        835                 840                 845

Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
```

```
    850                 855                 860

Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865                 870                 875                 880

Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
                885                 890                 895

Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
            900                 905                 910

Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
        915                 920                 925

Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
    930                 935                 940

Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945                 950                 955                 960

Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
                965                 970                 975

Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
            980                 985                 990

Thr Gln Cys Gln Gly Leu Pro Arg  Pro Glu Pro Gln Glu  Ala Cys
Ser
        995                 1000                1005

Leu Glu  Pro Cys Pro Pro Arg  Trp Lys Val Met Ser  Leu Gly Pro
    1010                1015                1020

Cys Ser  Ala Ser Cys Gly Leu  Gly Thr Ala Arg Arg  Ser Val Ala
    1025                1030                1035

Cys Val  Gln Leu Asp Gln Gly  Gln Asp Val Glu Val  Asp Glu Ala
    1040                1045                1050

Ala Cys  Ala Ala Leu Val Arg  Pro Glu Ala Ser Val  Pro Cys Leu
    1055                1060                1065

Ile Ala  Asp Cys Thr Tyr Arg  Trp His Val Gly Thr  Trp Met Glu
```

1070 1075 1080

Cys Ser Val Ser Cys Gly Asp Gly Ile Gln Arg Arg Arg Asp Thr
1085 1090 1095

Cys Leu Gly Pro Gln Ala Gln Ala Pro Val Pro Ala Asp Phe Cys
1100 1105 1110

Gln His Leu Pro Lys Pro Val Thr Val Arg Gly Cys Trp Ala Gly
1115 1120 1125

Pro Cys Val Gly Gln Gly Ala Cys Gly Arg Gln His Leu Glu Pro
1130 1135 1140

Thr Gly Thr Ile Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala
1145 1150 1155

Val Ala Ile Gly Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val
1160 1165 1170

Leu Glu Ser Ser Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu
1175 1180 1185

Trp Gly Arg Leu Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp
1190 1195 1200

Met Thr Phe Ser Ser Lys Thr Asn Thr Leu Val Val Arg Gln Arg
1205 1210 1215

Cys Gly Arg Pro Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser Gln
1220 1225 1230

Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe
1235 1240 1245

Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr
1250 1255 1260

Ser Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His
1265 1270 1275

Ala Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly
1280 1285 1290

```
Thr Glu  Gly Ala Asn Ala Ser  Tyr Ile Leu Ile Arg  Asp Thr His
    1295                1300                1305

Ser Leu  Arg Thr Thr Ala Phe  His Gly Gln Gln Val  Leu Tyr Trp
    1310                1315                1320

Glu Ser  Glu Ser Ser Gln Ala  Glu Met Glu Phe Ser  Glu Gly Phe
    1325                1330                1335

Leu Lys  Ala Gln Ala Ser Leu  Arg Gly Gln Tyr Trp  Thr Leu Gln
    1340                1345                1350

Ser Trp  Val Pro Glu Met Gln  Asp Pro Gln Ser Trp  Lys Gly Lys
    1355                1360                1365

Glu Gly  Thr
    1370
```

<210> 2255
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487185"

<400> 2255

```
Met Ala Ser Asp Gly Ala Ala Pro Arg Ala Gly Leu Ala Trp Ser Pro
1               5                  10                  15

Cys Ser Arg Arg Gln Leu Leu Ser Leu Leu Ser Ala Gly Arg Ala Arg
            20                  25                  30
```

```
Cys Val Trp Asp Pro Pro Arg Pro Gln Pro Gly Ser Ala Gly His Pro
        35                  40                  45

Pro Asp Ala Gln Pro Gly Leu Tyr Tyr Ser Ala Asn Glu Gln Cys Arg
    50                  55                  60

Val Ala Phe Gly Pro Lys Ala Val Ala Cys Thr Phe Ala Arg Glu His
65                  70                  75                  80

Leu Asp Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln
                85                  90                  95

Ser Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys
            100                 105                 110

Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val Glu
        115                 120                 125

Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp Gly Pro
    130                 135                 140

Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val Thr Arg Arg
145                 150                 155                 160

Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly Arg Ala Cys Val
                165                 170                 175

Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr Gln Ala Cys Glu Lys
            180                 185                 190

Thr Gln Leu Glu Phe Met Ser Gln Gln Cys Ala Arg Thr Asp Gly Gln
        195                 200                 205

Pro Leu Arg Ser Ser Pro Gly Gly Ala Ser Phe Tyr His Trp Gly Ala
    210                 215                 220

Ala Val Pro His Ser Gln Gly Asp Ala Leu Cys Arg His Met Cys Arg
225                 230                 235                 240

Ala Ile Gly Glu Ser Phe Ile Met Lys Arg Gly Asp Ser Phe Leu Asp
                245                 250                 255
```

```
Gly Thr Arg Cys Met Pro Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser
            260                 265                 270

Leu Cys Val Ser Gly Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met
        275                 280                 285

Asp Ser Gln Gln Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn
    290                 295                 300

Ser Thr Cys Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg
305                 310                 315                 320

Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr
                325                 330                 335

Ile Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly
            340                 345                 350

Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr Thr
        355                 360                 365

Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val Ala Leu
    370                 375                 380

Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro
385                 390                 395                 400

Leu Gln Glu Asp Ala Asp Ile Gln Val Gly Gly Val Arg Ala Gln Leu
                405                 410                 415

Met His Ile Ser Trp Trp Ser Arg Pro Gly Leu Gly Glu Arg Asp Leu
            420                 425                 430

Cys Ala Arg Gly Arg Trp Pro Gly Gly Ser Ser Asp
        435                 440


<210> 2256
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 556; "
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<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1,
motif 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487509"

<400> 2256

```
Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala Ile Gly Arg Pro
1               5                  10                  15

Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser Ser Leu Asn Cys
            20                  25                  30

Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu Thr Trp Arg Lys
        35                  40                  45

Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser Ser Lys Thr Asn Thr
    50                  55                  60

Leu Val Val Arg Gln Arg Cys Gly Arg Pro Gly Gly Gly Val Leu Leu
65                  70                  75                  80

Arg Tyr Gly Ser Gln Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp
                85                  90                  95

Met Gln Leu Phe Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser
            100                 105                 110

Pro Ala Thr Ser Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala
        115                 120                 125

Pro His Ala Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala
    130                 135                 140

Gly Thr Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His
145                 150                 155                 160

Ser Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu
                165                 170                 175
```

```
Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys
            180                 185                 190


Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val
        195                 200                 205


Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
    210                 215                 220


<210> 2257
<211> 967
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 557; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS1; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 1; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9UHI8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000284984"

<400> 2257
Met Gln Arg Ala Val Pro Glu Gly Phe Gly Arg Arg Lys Leu Gly Ser
1               5                   10                  15


Asp Met Gly Asn Ala Glu Arg Ala Pro Gly Ser Arg Ser Phe Gly Pro
            20                  25                  30


Val Pro Thr Leu Leu Leu Leu Ala Ala Ala Leu Leu Ala Val Ser Asp
        35                  40                  45


Ala Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro Glu
    50                  55                  60
```

```
Leu Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His Ala
65                  70                  75                  80

Phe Asp Gln Gln Leu Asp Leu Glu Leu Arg Pro Asp Ser Ser Phe Leu
                85                  90                  95

Ala Pro Gly Phe Thr Leu Gln Asn Val Gly Arg Lys Ser Gly Ser Glu
            100                 105                 110

Thr Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly Thr
        115                 120                 125

Val Asn Gly Asp Pro Ser Ser Ala Ala Ala Leu Ser Leu Cys Glu Gly
    130                 135                 140

Val Arg Gly Ala Phe Tyr Leu Leu Gly Glu Ala Tyr Phe Ile Gln Pro
145                 150                 155                 160

Leu Pro Ala Ala Ser Glu Arg Leu Ala Thr Ala Ala Pro Gly Glu Lys
                165                 170                 175

Pro Pro Ala Pro Leu Gln Phe His Leu Leu Arg Arg Asn Arg Gln Gly
            180                 185                 190

Asp Val Gly Gly Thr Cys Gly Val Val Asp Asp Glu Pro Arg Pro Thr
        195                 200                 205

Gly Lys Ala Glu Thr Glu Asp Glu Asp Glu Gly Thr Glu Gly Glu Asp
    210                 215                 220

Glu Gly Ala Gln Trp Ser Pro Gln Asp Pro Ala Leu Gln Gly Val Gly
225                 230                 235                 240

Gln Pro Thr Gly Thr Gly Ser Ile Arg Lys Lys Arg Phe Val Ser Ser
                245                 250                 255

His Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu
            260                 265                 270

Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val
        275                 280                 285
```

```
Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu
    290                 295                 300

Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu
305                 310                 315                 320

Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln
                325                 330                 335

Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr
            340                 345                 350

Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp
        355                 360                 365

Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser
    370                 375                 380

Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala
385                 390                 395                 400

His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln
                405                 410                 415

Cys Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser
            420                 425                 430

Met Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala
        435                 440                 445

Tyr Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met
    450                 455                 460

Asp Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr
465                 470                 475                 480

Ser Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser
                485                 490                 495

Lys His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr
            500                 505                 510

Gly Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp
```

```
        515                 520                 525

Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys
    530                 535                 540

Cys Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly
545                 550                 555                 560

Ser Trp Gly Met Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly
                565                 570                 575

Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys
            580                 585                 590

Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys
        595                 600                 605

Asn Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu
    610                 615                 620

Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly
625                 630                 635                 640

Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp
                645                 650                 655

Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val
            660                 665                 670

Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr
        675                 680                 685

Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile
    690                 695                 700

Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn
705                 710                 715                 720

Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro
                725                 730                 735

Gly Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu
            740                 745                 750
```

```
Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu
        755                 760                 765

Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr
    770                 775                 780

Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg
785                 790                 795                 800

Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro
                805                 810                 815

Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu
            820                 825                 830

Arg Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser
        835                 840                 845

Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly
    850                 855                 860

Glu Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu
865                 870                 875                 880

Cys Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val
                885                 890                 895

Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp
            900                 905                 910

Gln Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr
        915                 920                 925

Lys Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser
    930                 935                 940

His Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe
945                 950                 955                 960

Cys Thr Met Ala Glu Cys Ser
                965
```

<210> 2258
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 557; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS1; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403404"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2258
Xaa Cys Arg Ser Phe Leu Leu Arg Pro Ser Leu Cys Ala Val Leu Ile
1 5 10 15

Leu Gln Phe Phe Leu Phe His His Phe Gly Thr Gly Ser Ile Arg Lys
20 25 30

Lys Arg Phe Val Ser Ser His Arg Tyr Val Glu Thr Met Leu Val Ala
35 40 45

Asp Gln Ser Met Ala Glu Phe His Gly Ser Gly Leu Lys His Tyr Leu
50 55 60

Leu Thr Leu Phe Ser Val Ala Ala Arg Leu Tyr Lys His Pro Ser Ile
65 70 75 80

Arg Asn Ser Val Ser Leu Val Val Val Lys Ile Leu Val Ile His Asp
85 90 95

Glu Gln Lys Gly Pro Glu Val Thr Ser Asn Ala Ala Leu Thr Leu Arg
100 105 110

```
Asn Phe Cys Asn Trp Gln Lys Gln His Asn Pro Pro Ser Asp Arg Asp
        115                 120                 125

Ala Glu His Tyr Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys
    130                 135                 140

Gly Ser Gln Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly Thr Val
145                 150                 155                 160

Cys Asp Pro Ser Arg Ser Cys Ser Val Ile Glu Asp Asp Gly Leu Gln
                165                 170                 175

Ala Ala Phe Thr Thr Ala His Glu Leu Gly His Val Phe Asn Met Pro
            180                 185                 190

His Asp Asp Ala Lys Gln Cys Ala
        195                 200


<210> 2259
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 557; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS1; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000429557"

<400> 2259
Met Leu Val Ala Asp Gln Ser Met Ala Glu Phe His Gly Ser Gly Leu
1               5                   10                  15

Lys His Tyr Leu Leu Thr Leu Phe Ser Val Ala Ala Arg Leu Tyr Lys
            20                  25                  30
```

```
His Pro Ser Ile Arg Asn Ser Val Ser Leu Val Val Val Lys Ile Leu
        35                  40                  45

Val Ile His Asp Glu Gln Lys Gly Pro Glu Val Thr Ser Asn Ala Ala
    50                  55                  60

Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Lys Gln His Asn Pro Pro
65                  70                  75                  80

Ser Asp Arg Asp Ala Glu His Tyr Asp Thr Ala Ile Leu Phe Thr Arg
                85                  90                  95

Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp Thr Leu Gly Met Ala Asp
            100                 105                 110

Val Gly Thr Val Cys Asp Pro Ser Arg Ser Cys Ser Val Ile Glu Asp
        115                 120                 125

Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala His Glu Leu Gly His Val
    130                 135                 140

Phe Asn Met Pro His Asp Asp Ala Lys Gln Cys Ala Ser Leu Asn Gly
145                 150                 155                 160

Val Asn Gln Asp Ser His Met Met Ala Ser Met
                165                 170
```

<210> 2260
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 557; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS1; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000431065"

<400> 2260
Met Val Thr Trp Glu Gly Thr Gly Ser Ile Arg Lys Lys Arg Phe Val
1   5   10   15

Ser Ser His Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met
            20   25   30

Ala Glu Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe
        35   40   45

Ser Val Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val
    50   55   60

Ser Leu Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly
65   70   75   80

Pro Glu Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn
                85   90   95

Trp Gln Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr
            100   105   110

Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr
        115   120   125

<210> 2261
<211> 1103
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 558; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS10; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 10; "

<220>
<221> source

<223> /note="ENSP ID: ENSP00000270328"

<400> 2261

```
Met Ala Pro Ala Cys Gln Ile Leu Arg Trp Ala Leu Ala Leu Gly Leu
1               5                  10                  15

Gly Leu Met Phe Glu Val Thr His Ala Phe Arg Ser Gln Asp Glu Phe
            20                  25                  30

Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala Phe Pro Thr Arg Val Asp
        35                  40                  45

His Asn Gly Ala Leu Leu Ala Phe Ser Pro Pro Pro Pro Arg Arg Gln
    50                  55                  60

Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser Arg Leu Phe Tyr Lys Val
65                  70                  75                  80

Ala Ser Pro Ser Thr His Phe Leu Leu Asn Leu Thr Arg Ser Ser Arg
                85                  90                  95

Leu Leu Ala Gly His Val Ser Val Glu Tyr Trp Thr Arg Glu Gly Leu
            100                 105                 110

Ala Trp Gln Arg Ala Ala Arg Pro His Cys Leu Tyr Ala Gly His Leu
        115                 120                 125

Gln Gly Gln Ala Ser Ser Ser His Val Ala Ile Ser Thr Cys Gly Gly
    130                 135                 140

Leu His Gly Leu Ile Val Ala Asp Glu Glu Glu Tyr Leu Ile Glu Pro
145                 150                 155                 160

Leu His Gly Gly Pro Lys Gly Ser Arg Ser Pro Glu Glu Ser Gly Pro
                165                 170                 175

His Val Val Tyr Lys Arg Ser Ser Leu Arg His Pro His Leu Asp Thr
            180                 185                 190

Ala Cys Gly Val Arg Asp Glu Lys Pro Trp Lys Gly Arg Pro Trp Trp
        195                 200                 205

Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg Pro Leu Gly Asn Glu Thr
    210                 215                 220
```

```
Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser Val Ser Arg Glu Arg Tyr
225                 230                 235                 240

Val Glu Thr Leu Val Val Ala Asp Lys Met Met Val Ala Tyr His Gly
                245                 250                 255

Arg Arg Asp Val Glu Gln Tyr Val Leu Ala Ile Met Asn Ile Val Ala
            260                 265                 270

Lys Leu Phe Gln Asp Ser Ser Leu Gly Ser Thr Val Asn Ile Leu Val
        275                 280                 285

Thr Arg Leu Ile Leu Leu Thr Glu Asp Gln Pro Thr Leu Glu Ile Thr
    290                 295                 300

His His Ala Gly Lys Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser
305                 310                 315                 320

Ile Val Asn His Ser Gly His Gly Asn Ala Ile Pro Glu Asn Gly Val
                325                 330                 335

Ala Asn His Asp Thr Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Ile
            340                 345                 350

Tyr Lys Asn Lys Pro Cys Gly Thr Leu Gly Leu Ala Pro Val Gly Gly
        355                 360                 365

Met Cys Glu Arg Glu Arg Ser Cys Ser Val Asn Glu Asp Ile Gly Leu
    370                 375                 380

Ala Thr Ala Phe Thr Ile Ala His Glu Ile Gly His Thr Phe Gly Met
385                 390                 395                 400

Asn His Asp Gly Val Gly Asn Ser Cys Gly Ala Arg Gly Gln Asp Pro
                405                 410                 415

Ala Lys Leu Met Ala Ala His Ile Thr Met Lys Thr Asn Pro Phe Val
            420                 425                 430

Trp Ser Ser Cys Ser Arg Asp Tyr Ile Thr Ser Phe Leu Asp Ser Gly
        435                 440                 445
```

```
Leu Gly Leu Cys Leu Asn Asn Arg Pro Pro Arg Gln Asp Phe Val Tyr
    450                 455                 460

Pro Thr Val Ala Pro Gly Gln Ala Tyr Asp Ala Asp Glu Gln Cys Arg
465                 470                 475                 480

Phe Gln His Gly Val Lys Ser Arg Gln Cys Lys Tyr Gly Glu Val Cys
                485                 490                 495

Ser Glu Leu Trp Cys Leu Ser Lys Ser Asn Arg Cys Ile Thr Asn Ser
            500                 505                 510

Ile Pro Ala Ala Glu Gly Thr Leu Cys Gln Thr His Thr Ile Asp Lys
        515                 520                 525

Gly Trp Cys Tyr Lys Arg Val Cys Val Pro Phe Gly Ser Arg Pro Glu
    530                 535                 540

Gly Val Asp Gly Ala Trp Gly Pro Trp Thr Pro Trp Gly Asp Cys Ser
545                 550                 555                 560

Arg Thr Cys Gly Gly Gly Val Ser Ser Ser Ser Arg His Cys Asp Ser
                565                 570                 575

Pro Arg Pro Thr Ile Gly Gly Lys Tyr Cys Leu Gly Glu Arg Arg Arg
            580                 585                 590

His Arg Ser Cys Asn Thr Asp Asp Cys Pro Pro Gly Ser Gln Asp Phe
        595                 600                 605

Arg Glu Val Gln Cys Ser Glu Phe Asp Ser Ile Pro Phe Arg Gly Lys
    610                 615                 620

Phe Tyr Lys Trp Lys Thr Tyr Arg Gly Gly Gly Val Lys Ala Cys Ser
625                 630                 635                 640

Leu Thr Cys Leu Ala Glu Gly Phe Asn Phe Tyr Thr Glu Arg Ala Ala
                645                 650                 655

Ala Val Val Asp Gly Thr Pro Cys Arg Pro Asp Thr Val Asp Ile Cys
            660                 665                 670
```

```
Val Ser Gly Glu Cys Lys His Val Gly Cys Asp Arg Val Leu Gly Ser
        675                 680                 685

Asp Leu Arg Glu Asp Lys Cys Arg Val Cys Gly Gly Asp Gly Ser Ala
    690                 695                 700

Cys Glu Thr Ile Glu Gly Val Phe Ser Pro Ala Ser Pro Gly Ala Gly
705                 710                 715                 720

Tyr Glu Asp Val Val Trp Ile Pro Lys Gly Ser Val His Ile Phe Ile
                725                 730                 735

Gln Asp Leu Asn Leu Ser Leu Ser His Leu Ala Leu Lys Gly Asp Gln
            740                 745                 750

Glu Ser Leu Leu Leu Glu Gly Leu Pro Gly Thr Pro Gln Pro His Arg
        755                 760                 765

Leu Pro Leu Ala Gly Thr Thr Phe Gln Leu Arg Gln Gly Pro Asp Gln
    770                 775                 780

Val Gln Ser Leu Glu Ala Leu Gly Pro Ile Asn Ala Ser Leu Ile Val
785                 790                 795                 800

Met Val Leu Ala Arg Thr Glu Leu Pro Ala Leu Arg Tyr Arg Phe Asn
                805                 810                 815

Ala Pro Ile Ala Arg Asp Ser Leu Pro Pro Tyr Ser Trp His Tyr Ala
            820                 825                 830

Pro Trp Thr Lys Cys Ser Ala Gln Cys Ala Gly Gly Ser Gln Val Gln
        835                 840                 845

Ala Val Glu Cys Arg Asn Gln Leu Asp Ser Ser Ala Val Ala Pro His
    850                 855                 860

Tyr Cys Ser Ala His Ser Lys Leu Pro Lys Arg Gln Arg Ala Cys Asn
865                 870                 875                 880

Thr Glu Pro Cys Pro Pro Asp Trp Val Val Gly Asn Trp Ser Leu Cys
                885                 890                 895

Ser Arg Ser Cys Asp Ala Gly Val Arg Ser Arg Ser Val Val Cys Gln
```

900 905 910

Arg Arg Val Ser Ala Ala Glu Glu Lys Ala Leu Asp Asp Ser Ala Cys
915 920 925

Pro Gln Pro Arg Pro Pro Val Leu Glu Ala Cys His Gly Pro Thr Cys
930 935 940

Pro Pro Glu Trp Ala Ala Leu Asp Trp Ser Glu Cys Thr Pro Ser Cys
945 950 955 960

Gly Pro Gly Leu Arg His Arg Val Val Leu Cys Lys Ser Ala Asp His
965 970 975

Arg Ala Thr Leu Pro Pro Ala His Cys Ser Pro Ala Ala Lys Pro Pro
980 985 990

Ala Thr Met Arg Cys Asn Leu Arg Arg Cys Pro Pro Ala Arg Trp Val
995 1000 1005

Ala Gly Glu Trp Gly Glu Cys Ser Ala Gln Cys Gly Val Gly Gln
1010 1015 1020

Arg Gln Arg Ser Val Arg Cys Thr Ser His Thr Gly Gln Ala Ser
1025 1030 1035

His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr Thr Gln Gln Cys
1040 1045 1050

Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly Pro Glu Glu
1055 1060 1065

Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val Leu Lys
1070 1075 1080

Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys
1085 1090 1095

Thr Cys His Gly His
1100

<210> 2262

<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 558; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469516"

<400> 2262

Met	Gly	Pro	Thr	Ser	Val	Leu	Arg	Ala	Gly	Leu	Thr	Pro	Ser	Cys	Leu
1				5				10						15	

Pro	Pro	Pro	Ser	Gly	Ala	Thr	Asn	Gly	Ser	Val	Ser	Pro	Leu	Gly	Arg
			20					25					30		

Ala	Gln	Arg	Val	Trp	Thr	Glu	Pro	Gly	Gly	Arg	Gly	Leu	His	Gly	Ala
		35					40					45			

Thr	Ala	Ala	Gly	Pro	Val	Ala	Ala	Ala	Cys	Pro	Leu	Leu	Ala	Val	Thr
	50					55					60				

Ala	Thr	Ala	Pro	Gly	Gln	Pro	Ser	Gly	Ala	Ser	Thr	Val	Trp	Val	Arg
65				70					75					80	

Glu	Gly	Gly	Thr	Ala	Pro	Ala	Thr	Arg	Met	Thr	Val	Pro	Leu	Ala	Pro
				85					90					95	

Arg	Thr	Ser	Glu	Lys	Cys	Ser	Val	Leu	Asn	Leu	Thr	Ala	Ser	Leu	Ser
			100					105					110		

Val	Gly	Asn	Ser	Thr	Ser	Gly	Lys	Arg	Thr	Gly	Glu	Gly	Ala		
			115					120					125		

<210> 2263
<211> 289

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 558; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469559"

<400> 2263
Met Ala Pro Ala Cys Gln Ile Leu Arg Trp Ala Leu Ala Leu Gly Leu
1 5 10 15

Gly Leu Met Phe Glu Val Thr His Ala Phe Arg Ser Gln Asp Glu Phe
20 25 30

Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala Phe Pro Thr Arg Val Asp
35 40 45

His Asn Gly Ala Leu Leu Ala Phe Ser Pro Pro Pro Pro Arg Arg Gln
50 55 60

Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser Arg Leu Phe Tyr Lys Val
65 70 75 80

Ala Ser Pro Ser Thr His Phe Leu Leu Asn Leu Thr Arg Ser Ser Arg
85 90 95

Leu Leu Ala Gly His Val Ser Val Glu Tyr Trp Thr Arg Glu Gly Leu
100 105 110

Ala Trp Gln Arg Ala Ala Arg Pro His Cys Leu Tyr Ala Gly His Leu
115 120 125

Gln Gly Gln Ala Ser Ser Ser His Val Ala Ile Ser Thr Cys Gly Gly
130 135 140

```
Leu His Gly Leu Ile Val Ala Asp Glu Glu Glu Tyr Leu Ile Glu Pro
145                 150                 155                 160

Leu His Gly Gly Pro Lys Gly Ser Arg Ser Pro Glu Glu Ser Gly Pro
                165                 170                 175

His Val Val Tyr Lys Arg Ser Ser Leu Arg His Pro His Leu Asp Thr
            180                 185                 190

Ala Cys Gly Val Arg Asp Glu Lys Pro Trp Lys Gly Arg Pro Trp Trp
        195                 200                 205

Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg Pro Leu Gly Asn Glu Thr
    210                 215                 220

Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser Val Ser Arg Glu Arg Tyr
225                 230                 235                 240

Val Glu Thr Leu Val Val Ala Asp Lys Met Met Val Ala Tyr His Gly
                245                 250                 255

Arg Arg Asp Val Glu Gln Tyr Val Leu Ala Ile Met Asn Ile Val Arg
            260                 265                 270

Leu Pro Asn Phe Ser Arg Thr Arg Val Trp Glu Ala Pro Leu Thr Ser
        275                 280                 285

Ser
```

<210> 2264
<211> 289
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 558; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS10; "

<220>
<221> source
<223> /note="Gene Name:

ADAM metallopeptidase with thrombospondin type 1
motif, 10; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000469901"

<400> 2264

```
Met Ala Pro Ala Cys Gln Ile Leu Arg Trp Ala Leu Ala Leu Gly Leu
1               5                  10                  15

Gly Leu Met Phe Glu Val Thr His Ala Phe Arg Ser Gln Asp Glu Phe
            20                  25                  30

Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala Phe Pro Thr Arg Val Asp
        35                  40                  45

His Asn Gly Ala Leu Leu Ala Phe Ser Pro Pro Pro Pro Arg Arg Gln
    50                  55                  60

Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser Arg Leu Phe Tyr Lys Val
65                  70                  75                  80

Ala Ser Pro Ser Thr His Phe Leu Leu Asn Leu Thr Arg Ser Ser Arg
                85                  90                  95

Leu Leu Ala Gly His Val Ser Val Glu Tyr Trp Thr Arg Glu Gly Leu
            100                 105                 110

Ala Trp Gln Arg Ala Ala Arg Pro His Cys Leu Tyr Ala Gly His Leu
        115                 120                 125

Gln Gly Gln Ala Ser Ser Ser His Val Ala Ile Ser Thr Cys Gly Gly
    130                 135                 140

Leu His Gly Leu Ile Val Ala Asp Glu Glu Glu Tyr Leu Ile Glu Pro
145                 150                 155                 160

Leu His Gly Gly Pro Lys Gly Ser Arg Ser Pro Glu Glu Ser Gly Pro
                165                 170                 175

His Val Val Tyr Lys Arg Ser Ser Leu Arg His Pro His Leu Asp Thr
            180                 185                 190

Ala Cys Gly Val Arg Asp Glu Lys Pro Trp Lys Gly Arg Pro Trp Trp
```

```
        195                 200                 205

Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg Pro Leu Gly Asn Glu Thr
    210                 215                 220

Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser Val Ser Arg Glu Arg Tyr
225                 230                 235                 240

Val Glu Thr Leu Val Val Ala Asp Lys Met Met Val Ala Tyr His Gly
                245                 250                 255

Arg Arg Asp Val Glu Gln Tyr Val Leu Ala Ile Met Asn Ile Val Arg
            260                 265                 270

Leu Pro Asn Phe Ser Arg Thr Arg Val Trp Glu Ala Pro Leu Thr Ser
        275                 280                 285

Ser
```

<210> 2265
<211> 590
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 558; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS10; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 10; "

<220>
<221> source
<223> /note="Uniprot ID: Q9H324; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000470501"

<400> 2265

```
Met Gly Pro Thr Ser Val Leu Arg Ala Gly Leu Thr Pro Ser Cys Leu
1               5                  10                  15
```

```
Pro Pro Pro Ser Gly Ala Thr Asn Gly Ser Val Ser Pro Leu Gly Arg
            20                  25                  30

Ala Gln Arg Val Trp Thr Glu Pro Gly Gly Arg Gly Leu His Gly Ala
        35                  40                  45

Thr Ala Ala Gly Pro Val Ala Ala Ala Cys Pro Leu Leu Ala Val Thr
    50                  55                  60

Ala Thr Ala Pro Gly Gln Pro Ser Gly Ala Ser Thr Val Trp Val Arg
65                  70                  75                  80

Glu Gly Gly Thr Ala Pro Ala Thr Arg Met Thr Val Pro Leu Ala Pro
                85                  90                  95

Arg Thr Ser Glu Lys Cys Ser Val Leu Asn Leu Thr Ala Ser Leu Ser
            100                 105                 110

Val Gly Asn Ser Thr Ser Gly Lys Arg Thr Gly Glu Ala Cys Ser Leu
        115                 120                 125

Thr Cys Leu Ala Glu Gly Phe Asn Phe Tyr Thr Glu Arg Ala Ala Ala
    130                 135                 140

Val Val Asp Gly Thr Pro Cys Arg Pro Asp Thr Val Asp Ile Cys Val
145                 150                 155                 160

Ser Gly Glu Cys Lys His Val Gly Cys Asp Arg Val Leu Gly Ser Asp
                165                 170                 175

Leu Arg Glu Asp Lys Cys Arg Val Cys Gly Gly Asp Gly Ser Ala Cys
            180                 185                 190

Glu Thr Ile Glu Gly Val Phe Ser Pro Ala Ser Pro Gly Ala Gly Tyr
        195                 200                 205

Glu Asp Val Val Trp Ile Pro Lys Gly Ser Val His Ile Phe Ile Gln
    210                 215                 220

Asp Leu Asn Leu Ser Leu Ser His Leu Ala Leu Lys Gly Asp Gln Glu
225                 230                 235                 240
```

```
Ser Leu Leu Leu Glu Gly Leu Pro Gly Thr Pro Gln Pro His Arg Leu
                245                 250                 255

Pro Leu Ala Gly Thr Thr Phe Gln Leu Arg Gln Gly Pro Asp Gln Val
            260                 265                 270

Gln Ser Leu Glu Ala Leu Gly Pro Ile Asn Ala Ser Leu Ile Val Met
        275                 280                 285

Val Leu Ala Arg Thr Glu Leu Pro Ala Leu Arg Tyr Arg Phe Asn Ala
    290                 295                 300

Pro Ile Ala Arg Asp Ser Leu Pro Pro Tyr Ser Trp His Tyr Ala Pro
305                 310                 315                 320

Trp Thr Lys Cys Ser Ala Gln Cys Ala Gly Gly Ser Gln Val Gln Ala
                325                 330                 335

Val Glu Cys Arg Asn Gln Leu Asp Ser Ser Ala Val Ala Pro His Tyr
            340                 345                 350

Cys Ser Ala His Ser Lys Leu Pro Lys Arg Gln Arg Ala Cys Asn Thr
        355                 360                 365

Glu Pro Cys Pro Pro Asp Trp Val Val Gly Asn Trp Ser Leu Cys Ser
    370                 375                 380

Arg Ser Cys Asp Ala Gly Val Arg Ser Arg Ser Val Val Cys Gln Arg
385                 390                 395                 400

Arg Val Ser Ala Ala Glu Glu Lys Ala Leu Asp Asp Ser Ala Cys Pro
                405                 410                 415

Gln Pro Arg Pro Pro Val Leu Glu Ala Cys His Gly Pro Thr Cys Pro
            420                 425                 430

Pro Glu Trp Ala Ala Leu Asp Trp Ser Glu Cys Thr Pro Ser Cys Gly
        435                 440                 445

Pro Gly Leu Arg His Arg Val Val Leu Cys Lys Ser Ala Asp His Arg
    450                 455                 460
```

```
Ala Thr Leu Pro Pro Ala His Cys Ser Pro Ala Ala Lys Pro Pro Ala
465                 470                 475                 480

Thr Met Arg Cys Asn Leu Arg Arg Cys Pro Pro Ala Arg Trp Val Ala
                485                 490                 495

Gly Glu Trp Gly Glu Cys Ser Ala Gln Cys Gly Val Gly Gln Arg Gln
            500                 505                 510

Arg Ser Val Arg Cys Thr Ser His Thr Gly Gln Ala Ser His Glu Cys
        515                 520                 525

Thr Glu Ala Leu Arg Pro Pro Thr Thr Gln Gln Cys Glu Ala Lys Cys
    530                 535                 540

Asp Ser Pro Thr Pro Gly Asp Gly Pro Glu Glu Cys Lys Asp Val Asn
545                 550                 555                 560

Lys Val Ala Tyr Cys Pro Leu Val Leu Lys Phe Gln Phe Cys Ser Arg
                565                 570                 575

Ala Tyr Phe Arg Gln Met Cys Cys Lys Thr Cys His Gly His
            580                 585                 590


<210> 2266
<211> 1103
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ADAMTS10; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 10; "

<220>
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<223> /note="ENSP ID: ENSP00000471851"

<400> 2266
Met Ala Pro Ala Cys Gln Ile Leu Arg Trp Ala Leu Ala Leu Gly Leu
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```
1               5                   10                  15

Gly Leu Met Phe Glu Val Thr His Ala Phe Arg Ser Gln Asp Glu Phe
            20                  25                  30

Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala Phe Pro Thr Arg Val Asp
        35                  40                  45

His Asn Gly Ala Leu Leu Ala Phe Ser Pro Pro Pro Pro Arg Arg Gln
    50                  55                  60

Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser Arg Leu Phe Tyr Lys Val
65                  70                  75                  80

Ala Ser Pro Ser Thr His Phe Leu Leu Asn Leu Thr Arg Ser Ser Arg
                85                  90                  95

Leu Leu Ala Gly His Val Ser Val Glu Tyr Trp Thr Arg Glu Gly Leu
            100                 105                 110

Ala Trp Gln Arg Ala Ala Arg Pro His Cys Leu Tyr Ala Gly His Leu
        115                 120                 125

Gln Gly Gln Ala Ser Ser Ser His Val Ala Ile Ser Thr Cys Gly Gly
    130                 135                 140

Leu His Gly Leu Ile Val Ala Asp Glu Glu Glu Tyr Leu Ile Glu Pro
145                 150                 155                 160

Leu His Gly Gly Pro Lys Gly Ser Arg Ser Pro Glu Glu Ser Gly Pro
                165                 170                 175

His Val Val Tyr Lys Arg Ser Ser Leu Arg His Pro His Leu Asp Thr
            180                 185                 190

Ala Cys Gly Val Arg Asp Glu Lys Pro Trp Lys Gly Arg Pro Trp Trp
        195                 200                 205

Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg Pro Leu Gly Asn Glu Thr
    210                 215                 220

Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser Val Ser Arg Glu Arg Tyr
225                 230                 235                 240
```

```
Val Glu Thr Leu Val Val Ala Asp Lys Met Met Val Ala Tyr His Gly
                245                 250                 255

Arg Arg Asp Val Glu Gln Tyr Val Leu Ala Ile Met Asn Ile Val Ala
            260                 265                 270

Lys Leu Phe Gln Asp Ser Ser Leu Gly Ser Thr Val Asn Ile Leu Val
        275                 280                 285

Thr Arg Leu Ile Leu Leu Thr Glu Asp Gln Pro Thr Leu Glu Ile Thr
    290                 295                 300

His His Ala Gly Lys Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser
305                 310                 315                 320

Ile Val Asn His Ser Gly His Gly Asn Ala Ile Pro Glu Asn Gly Val
                325                 330                 335

Ala Asn His Asp Thr Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Ile
            340                 345                 350

Tyr Lys Asn Lys Pro Cys Gly Thr Leu Gly Leu Ala Pro Val Gly Gly
        355                 360                 365

Met Cys Glu Arg Glu Arg Ser Cys Ser Val Asn Glu Asp Ile Gly Leu
    370                 375                 380

Ala Thr Ala Phe Thr Ile Ala His Glu Ile Gly His Thr Phe Gly Met
385                 390                 395                 400

Asn His Asp Gly Val Gly Asn Ser Cys Gly Ala Arg Gly Gln Asp Pro
                405                 410                 415

Ala Lys Leu Met Ala Ala His Ile Thr Met Lys Thr Asn Pro Phe Val
            420                 425                 430

Trp Ser Ser Cys Ser Arg Asp Tyr Ile Thr Ser Phe Leu Asp Ser Gly
        435                 440                 445

Leu Gly Leu Cys Leu Asn Asn Arg Pro Pro Arg Gln Asp Phe Val Tyr
    450                 455                 460
```

```
Pro Thr Val Ala Pro Gly Gln Ala Tyr Asp Ala Asp Glu Gln Cys Arg
465                 470                 475                 480

Phe Gln His Gly Val Lys Ser Arg Gln Cys Lys Tyr Gly Glu Val Cys
                485                 490                 495

Ser Glu Leu Trp Cys Leu Ser Lys Ser Asn Arg Cys Ile Thr Asn Ser
            500                 505                 510

Ile Pro Ala Ala Glu Gly Thr Leu Cys Gln Thr His Thr Ile Asp Lys
        515                 520                 525

Gly Trp Cys Tyr Lys Arg Val Cys Val Pro Phe Gly Ser Arg Pro Glu
    530                 535                 540

Gly Val Asp Gly Ala Trp Gly Pro Trp Thr Pro Trp Gly Asp Cys Ser
545                 550                 555                 560

Arg Thr Cys Gly Gly Gly Val Ser Ser Ser Ser Arg His Cys Asp Ser
                565                 570                 575

Pro Arg Pro Thr Ile Gly Gly Lys Tyr Cys Leu Gly Glu Arg Arg Arg
            580                 585                 590

His Arg Ser Cys Asn Thr Asp Asp Cys Pro Pro Gly Ser Gln Asp Phe
        595                 600                 605

Arg Glu Val Gln Cys Ser Glu Phe Asp Ser Ile Pro Phe Arg Gly Lys
    610                 615                 620

Phe Tyr Lys Trp Lys Thr Tyr Arg Gly Gly Gly Val Lys Ala Cys Ser
625                 630                 635                 640

Leu Thr Cys Leu Ala Glu Gly Phe Asn Phe Tyr Thr Glu Arg Ala Ala
                645                 650                 655

Ala Val Val Asp Gly Thr Pro Cys Arg Pro Asp Thr Val Asp Ile Cys
            660                 665                 670

Val Ser Gly Glu Cys Lys His Val Gly Cys Asp Arg Val Leu Gly Ser
        675                 680                 685
```

```
Asp Leu Arg Glu Asp Lys Cys Arg Val Cys Gly Gly Asp Gly Ser Ala
     690                 695                 700

Cys Glu Thr Ile Glu Gly Val Phe Ser Pro Ala Ser Pro Gly Ala Gly
705                 710                 715                 720

Tyr Glu Asp Val Val Trp Ile Pro Lys Gly Ser Val His Ile Phe Ile
                725                 730                 735

Gln Asp Leu Asn Leu Ser Leu Ser His Leu Ala Leu Lys Gly Asp Gln
            740                 745                 750

Glu Ser Leu Leu Leu Glu Gly Leu Pro Gly Thr Pro Gln Pro His Arg
        755                 760                 765

Leu Pro Leu Ala Gly Thr Thr Phe Gln Leu Arg Gln Gly Pro Asp Gln
    770                 775                 780

Val Gln Ser Leu Glu Ala Leu Gly Pro Ile Asn Ala Ser Leu Ile Val
785                 790                 795                 800

Met Val Leu Ala Arg Thr Glu Leu Pro Ala Leu Arg Tyr Arg Phe Asn
                805                 810                 815

Ala Pro Ile Ala Arg Asp Ser Leu Pro Pro Tyr Ser Trp His Tyr Ala
            820                 825                 830

Pro Trp Thr Lys Cys Ser Ala Gln Cys Ala Gly Gly Ser Gln Val Gln
        835                 840                 845

Ala Val Glu Cys Arg Asn Gln Leu Asp Ser Ser Ala Val Ala Pro His
    850                 855                 860

Tyr Cys Ser Ala His Ser Lys Leu Pro Lys Arg Gln Arg Ala Cys Asn
865                 870                 875                 880

Thr Glu Pro Cys Pro Pro Asp Trp Val Val Gly Asn Trp Ser Leu Cys
                885                 890                 895

Ser Arg Ser Cys Asp Ala Gly Val Arg Ser Arg Ser Val Val Cys Gln
            900                 905                 910

Arg Arg Val Ser Ala Ala Glu Glu Lys Ala Leu Asp Asp Ser Ala Cys
```

915 920 925

Pro Gln Pro Arg Pro Pro Val Leu Glu Ala Cys His Gly Pro Thr Cys
930 935 940

Pro Pro Glu Trp Ala Ala Leu Asp Trp Ser Glu Cys Thr Pro Ser Cys
945 950 955 960

Gly Pro Gly Leu Arg His Arg Val Val Leu Cys Lys Ser Ala Asp His
965 970 975

Arg Ala Thr Leu Pro Pro Ala His Cys Ser Pro Ala Ala Lys Pro Pro
980 985 990

Ala Thr Met Arg Cys Asn Leu Arg Arg Cys Pro Pro Ala Arg Trp
Val
995 1000 1005

Ala Gly Glu Trp Gly Glu Cys Ser Ala Gln Cys Gly Val Gly Gln
1010 1015 1020

Arg Gln Arg Ser Val Arg Cys Thr Ser His Thr Gly Gln Ala Ser
1025 1030 1035

His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr Thr Gln Gln Cys
1040 1045 1050

Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly Pro Glu Glu
1055 1060 1065

Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val Leu Lys
1070 1075 1080

Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys
1085 1090 1095

Thr Cys His Gly His
1100

<210> 2267
<211> 1509
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 559; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS12; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 12; "

<220>
<221> source
<223> /note="Uniprot ID: P58397; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000344847"

<400> 2267
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1   5   10   15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
            20   25   30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
        35   40   45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
    50   55   60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
65   70   75   80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
                85   90   95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
            100   105   110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
        115   120   125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
    130   135   140

```
Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
145                 150                 155                 160

His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
                165                 170                 175

Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
            180                 185                 190

Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
        195                 200                 205

Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg
    210                 215                 220

Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg
225                 230                 235                 240

Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr
                245                 250                 255

Lys Met Ile Glu Tyr His Gly Ser Glu Asn Val Glu Ser Tyr Ile Leu
            260                 265                 270

Thr Ile Met Asn Met Val Thr Gly Leu Phe His Asn Pro Ser Ile Gly
        275                 280                 285

Asn Ala Ile His Ile Val Val Val Arg Leu Ile Leu Leu Glu Glu Glu
    290                 295                 300

Glu Gln Gly Leu Lys Ile Val His His Ala Glu Lys Thr Leu Ser Ser
305                 310                 315                 320

Phe Cys Lys Trp Gln Lys Ser Ile Asn Pro Lys Ser Asp Leu Asn Pro
                325                 330                 335

Val His His Asp Val Ala Val Leu Leu Thr Arg Lys Asp Ile Cys Ala
            340                 345                 350

Gly Phe Asn Arg Pro Cys Glu Thr Leu Gly Leu Ser His Leu Ser Gly
        355                 360                 365
```

```
Met Cys Gln Pro His Arg Ser Cys Asn Ile Asn Glu Asp Ser Gly Leu
    370                 375                 380

Pro Leu Ala Phe Thr Ile Ala His Glu Leu Gly His Ser Phe Gly Ile
385                 390                 395                 400

Gln His Asp Gly Lys Glu Asn Asp Cys Glu Pro Val Gly Arg His Pro
                405                 410                 415

Tyr Ile Met Ser Arg Gln Leu Gln Tyr Asp Pro Thr Pro Leu Thr Trp
            420                 425                 430

Ser Lys Cys Ser Glu Glu Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp
        435                 440                 445

Gly Phe Cys Leu Asp Asp Ile Pro Lys Lys Lys Gly Leu Lys Ser Lys
    450                 455                 460

Val Ile Ala Pro Gly Val Ile Tyr Asp Val His His Gln Cys Gln Leu
465                 470                 475                 480

Gln Tyr Gly Pro Asn Ala Thr Phe Cys Gln Glu Val Glu Asn Val Cys
                485                 490                 495

Gln Thr Leu Trp Cys Ser Val Lys Gly Phe Cys Arg Ser Lys Leu Asp
            500                 505                 510

Ala Ala Ala Asp Gly Thr Gln Cys Gly Glu Lys Lys Trp Cys Met Ala
        515                 520                 525

Gly Lys Cys Ile Thr Val Gly Lys Lys Pro Glu Ser Ile Pro Gly Gly
    530                 535                 540

Trp Gly Arg Trp Ser Pro Trp Ser His Cys Ser Arg Thr Cys Gly Ala
545                 550                 555                 560

Gly Val Gln Ser Ala Glu Arg Leu Cys Asn Asn Pro Glu Pro Lys Phe
                565                 570                 575

Gly Gly Lys Tyr Cys Thr Gly Glu Arg Lys Arg Tyr Arg Leu Cys Asn
            580                 585                 590
```

```
Val His Pro Cys Arg Ser Glu Ala Pro Thr Phe Arg Gln Met Gln Cys
        595                 600                 605

Ser Glu Phe Asp Thr Val Pro Tyr Lys Asn Glu Leu Tyr His Trp Phe
    610                 615                 620

Pro Ile Phe Asn Pro Gly Tyr Val Asp Ile Gly Leu Ile Pro Lys Gly
625                 630                 635                 640

Ala Arg Asp Ile Arg Val Met Glu Ile Glu Gly Ala Gly Asn Phe Leu
                645                 650                 655

Ala Ile Arg Ser Glu Asp Pro Glu Lys Tyr Tyr Leu Asn Gly Gly Phe
            660                 665                 670

Ile Ile Gln Trp Asn Gly Asn Tyr Lys Leu Ala Gly Thr Val Phe Gln
        675                 680                 685

Tyr Asp Arg Lys Gly Asp Leu Glu Lys Leu Met Ala Thr Gly Pro Thr
    690                 695                 700

Asn Glu Ser Val Trp Ile Gln Leu Leu Phe Gln Val Thr Asn Pro Gly
705                 710                 715                 720

Ile Lys Tyr Glu Tyr Thr Ile Gln Lys Asp Gly Leu Asp Asn Asp Val
                725                 730                 735

Glu Gln Gln Met Tyr Phe Trp Gln Tyr Gly His Trp Thr Glu Cys Ser
            740                 745                 750

Val Thr Cys Gly Thr Gly Ile Arg Arg Gln Thr Ala His Cys Ile Lys
        755                 760                 765

Lys Gly Arg Gly Met Val Lys Ala Thr Phe Cys Asp Pro Glu Thr Gln
    770                 775                 780

Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala Cys Pro Pro Arg
785                 790                 795                 800

Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr Cys Gly Pro His
                805                 810                 815

Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr Met Val Ser Asp
```

```
            820                 825                 830

Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu Leu Lys Pro Lys
        835                 840                 845

Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro Ser Asp Trp Thr
    850                 855                 860

Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Val Arg
865                 870                 875                 880

Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu Pro Cys Asp Val
                885                 890                 895

Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu Gln Gln Cys Pro
            900                 905                 910

Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr Ile Ser Asn Gly
        915                 920                 925

Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro Thr Ser Arg Pro
    930                 935                 940

Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met Ser Thr Ser Thr
945                 950                 955                 960

Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser Lys Glu Gly Asp
                965                 970                 975

Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln Pro Glu Leu Ser
            980                 985                 990

Ser Arg Tyr Leu Ile Ser Thr Gly  Ser Thr Ser Gln Pro  Ile Leu
Thr
        995                 1000                1005

Ser Gln  Ser Leu Ser Ile Gln  Pro Ser Glu Glu Asn  Val Ser Ser
    1010                1015                1020

Ser Asp  Thr Gly Pro Thr Ser  Glu Gly Gly Leu Val  Ala Thr Thr
    1025                1030                1035

Thr Ser  Gly Ser Gly Leu Ser  Ser Ser Arg Asn Pro  Ile Thr Trp
```

1040 1045 1050

Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met
1055 1060 1065

Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp
1070 1075 1080

Lys Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro
1085 1090 1095

Gly Asn Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro
1100 1105 1110

Pro Leu Thr Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe
1115 1120 1125

Ser Thr Val Met Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr
1130 1135 1140

Ser Glu Thr Gly Thr Pro Arg Val Glu Gly Met Val Thr Glu Lys
1145 1150 1155

Pro Ala Asn Thr Leu Leu Pro Leu Gly Gly Asp His Gln Pro Glu
1160 1165 1170

Pro Ser Gly Lys Thr Ala Asn Arg Asn His Leu Lys Leu Pro Asn
1175 1180 1185

Asn Met Asn Gln Thr Lys Ser Ser Glu Pro Val Leu Thr Glu Glu
1190 1195 1200

Asp Ala Thr Ser Leu Ile Thr Glu Gly Phe Leu Leu Asn Ala Ser
1205 1210 1215

Asn Tyr Lys Gln Leu Thr Asn Gly His Gly Ser Ala His Trp Ile
1220 1225 1230

Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys Gly Leu Gly Ala
1235 1240 1245

Tyr Trp Arg Arg Val Glu Cys Ser Thr Gln Met Asp Ser Asp Cys
1250 1255 1260

```
Ala Ala  Ile Gln Arg Pro Asp  Pro Ala Lys Arg Cys  His Leu Arg
    1265                1270                1275

Pro Cys  Ala Gly Trp Lys Val  Gly Asn Trp Ser Lys  Cys Ser Arg
    1280                1285                1290

Asn Cys  Ser Gly Gly Phe Lys  Ile Arg Glu Ile Gln  Cys Val Asp
    1295                1300                1305

Ser Arg  Asp His Arg Asn Leu  Arg Pro Phe His Cys  Gln Phe Leu
    1310                1315                1320

Ala Gly  Ile Pro Pro Pro Leu  Ser Met Ser Cys Asn  Pro Glu Pro
    1325                1330                1335

Cys Glu  Ala Trp Gln Val Glu  Pro Trp Ser Gln Cys  Ser Arg Ser
    1340                1345                1350

Cys Gly  Gly Gly Val Gln Glu  Arg Gly Val Phe Cys  Pro Gly Gly
    1355                1360                1365

Leu Cys  Asp Trp Thr Lys Arg  Pro Thr Ser Thr Met  Ser Cys Asn
    1370                1375                1380

Glu His  Leu Cys Cys His Trp  Ala Thr Gly Asn Trp  Asp Leu Cys
    1385                1390                1395

Ser Thr  Ser Cys Gly Gly Gly  Phe Gln Lys Arg Thr  Val Gln Cys
    1400                1405                1410

Val Pro  Ser Glu Gly Asn Lys  Thr Glu Asp Gln Asp  Gln Cys Leu
    1415                1420                1425

Cys Asp  His Lys Pro Arg Pro  Pro Glu Phe Lys Lys  Cys Asn Gln
    1430                1435                1440

Gln Ala  Cys Lys Lys Ser Ala  Asp Leu Leu Cys Thr  Lys Asp Lys
    1445                1450                1455

Leu Ser  Ala Ser Phe Cys Gln  Thr Leu Lys Ala Met  Lys Lys Cys
    1460                1465                1470
```

Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe Ser Cys Pro Gln
1475 1480 1485

Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln Arg Leu Leu
1490 1495 1500

Gln Lys Ser Lys Glu Leu
1505

<210> 2268
<211> 232
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 559; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS12; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421638"

<400> 2268
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1 5 10 15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
65 70 75 80

```
Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
                85                  90                  95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
            100                 105                 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
        115                 120                 125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
    130                 135                 140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
145                 150                 155                 160

His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
                165                 170                 175

Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
            180                 185                 190

Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
        195                 200                 205

Gly Leu Lys Gly Ile Val Thr His Met Ser Ser Trp Val Glu Glu Ser
    210                 215                 220

Val Leu Phe Phe Trp Leu Phe Tyr
225                 230


<210> 2269
<211> 1594
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
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motif, 12; "

<220>
<221> source
<223> /note="Uniprot ID: P58397; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422554"

<400> 2269
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1   5   10   15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
            20   25   30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
        35   40   45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
    50   55   60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
65   70   75   80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
                85   90   95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
            100   105   110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
        115   120   125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
    130   135   140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
145   150   155   160

His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
                165   170   175

Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
            180   185   190

```
Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
        195                 200                 205

Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg
    210                 215                 220

Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg
225                 230                 235                 240

Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr
                245                 250                 255

Lys Met Ile Glu Tyr His Gly Ser Glu Asn Val Glu Ser Tyr Ile Leu
            260                 265                 270

Thr Ile Met Asn Met Val Thr Gly Leu Phe His Asn Pro Ser Ile Gly
        275                 280                 285

Asn Ala Ile His Ile Val Val Val Arg Leu Ile Leu Leu Glu Glu Glu
    290                 295                 300

Glu Gln Gly Leu Lys Ile Val His His Ala Glu Lys Thr Leu Ser Ser
305                 310                 315                 320

Phe Cys Lys Trp Gln Lys Ser Ile Asn Pro Lys Ser Asp Leu Asn Pro
                325                 330                 335

Val His His Asp Val Ala Val Leu Leu Thr Arg Lys Asp Ile Cys Ala
            340                 345                 350

Gly Phe Asn Arg Pro Cys Glu Thr Leu Gly Leu Ser His Leu Ser Gly
        355                 360                 365

Met Cys Gln Pro His Arg Ser Cys Asn Ile Asn Glu Asp Ser Gly Leu
    370                 375                 380

Pro Leu Ala Phe Thr Ile Ala His Glu Leu Gly His Ser Phe Gly Ile
385                 390                 395                 400

Gln His Asp Gly Lys Glu Asn Asp Cys Glu Pro Val Gly Arg His Pro
                405                 410                 415
```

```
Tyr Ile Met Ser Arg Gln Leu Gln Tyr Asp Pro Thr Pro Leu Thr Trp
            420                 425                 430

Ser Lys Cys Ser Glu Glu Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp
        435                 440                 445

Gly Phe Cys Leu Asp Asp Ile Pro Lys Lys Lys Gly Leu Lys Ser Lys
    450                 455                 460

Val Ile Ala Pro Gly Val Ile Tyr Asp Val His His Gln Cys Gln Leu
465                 470                 475                 480

Gln Tyr Gly Pro Asn Ala Thr Phe Cys Gln Glu Val Glu Asn Val Cys
                485                 490                 495

Gln Thr Leu Trp Cys Ser Val Lys Gly Phe Cys Arg Ser Lys Leu Asp
            500                 505                 510

Ala Ala Ala Asp Gly Thr Gln Cys Gly Glu Lys Lys Trp Cys Met Ala
        515                 520                 525

Gly Lys Cys Ile Thr Val Gly Lys Lys Pro Glu Ser Ile Pro Gly Gly
    530                 535                 540

Trp Gly Arg Trp Ser Pro Trp Ser His Cys Ser Arg Thr Cys Gly Ala
545                 550                 555                 560

Gly Val Gln Ser Ala Glu Arg Leu Cys Asn Asn Pro Glu Pro Lys Phe
                565                 570                 575

Gly Gly Lys Tyr Cys Thr Gly Glu Arg Lys Arg Tyr Arg Leu Cys Asn
            580                 585                 590

Val His Pro Cys Arg Ser Glu Ala Pro Thr Phe Arg Gln Met Gln Cys
        595                 600                 605

Ser Glu Phe Asp Thr Val Pro Tyr Lys Asn Glu Leu Tyr His Trp Phe
    610                 615                 620

Pro Ile Phe Asn Pro Ala His Pro Cys Glu Leu Tyr Cys Arg Pro Ile
625                 630                 635                 640
```

```
Asp Gly Gln Phe Ser Glu Lys Met Leu Asp Ala Val Ile Asp Gly Thr
                645                 650                 655

Pro Cys Phe Glu Gly Gly Asn Ser Arg Asn Val Cys Ile Asn Gly Ile
            660                 665                 670

Cys Lys Met Val Gly Cys Asp Tyr Glu Ile Asp Ser Asn Ala Thr Glu
        675                 680                 685

Asp Arg Cys Gly Val Cys Leu Gly Asp Gly Ser Ser Cys Gln Thr Val
    690                 695                 700

Arg Lys Met Phe Lys Gln Lys Glu Gly Ser Gly Tyr Val Asp Ile Gly
705                 710                 715                 720

Leu Ile Pro Lys Gly Ala Arg Asp Ile Arg Val Met Glu Ile Glu Gly
                725                 730                 735

Ala Gly Asn Phe Leu Ala Ile Arg Ser Glu Asp Pro Glu Lys Tyr Tyr
            740                 745                 750

Leu Asn Gly Gly Phe Ile Ile Gln Trp Asn Gly Asn Tyr Lys Leu Ala
        755                 760                 765

Gly Thr Val Phe Gln Tyr Asp Arg Lys Gly Asp Leu Glu Lys Leu Met
    770                 775                 780

Ala Thr Gly Pro Thr Asn Glu Ser Val Trp Ile Gln Leu Leu Phe Gln
785                 790                 795                 800

Val Thr Asn Pro Gly Ile Lys Tyr Glu Tyr Thr Ile Gln Lys Asp Gly
                805                 810                 815

Leu Asp Asn Asp Val Glu Gln Gln Met Tyr Phe Trp Gln Tyr Gly His
            820                 825                 830

Trp Thr Glu Cys Ser Val Thr Cys Gly Thr Gly Ile Arg Arg Gln Thr
        835                 840                 845

Ala His Cys Ile Lys Lys Gly Arg Gly Met Val Lys Ala Thr Phe Cys
    850                 855                 860

Asp Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys
```

865 870 875 880

Ala Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala
885 890 895

Thr Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln
900 905 910

Thr Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His
915 920 925

Leu Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys
930 935 940

Pro Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys
945 950 955 960

Gly Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp
965 970 975

Glu Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly
980 985 990

Leu Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys
Gly
995 1000 1005

Thr Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro
1010 1015 1020

Pro Pro Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro
1025 1030 1035

Glu Ser Met Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro
1040 1045 1050

Thr Thr Ala Ser Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln
1055 1060 1065

Asp Ser Ser Thr Gln Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser
1070 1075 1080

Thr Gly Ser Thr Ser Gln Pro Ile Leu Thr Ser Gln Ser Leu Ser

1085 1090 1095

Ile Gln Pro Ser Glu Glu Asn Val Ser Ser Ser Asp Thr Gly Pro
1100 1105 1110

Thr Ser Glu Gly Gly Leu Val Ala Thr Thr Thr Ser Gly Ser Gly
1115 1120 1125

Leu Ser Ser Ser Arg Asn Pro Ile Thr Trp Pro Val Thr Pro Phe
1130 1135 1140

Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met Glu Ile His Ser Gly
1145 1150 1155

Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys Asp Glu Ser Asn
1160 1165 1170

Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn Asp Ala Pro
1175 1180 1185

Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr Pro Asp
1190 1195 1200

Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met Glu
1205 1210 1215

Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr
1220 1225 1230

Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu
1235 1240 1245

Leu Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr
1250 1255 1260

Ala Asn Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr
1265 1270 1275

Lys Ser Ser Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu
1280 1285 1290

Ile Thr Glu Gly Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu
1295 1300 1305

```
Thr Asn  Gly His Gly Ser Ala  His Trp Ile Val Gly  Asn Trp Ser
    1310                1315                1320

Glu Cys  Ser Thr Thr Cys Gly  Leu Gly Ala Tyr Trp  Arg Arg Val
    1325                1330                1335

Glu Cys  Ser Thr Gln Met Asp  Ser Asp Cys Ala Ala  Ile Gln Arg
    1340                1345                1350

Pro Asp  Pro Ala Lys Arg Cys  His Leu Arg Pro Cys  Ala Gly Trp
    1355                1360                1365

Lys Val  Gly Asn Trp Ser Lys  Cys Ser Arg Asn Cys  Ser Gly Gly
    1370                1375                1380

Phe Lys  Ile Arg Glu Ile Gln  Cys Val Asp Ser Arg  Asp His Arg
    1385                1390                1395

Asn Leu  Arg Pro Phe His Cys  Gln Phe Leu Ala Gly  Ile Pro Pro
    1400                1405                1410

Pro Leu  Ser Met Ser Cys Asn  Pro Glu Pro Cys Glu  Ala Trp Gln
    1415                1420                1425

Val Glu  Pro Trp Ser Gln Cys  Ser Arg Ser Cys Gly  Gly Gly Val
    1430                1435                1440

Gln Glu  Arg Gly Val Phe Cys  Pro Gly Gly Leu Cys  Asp Trp Thr
    1445                1450                1455

Lys Arg  Pro Thr Ser Thr Met  Ser Cys Asn Glu His  Leu Cys Cys
    1460                1465                1470

His Trp  Ala Thr Gly Asn Trp  Asp Leu Cys Ser Thr  Ser Cys Gly
    1475                1480                1485

Gly Gly  Phe Gln Lys Arg Thr  Val Gln Cys Val Pro  Ser Glu Gly
    1490                1495                1500

Asn Lys  Thr Glu Asp Gln Asp  Gln Cys Leu Cys Asp  His Lys Pro
    1505                1510                1515
```

```
Arg Pro  Pro Glu Phe Lys Lys  Cys Asn Gln Gln Ala  Cys Lys Lys
    1520                1525                1530

Ser Ala  Asp Leu Leu Cys Thr  Lys Asp Lys Leu Ser  Ala Ser Phe
    1535                1540                1545

Cys Gln  Thr Leu Lys Ala Met  Lys Lys Cys Ser Val  Pro Thr Val
    1550                1555                1560

Arg Ala  Glu Cys Cys Phe Ser  Cys Pro Gln Thr His  Ile Thr His
    1565                1570                1575

Thr Gln  Arg Gln Arg Arg Gln  Arg Leu Leu Gln Lys  Ser Lys Glu
    1580                1585                1590

Leu
```

<210> 2270
<211> 163
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 559; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS12; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 12; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486213"

<400> 2270

```
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1               5                  10                  15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
            20                  25                  30
```

```
Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
        35                  40                  45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
    50                  55                  60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
65                  70                  75                  80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
                85                  90                  95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
            100                 105                 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
        115                 120                 125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
    130                 135                 140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
145                 150                 155                 160

His Gly Leu
```

<210> 2271
<211> 163
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
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ADAM metallopeptidase with thrombospondin type 1
motif, 12; "

<220>
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<223> /note="ENSP ID: ENSP00000486915"

<400> 2271
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1 5 10 15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
65 70 75 80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
85 90 95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
100 105 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
115 120 125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
130 135 140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
145 150 155 160

His Gly Leu

<210> 2272
<211> 1371
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 560; "

<220>

<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
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ADAM metallopeptidase with thrombospondin type 1
motif, 13; "

<220>
<221> source
<223> /note="Uniprot ID: Q76LX8; "

<220>
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<223> /note="ENSP ID: ENSP00000347927"

<400> 2272

Met	His	Gln	Arg	His	Pro	Arg	Ala	Arg	Cys	Pro	Pro	Leu	Cys	Val	Ala
1				5				10					15		
Gly	Ile	Leu	Ala	Cys	Gly	Phe	Leu	Leu	Gly	Cys	Trp	Gly	Pro	Ser	His
			20					25				30			
Phe	Gln	Gln	Ser	Cys	Leu	Gln	Ala	Leu	Glu	Pro	Gln	Ala	Val	Ser	Ser
		35					40					45			
Tyr	Leu	Ser	Pro	Gly	Ala	Pro	Leu	Lys	Gly	Arg	Pro	Pro	Ser	Pro	Gly
	50					55					60				
Phe	Gln	Arg	Gln	Arg	Gln	Arg	Gln	Arg	Arg	Ala	Ala	Gly	Gly	Ile	Leu
65					70					75					80
His	Leu	Glu	Leu	Leu	Val	Ala	Val	Gly	Pro	Asp	Val	Phe	Gln	Ala	His
				85					90					95	
Gln	Glu	Asp	Thr	Glu	Arg	Tyr	Val	Leu	Thr	Asn	Leu	Asn	Ile	Gly	Ala
			100					105					110		
Glu	Leu	Leu	Arg	Asp	Pro	Ser	Leu	Gly	Ala	Gln	Phe	Arg	Val	His	Leu
		115					120					125			
Val	Lys	Met	Val	Ile	Leu	Thr	Glu	Pro	Glu	Gly	Ala	Pro	Asn	Ile	Thr
	130					135					140				
Ala	Asn	Leu	Thr	Ser	Ser	Leu	Leu	Ser	Val	Cys	Gly	Trp	Ser	Gln	Thr
145					150					155					160

```
Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
        275                 280                 285

Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290                 295                 300

Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305                 310                 315                 320

Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325                 330                 335

Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
            340                 345                 350

Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
        355                 360                 365

Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
    370                 375                 380
```

```
Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385                 390                 395                 400

Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
                405                 410                 415

Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
            420                 425                 430

Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
        435                 440                 445

Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
    450                 455                 460

Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465                 470                 475                 480

Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
                485                 490                 495

Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
            500                 505                 510

Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
        515                 520                 525

Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
    530                 535                 540

Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545                 550                 555                 560

Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
                565                 570                 575

Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
            580                 585                 590

Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
        595                 600                 605

Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
```

610 615 620

Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625 630 635 640

Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
645 650 655

Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
660 665 670

Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
675 680 685

Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
690 695 700

Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705 710 715 720

Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
725 730 735

Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
740 745 750

Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
755 760 765

Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
770 775 780

Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785 790 795 800

Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
805 810 815

Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
820 825 830

Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
835 840 845

```
Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
    850                 855                 860

Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865                 870                 875                 880

Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
                885                 890                 895

Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
            900                 905                 910

Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
        915                 920                 925

Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
    930                 935                 940

Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945                 950                 955                 960

Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
                965                 970                 975

Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
            980                 985                 990

Thr Gln Cys Gln Gly Leu Pro Arg  Pro Glu Pro Gln Glu  Ala Cys
Ser
        995                 1000                1005

Leu Glu  Pro Cys Pro Pro Arg  Trp Lys Val Met Ser  Leu Gly Pro
    1010                1015                1020

Cys Ser  Ala Ser Cys Gly Leu  Gly Thr Ala Arg Arg  Ser Val Ala
    1025                1030                1035

Cys Val  Gln Leu Asp Gln Gly  Gln Asp Val Glu Val  Asp Glu Ala
    1040                1045                1050

Ala Cys  Ala Ala Leu Val Arg  Pro Glu Ala Ser Val  Pro Cys Leu
    1055                1060                1065
```

```
Ile Ala  Asp Cys Thr Tyr Arg  Trp His Val Gly Thr  Trp Met Glu
    1070                1075                1080

Cys Ser  Val Ser Cys Gly Asp  Gly Ile Gln Arg Arg  Arg Asp Thr
    1085                1090                1095

Cys Leu  Gly Pro Gln Ala Gln  Ala Pro Val Pro Ala  Asp Phe Cys
    1100                1105                1110

Gln His  Leu Pro Lys Pro Val  Thr Val Arg Gly Cys  Trp Ala Gly
    1115                1120                1125

Pro Cys  Val Gly Gln Gly Ala  Cys Gly Arg Gln His  Leu Glu Pro
    1130                1135                1140

Thr Gly  Thr Ile Asp Met Arg  Gly Pro Gly Gln Ala  Asp Cys Ala
    1145                1150                1155

Val Ala  Ile Gly Arg Pro Leu  Gly Glu Val Val Thr  Leu Arg Val
    1160                1165                1170

Leu Glu  Ser Ser Leu Asn Cys  Ser Ala Gly Asp Met  Leu Leu Leu
    1175                1180                1185

Trp Gly  Arg Leu Thr Trp Arg  Lys Met Cys Arg Lys  Leu Leu Asp
    1190                1195                1200

Met Thr  Phe Ser Ser Lys Thr  Asn Thr Leu Val Val  Arg Gln Arg
    1205                1210                1215

Cys Gly  Arg Pro Gly Gly Gly  Val Leu Leu Arg Tyr  Gly Ser Gln
    1220                1225                1230

Leu Ala  Pro Glu Thr Phe Tyr  Arg Glu Cys Asp Met  Gln Leu Phe
    1235                1240                1245

Gly Pro  Trp Gly Glu Ile Val  Ser Pro Ser Leu Ser  Pro Ala Thr
    1250                1255                1260

Ser Asn  Ala Gly Gly Cys Arg  Leu Phe Ile Asn Val  Ala Pro His
    1265                1270                1275
```

```
Ala Arg  Ile Ala Ile His Ala  Leu Ala Thr Asn Met  Gly Ala Gly
    1280                1285                1290

Thr Glu  Gly Ala Asn Ala Ser  Tyr Ile Leu Ile Arg  Asp Thr His
    1295                1300                1305

Ser Leu  Arg Thr Thr Ala Phe  His Gly Gln Gln Val  Leu Tyr Trp
    1310                1315                1320

Glu Ser  Glu Ser Ser Gln Ala  Glu Met Glu Phe Ser  Glu Gly Phe
    1325                1330                1335

Leu Lys  Ala Gln Ala Ser Leu  Arg Gly Gln Tyr Trp  Thr Leu Gln
    1340                1345                1350

Ser Trp  Val Pro Glu Met Gln  Asp Pro Gln Ser Trp  Lys Gly Lys
    1355                1360                1365

Glu Gly  Thr
    1370
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<210> 2273
<211> 1340
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 560; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 13; "

<220>
<221> source
<223> /note="Uniprot ID: Q76LX8; "

<220>
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<223> /note="ENSP ID: ENSP00000348997"

<400> 2273

```
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                  10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
```

225 230 235 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
245 250 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
260 265 270

Leu Leu Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala
275 280 285

Val Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu
290 295 300

Ser Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu
305 310 315 320

Val Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser
325 330 335

Lys Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val
340 345 350

His Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser
355 360 365

Cys Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg
370 375 380

Pro Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu
385 390 395 400

Met Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser
405 410 415

Gln Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly
420 425 430

Gly Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly
435 440 445

Asp Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile
450 455 460

```
Met Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser
465                 470                 475                 480

Gly Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys
                485                 490                 495

Arg Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp
            500                 505                 510

Arg Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys
        515                 520                 525

Gly Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr
    530                 535                 540

Val Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu
545                 550                 555                 560

Phe Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly
                565                 570                 575

Lys Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp
            580                 585                 590

Gly Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg
        595                 600                 605

Leu Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile
    610                 615                 620

Gln Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro
625                 630                 635                 640

Asp Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val
                645                 650                 655

Trp Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu
            660                 665                 670

Arg Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val
        675                 680                 685
```

```
Glu Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu
    690                 695                 700

Ala Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe
705                 710                 715                 720

Gly Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val
                725                 730                 735

Arg Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala
            740                 745                 750

Arg Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys
        755                 760                 765

Asn Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser
    770                 775                 780

Cys Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys
785                 790                 795                 800

Val Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly
                805                 810                 815

Ser Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser
            820                 825                 830

Cys Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys
        835                 840                 845

Ala Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His
    850                 855                 860

Val Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly
865                 870                 875                 880

Leu Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro
                885                 890                 895

Val Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg
            900                 905                 910
```

```
Glu Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu
        915                 920                 925

Ala Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu
    930                 935                 940

Tyr Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu
945                 950                 955                 960

Asp Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys
                965                 970                 975

Ser Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser Leu Gly Pro
            980                 985                 990

Cys Ser Ala Ser Cys Gly Leu Gly  Thr Ala Arg Arg Ser  Val Ala
Cys
        995                 1000                1005

Val Gln  Leu Asp Gln Gly Gln  Asp Val Glu Val Asp  Glu Ala Ala
    1010                1015                1020

Cys Ala  Ala Leu Val Arg Pro  Glu Ala Ser Val Pro  Cys Leu Ile
    1025                1030                1035

Ala Asp  Cys Thr Tyr Arg Trp  His Val Gly Thr Trp  Met Glu Cys
    1040                1045                1050

Ser Val  Ser Cys Gly Asp Gly  Ile Gln Arg Arg Arg  Asp Thr Cys
    1055                1060                1065

Leu Gly  Pro Gln Ala Gln Ala  Pro Val Pro Ala Asp  Phe Cys Gln
    1070                1075                1080

His Leu  Pro Lys Pro Val Thr  Val Arg Gly Cys Trp  Ala Gly Pro
    1085                1090                1095

Cys Val  Gly Gln Gly Ala Cys  Gly Arg Gln His Leu  Glu Pro Thr
    1100                1105                1110

Gly Thr  Ile Asp Met Arg Gly  Pro Gly Gln Ala Asp  Cys Ala Val
    1115                1120                1125
```

```
Ala Ile  Gly Arg Pro Leu Gly  Glu Val Val Thr Leu  Arg Val Leu
    1130                1135                1140

Glu Ser  Ser Leu Asn Cys Ser  Ala Gly Asp Met Leu  Leu Leu Trp
    1145                1150                1155

Gly Arg  Leu Thr Trp Arg Lys  Met Cys Arg Lys Leu  Leu Asp Met
    1160                1165                1170

Thr Phe  Ser Ser Lys Thr Asn  Thr Leu Val Val Arg  Gln Arg Cys
    1175                1180                1185

Gly Arg  Pro Gly Gly Gly Val  Leu Leu Arg Tyr Gly  Ser Gln Leu
    1190                1195                1200

Ala Pro  Glu Thr Phe Tyr Arg  Glu Cys Asp Met Gln  Leu Phe Gly
    1205                1210                1215

Pro Trp  Gly Glu Ile Val Ser  Pro Ser Leu Ser Pro  Ala Thr Ser
    1220                1225                1230

Asn Ala  Gly Gly Cys Arg Leu  Phe Ile Asn Val Ala  Pro His Ala
    1235                1240                1245

Arg Ile  Ala Ile His Ala Leu  Ala Thr Asn Met Gly  Ala Gly Thr
    1250                1255                1260

Glu Gly  Ala Asn Ala Ser Tyr  Ile Leu Ile Arg Asp  Thr His Ser
    1265                1270                1275

Leu Arg  Thr Thr Ala Phe His  Gly Gln Gln Val Leu  Tyr Trp Glu
    1280                1285                1290

Ser Glu  Ser Ser Gln Ala Glu  Met Glu Phe Ser Glu  Gly Phe Leu
    1295                1300                1305

Lys Ala  Gln Ala Ser Leu Arg  Gly Gln Tyr Trp Thr  Leu Gln Ser
    1310                1315                1320

Trp Val  Pro Glu Met Gln Asp  Pro Gln Ser Trp Lys  Gly Lys Glu
    1325                1330                1335

Gly Thr
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1340

<210> 2274
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 560; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 13; "

<220>
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<223> /note="ENSP ID: ENSP00000360978"

<400> 2274
Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala Ile Gly Arg Pro
1 5 10 15

Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser Ser Leu Asn Cys
20 25 30

Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu Thr Trp Arg Lys
35 40 45

Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser Ser Lys Thr Asn Thr
50 55 60

Leu Val Val Arg Gln Arg Cys Gly Arg Pro Gly Gly Gly Val Leu Leu
65 70 75 80

Arg Tyr Gly Ser Gln Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp
85 90 95

Met Gln Leu Phe Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser
100 105 110

Pro Ala Thr Ser Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala
115 120 125

```
Pro His Ala Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala
    130                 135                 140

Gly Thr Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His
145                 150                 155                 160

Ser Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu
                165                 170                 175

Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys
            180                 185                 190

Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val
        195                 200                 205

Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
    210                 215                 220


<210> 2275
<211> 344
<212> PRT
<213> Homo sapiens

<220>
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      motif, 13; "

<220>
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<400> 2275
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                   10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30
```

```
Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255
```

```
Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Arg Pro Val Pro Pro Ser Pro Leu Pro Leu Leu Ala Thr His
        275                 280                 285

Leu Cys Ala Gly Arg Ser Leu Ser Leu Gly Pro Ser Gln Glu Pro Ala
    290                 295                 300

Pro Gly Gly Gly Arg Gly Pro Arg Thr Pro Val Pro Thr His Lys Arg
305                 310                 315                 320

Pro Arg Phe Gln Thr Leu Pro Ser Ser Cys Pro Leu Leu Arg Pro Ala
                325                 330                 335

Ser Ser Arg Cys Thr Pro Arg Asp
            340


<210> 2276
<211> 444
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 13; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000360984"

<400> 2276
Met Ala Ser Asp Gly Ala Ala Pro Arg Ala Gly Leu Ala Trp Ser Pro
1               5                   10                  15

Cys Ser Arg Arg Gln Leu Leu Ser Leu Leu Ser Ala Gly Arg Ala Arg
            20                  25                  30

Cys Val Trp Asp Pro Pro Arg Pro Gln Pro Gly Ser Ala Gly His Pro
```

```
        35                  40                  45

Pro Asp Ala Gln Pro Gly Leu Tyr Tyr Ser Ala Asn Glu Gln Cys Arg
    50                  55                  60

Val Ala Phe Gly Pro Lys Ala Val Ala Cys Thr Phe Ala Arg Glu His
65                  70                  75                  80

Leu Asp Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln
                85                  90                  95

Ser Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys
            100                 105                 110

Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val Glu
        115                 120                 125

Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp Gly Pro
    130                 135                 140

Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val Thr Arg Arg
145                 150                 155                 160

Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly Arg Ala Cys Val
                165                 170                 175

Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr Gln Ala Cys Glu Lys
            180                 185                 190

Thr Gln Leu Glu Phe Met Ser Gln Gln Cys Ala Arg Thr Asp Gly Gln
        195                 200                 205

Pro Leu Arg Ser Ser Pro Gly Gly Ala Ser Phe Tyr His Trp Gly Ala
    210                 215                 220

Ala Val Pro His Ser Gln Gly Asp Ala Leu Cys Arg His Met Cys Arg
225                 230                 235                 240

Ala Ile Gly Glu Ser Phe Ile Met Lys Arg Gly Asp Ser Phe Leu Asp
                245                 250                 255

Gly Thr Arg Cys Met Pro Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser
            260                 265                 270
```

```
Leu Cys Val Ser Gly Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met
        275                 280                 285

Asp Ser Gln Gln Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn
    290                 295                 300

Ser Thr Cys Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg
305                 310                 315                 320

Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr
                325                 330                 335

Ile Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly
            340                 345                 350

Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr Thr
        355                 360                 365

Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val Ala Leu
    370                 375                 380

Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro
385                 390                 395                 400

Leu Gln Glu Asp Ala Asp Ile Gln Val Gly Gly Val Arg Ala Gln Leu
                405                 410                 415

Met His Ile Ser Trp Trp Ser Arg Pro Gly Leu Gly Glu Arg Asp Leu
            420                 425                 430

Cys Ala Arg Gly Arg Trp Pro Gly Gly Ser Ser Asp
        435                 440


<210> 2277
<211> 1427
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 560; "

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<223> /note="Gene Symbol: ADAMTS13; "

<220>
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ADAM metallopeptidase with thrombospondin type 1
motif, 13; "

<220>
<221> source
<223> /note="Uniprot ID: Q76LX8; "

<220>
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<223> /note="ENSP ID: ENSP00000360997"

<400> 2277

```
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                   10                  15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35                  40                  45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115                 120                 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160
```

```
Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195                 200                 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
        275                 280                 285

Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290                 295                 300

Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305                 310                 315                 320

Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325                 330                 335

Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
            340                 345                 350

Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
        355                 360                 365

Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
    370                 375                 380

Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
```

385 390 395 400

Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
405 410 415

Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
420 425 430

Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
435 440 445

Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
450 455 460

Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465 470 475 480

Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
485 490 495

Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
500 505 510

Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
515 520 525

Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
530 535 540

Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545 550 555 560

Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
565 570 575

Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
580 585 590

Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
595 600 605

Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
610 615 620

```
Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625                 630                 635                 640

Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
                645                 650                 655

Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
            660                 665                 670

Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
        675                 680                 685

Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
    690                 695                 700

Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705                 710                 715                 720

Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
                725                 730                 735

Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
            740                 745                 750

Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
        755                 760                 765

Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
    770                 775                 780

Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785                 790                 795                 800

Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
                805                 810                 815

Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
            820                 825                 830

Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
        835                 840                 845
```

```
Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
    850                 855                 860

Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865                 870                 875                 880

Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
                885                 890                 895

Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
            900                 905                 910

Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
        915                 920                 925

Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
    930                 935                 940

Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945                 950                 955                 960

Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
                965                 970                 975

Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
            980                 985                 990

Thr Gln Cys Gln Gly Leu Pro Arg  Pro Glu Pro Gln Glu  Ala Cys
Ser
        995                 1000                1005

Leu Glu  Pro Cys Pro Pro Arg  Trp Lys Val Met Ser  Leu Gly Pro
    1010                1015                1020

Cys Ser  Ala Ser Cys Gly Leu  Gly Thr Ala Arg Arg  Ser Val Ala
    1025                1030                1035

Cys Val  Gln Leu Asp Gln Gly  Gln Asp Val Glu Val  Asp Glu Ala
    1040                1045                1050

Ala Cys  Ala Ala Leu Val Arg  Pro Glu Ala Ser Val  Pro Cys Leu
    1055                1060                1065
```

```
Ile Ala  Asp Cys Thr Tyr Arg  Trp His Val Gly Thr  Trp Met Glu
    1070                1075                1080

Cys Ser  Val Ser Cys Gly Asp  Gly Ile Gln Arg Arg  Arg Asp Thr
    1085                1090                1095

Cys Leu  Gly Pro Gln Ala Gln  Ala Pro Val Pro Ala  Asp Phe Cys
    1100                1105                1110

Gln His  Leu Pro Lys Pro Val  Thr Val Arg Gly Cys  Trp Ala Gly
    1115                1120                1125

Pro Cys  Val Gly Gln Gly Thr  Pro Ser Leu Val Pro  His Glu Glu
    1130                1135                1140

Ala Ala  Ala Pro Gly Arg Thr  Thr Ala Thr Pro Ala  Gly Ala Ser
    1145                1150                1155

Leu Glu  Trp Ser Gln Ala Arg  Gly Leu Leu Phe Ser  Pro Ala Pro
    1160                1165                1170

Gln Pro  Arg Arg Leu Leu Pro  Gly Pro Gln Glu Asn  Ser Val Gln
    1175                1180                1185

Ser Ser  Ala Cys Gly Arg Gln  His Leu Glu Pro Thr  Gly Thr Ile
    1190                1195                1200

Asp Met  Arg Gly Pro Gly Gln  Ala Asp Cys Ala Val  Ala Ile Gly
    1205                1210                1215

Arg Pro  Leu Gly Glu Val Val  Thr Leu Arg Val Leu  Glu Ser Ser
    1220                1225                1230

Leu Asn  Cys Ser Ala Gly Asp  Met Leu Leu Leu Trp  Gly Arg Leu
    1235                1240                1245

Thr Trp  Arg Lys Met Cys Arg  Lys Leu Leu Asp Met  Thr Phe Ser
    1250                1255                1260

Ser Lys  Thr Asn Thr Leu Val  Val Arg Gln Arg Cys  Gly Arg Pro
    1265                1270                1275
```

```
Gly Gly  Gly Val Leu Leu Arg  Tyr Gly Ser Gln Leu  Ala Pro Glu
    1280                 1285                 1290

Thr Phe  Tyr Arg Glu Cys Asp  Met Gln Leu Phe Gly  Pro Trp Gly
    1295                 1300                 1305

Glu Ile  Val Ser Pro Ser Leu  Ser Pro Ala Thr Ser  Asn Ala Gly
    1310                 1315                 1320

Gly Cys  Arg Leu Phe Ile Asn  Val Ala Pro His Ala  Arg Ile Ala
    1325                 1330                 1335

Ile His  Ala Leu Ala Thr Asn  Met Gly Ala Gly Thr  Glu Gly Ala
    1340                 1345                 1350

Asn Ala  Ser Tyr Ile Leu Ile  Arg Asp Thr His Ser  Leu Arg Thr
    1355                 1360                 1365

Thr Ala  Phe His Gly Gln Gln  Val Leu Tyr Trp Glu  Ser Glu Ser
    1370                 1375                 1380

Ser Gln  Ala Glu Met Glu Phe  Ser Glu Gly Phe Leu  Lys Ala Gln
    1385                 1390                 1395

Ala Ser  Leu Arg Gly Gln Tyr  Trp Thr Leu Gln Ser  Trp Val Pro
    1400                 1405                 1410

Glu Met  Gln Asp Pro Gln Ser  Trp Lys Gly Lys Glu  Gly Thr
    1415                 1420                 1425


<210> 2278
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 560; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS13; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
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motif, 13; "

<220>
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<223> /note="ENSP ID: ENSP00000435274"

<400> 2278
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1 5 10 15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
20 25 30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
35 40 45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
50 55 60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65 70 75 80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
85 90 95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
100 105 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
115 120 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
130 135 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145 150 155 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
165 170 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
180 185 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
195 200 205

```
Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270

Leu Leu Arg Pro Val Pro Pro Ser Pro Leu Pro Leu Leu Ala Thr His
        275                 280                 285

Leu Cys Ala Gly Arg Ser Leu Ser Leu Gly Pro Ser Gln Glu Pro Ala
    290                 295                 300

Pro Gly Gly Gly Arg Gly Pro Arg Thr Pro Val Pro Thr His Lys Arg
305                 310                 315                 320

Pro Arg Phe Gln Thr Leu Pro Ser Ser Cys Pro Leu Leu Arg Pro Ala
                325                 330                 335

Ser Ser Arg Cys Thr Pro Arg Asp
            340


<210> 2279
<211> 276
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      motif, 13; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000435305"

<400> 2279
Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val Ala
1   5   10   15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20   25   30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35   40   45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50   55   60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65   70   75   80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85   90   95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100   105   110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
        115   120   125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130   135   140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145   150   155   160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165   170   175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180   185   190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195   200   205

```
Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220

Glu Ile Gly His Arg Ile Cys Ala Arg Pro Ser Pro Ala Thr Gln Thr
225                 230                 235                 240

Arg Trp Thr Lys Ala Ala Ala Ala Ala Ser Ser Phe Leu Ser Trp Met
                245                 250                 255

Gly Gln Asn Val Ala Trp Arg Ser Gly Ala Pro Arg Val Ala Ala Ala
            260                 265                 270

Pro Trp Trp Ser
        275


<210> 2280
<211> 1223
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 561; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS14; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 14; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8WXS8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000362303"

<400> 2280
Met Ala Pro Leu Arg Ala Leu Leu Ser Tyr Leu Leu Pro Leu His Cys
1               5                   10                  15

Ala Leu Cys Ala Ala Ala Gly Ser Arg Thr Pro Glu Leu His Leu Ser
            20                  25                  30

Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
```

```
        35                  40                  45

Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
    50                  55                  60

Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
65                  70                  75                  80

Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
                85                  90                  95

Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
            100                 105                 110

Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
        115                 120                 125

Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
    130                 135                 140

Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
145                 150                 155                 160

Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
                165                 170                 175

Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
            180                 185                 190

Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
        195                 200                 205

Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
    210                 215                 220

Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
225                 230                 235                 240

Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
                245                 250                 255

Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
            260                 265                 270
```

```
Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
        275                 280                 285

Asn Ile Val Asp Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile
    290                 295                 300

Asn Ile Ala Leu Val Arg Leu Ile Met Val Gly Tyr Arg Gln Ser Leu
305                 310                 315                 320

Ser Leu Ile Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Gln Val Cys
                325                 330                 335

Arg Trp Ala His Ser Gln Gln Arg Gln Asp Pro Ser His Ala Glu His
            340                 345                 350

His Asp His Val Val Phe Leu Thr Arg Gln Asp Phe Gly Pro Ser Gly
        355                 360                 365

Tyr Ala Pro Val Thr Gly Met Cys His Pro Leu Arg Ser Cys Ala Leu
    370                 375                 380

Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Ile Ala His Glu Thr
385                 390                 395                 400

Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Gly Cys Ala
                405                 410                 415

Asp Glu Thr Ser Leu Gly Ser Val Met Ala Pro Leu Val Gln Ala Ala
            420                 425                 430

Phe His Arg Phe His Trp Ser Arg Cys Ser Lys Leu Glu Leu Ser Arg
        435                 440                 445

Tyr Leu Pro Ser Tyr Asp Cys Leu Leu Asp Asp Pro Phe Asp Pro Ala
    450                 455                 460

Trp Pro Gln Pro Pro Glu Leu Pro Gly Ile Asn Tyr Ser Met Asp Glu
465                 470                 475                 480

Gln Cys Arg Phe Asp Phe Gly Ser Gly Tyr Gln Thr Cys Leu Ala Phe
                485                 490                 495
```

```
Arg Thr Phe Glu Pro Cys Lys Gln Leu Trp Cys Ser His Pro Asp Asn
            500                 505                 510

Pro Tyr Phe Cys Lys Thr Lys Lys Gly Pro Pro Leu Asp Gly Thr Glu
        515                 520                 525

Cys Ala Pro Gly Lys Trp Cys Phe Lys Gly His Cys Ile Trp Lys Ser
    530                 535                 540

Pro Glu Gln Thr Tyr Gly Gln Asp Gly Gly Trp Ser Ser Trp Thr Lys
545                 550                 555                 560

Phe Gly Ser Cys Ser Arg Ser Cys Gly Gly Gly Val Arg Ser Arg Ser
                565                 570                 575

Arg Ser Cys Asn Asn Pro Ser Pro Ala Tyr Gly Gly Arg Leu Cys Leu
            580                 585                 590

Gly Pro Met Phe Glu Tyr Gln Val Cys Asn Ser Glu Glu Cys Pro Gly
        595                 600                 605

Thr Tyr Glu Asp Phe Arg Ala Gln Gln Cys Ala Lys Arg Asn Ser Tyr
    610                 615                 620

Tyr Val His Gln Asn Ala Lys His Ser Trp Val Pro Tyr Glu Pro Asp
625                 630                 635                 640

Asp Asp Ala Gln Lys Cys Glu Leu Ile Cys Gln Ser Ala Asp Thr Gly
                645                 650                 655

Asp Val Val Phe Met Asn Gln Val Val His Asp Gly Thr Arg Cys Ser
            660                 665                 670

Tyr Arg Asp Pro Tyr Ser Val Cys Ala Arg Gly Glu Cys Val Pro Val
        675                 680                 685

Gly Cys Asp Lys Glu Val Gly Ser Met Lys Ala Asp Asp Lys Cys Gly
    690                 695                 700

Val Cys Gly Gly Asp Asn Ser His Cys Arg Thr Val Lys Gly Thr Leu
705                 710                 715                 720
```

```
Gly Lys Ala Ser Lys Gln Ala Gly Ala Leu Lys Leu Val Gln Ile Pro
                725                 730                 735

Ala Gly Ala Arg His Ile Gln Ile Glu Ala Leu Glu Lys Ser Pro His
            740                 745                 750

Arg Ile Val Val Lys Asn Gln Val Thr Gly Ser Phe Ile Leu Asn Pro
        755                 760                 765

Lys Gly Lys Glu Ala Thr Ser Arg Thr Phe Thr Ala Met Gly Leu Glu
    770                 775                 780

Trp Glu Asp Ala Val Glu Asp Ala Lys Glu Ser Leu Lys Thr Ser Gly
785                 790                 795                 800

Pro Leu Pro Glu Ala Ile Ala Ile Leu Ala Leu Pro Pro Thr Glu Gly
                805                 810                 815

Gly Pro Arg Ser Ser Leu Ala Tyr Lys Tyr Val Ile His Glu Asp Leu
            820                 825                 830

Leu Pro Leu Ile Gly Ser Asn Asn Val Leu Leu Glu Glu Met Asp Thr
        835                 840                 845

Tyr Glu Trp Ala Leu Lys Ser Trp Ala Pro Cys Ser Lys Ala Cys Gly
    850                 855                 860

Gly Gly Ile Gln Phe Thr Lys Tyr Gly Cys Arg Arg Arg Arg Asp His
865                 870                 875                 880

His Met Val Gln Arg His Leu Cys Asp His Lys Lys Arg Pro Lys Pro
                885                 890                 895

Ile Arg Arg Arg Cys Asn Gln His Pro Cys Ser Gln Pro Val Trp Val
            900                 905                 910

Thr Glu Glu Trp Gly Ala Cys Ser Arg Ser Cys Gly Lys Leu Gly Val
        915                 920                 925

Gln Thr Arg Gly Ile Gln Cys Leu Leu Pro Leu Ser Asn Gly Thr His
    930                 935                 940

Lys Val Met Pro Ala Lys Ala Cys Ala Gly Asp Arg Pro Glu Ala Arg
```

945 950 955 960

Arg Pro Cys Leu Arg Val Pro Cys Pro Ala Gln Trp Arg Leu Gly Ala
965 970 975

Trp Ser Gln Cys Ser Ala Thr Cys Gly Glu Gly Ile Gln Gln Arg Gln
980 985 990

Val Val Cys Arg Thr Asn Ala Asn Ser Leu Gly His Cys Glu Gly Asp
995 1000 1005

Arg Pro Asp Thr Val Gln Val Cys Ser Leu Pro Ala Cys Gly Gly
1010 1015 1020

Asn His Gln Asn Ser Thr Val Arg Ala Asp Val Trp Glu Leu Gly
1025 1030 1035

Thr Pro Glu Gly Gln Trp Val Pro Gln Ser Glu Pro Leu His Pro
1040 1045 1050

Ile Asn Lys Ile Ser Ser Thr Glu Pro Cys Thr Gly Asp Arg Ser
1055 1060 1065

Val Phe Cys Gln Met Glu Val Leu Asp Arg Tyr Cys Ser Ile Pro
1070 1075 1080

Gly Tyr His Arg Leu Cys Cys Val Ser Cys Ile Lys Lys Ala Ser
1085 1090 1095

Gly Pro Asn Pro Gly Pro Asp Pro Gly Pro Thr Ser Leu Pro Pro
1100 1105 1110

Phe Ser Thr Pro Gly Ser Pro Leu Pro Gly Pro Gln Asp Pro Ala
1115 1120 1125

Asp Ala Ala Glu Pro Pro Gly Lys Pro Thr Gly Ser Glu Asp His
1130 1135 1140

Gln His Gly Arg Ala Thr Gln Leu Pro Gly Ala Leu Asp Thr Ser
1145 1150 1155

Ser Pro Gly Thr Gln His Pro Phe Ala Pro Glu Thr Pro Ile Pro

```
    1160                1165                1170

Gly Ala  Ser Trp Ser Ile Ser  Pro Thr Thr Pro Gly  Gly Leu Pro
    1175                1180                1185

Trp Gly  Trp Thr Gln Thr Pro  Thr Pro Val Pro Glu  Asp Lys Gly
    1190                1195                1200

Gln Pro  Gly Glu Asp Leu Arg  His Pro Gly Thr Ser  Leu Pro Ala
    1205                1210                1215

Ala Ser  Pro Val Thr
    1220


<210> 2281
<211> 1226
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 561; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS14; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 14; "

<220>
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<223> /note="Uniprot ID:  Q8WXS8; "

<220>
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<400> 2281
Met Ala Pro Leu Arg Ala Leu Leu Ser Tyr Leu Leu Pro Leu His Cys
1               5                  10                  15

Ala Leu Cys Ala Ala Ala Gly Ser Arg Thr Pro Glu Leu His Leu Ser
            20                  25                  30

Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
        35                  40                  45
```

```
Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
    50                  55                  60

Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
65                  70                  75                  80

Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
                85                  90                  95

Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
            100                 105                 110

Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
        115                 120                 125

Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
    130                 135                 140

Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
145                 150                 155                 160

Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
                165                 170                 175

Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
            180                 185                 190

Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
        195                 200                 205

Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
    210                 215                 220

Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
225                 230                 235                 240

Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
                245                 250                 255

Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
            260                 265                 270
```

```
Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
        275                 280                 285

Asn Ile Val Asp Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile
    290                 295                 300

Asn Ile Ala Leu Val Arg Leu Ile Met Val Gly Tyr Arg Gln Ser Leu
305                 310                 315                 320

Ser Leu Ile Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Gln Val Cys
                325                 330                 335

Arg Trp Ala His Ser Gln Gln Arg Gln Asp Pro Ser His Ala Glu His
            340                 345                 350

His Asp His Val Val Phe Leu Thr Arg Gln Asp Phe Gly Pro Ser Gly
        355                 360                 365

Met Gln Gly Tyr Ala Pro Val Thr Gly Met Cys His Pro Leu Arg Ser
    370                 375                 380

Cys Ala Leu Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Ile Ala
385                 390                 395                 400

His Glu Thr Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn
                405                 410                 415

Gly Cys Ala Asp Glu Thr Ser Leu Gly Ser Val Met Ala Pro Leu Val
            420                 425                 430

Gln Ala Ala Phe His Arg Phe His Trp Ser Arg Cys Ser Lys Leu Glu
        435                 440                 445

Leu Ser Arg Tyr Leu Pro Ser Tyr Asp Cys Leu Leu Asp Asp Pro Phe
    450                 455                 460

Asp Pro Ala Trp Pro Gln Pro Pro Glu Leu Pro Gly Ile Asn Tyr Ser
465                 470                 475                 480

Met Asp Glu Gln Cys Arg Phe Asp Phe Gly Ser Gly Tyr Gln Thr Cys
                485                 490                 495
```

```
Leu Ala Phe Arg Thr Phe Glu Pro Cys Lys Gln Leu Trp Cys Ser His
            500                 505                 510

Pro Asp Asn Pro Tyr Phe Cys Lys Thr Lys Lys Gly Pro Pro Leu Asp
        515                 520                 525

Gly Thr Glu Cys Ala Pro Gly Lys Trp Cys Phe Lys Gly His Cys Ile
    530                 535                 540

Trp Lys Ser Pro Glu Gln Thr Tyr Gly Gln Asp Gly Gly Trp Ser Ser
545                 550                 555                 560

Trp Thr Lys Phe Gly Ser Cys Ser Arg Ser Cys Gly Gly Gly Val Arg
                565                 570                 575

Ser Arg Ser Arg Ser Cys Asn Asn Pro Ser Pro Ala Tyr Gly Gly Arg
            580                 585                 590

Leu Cys Leu Gly Pro Met Phe Glu Tyr Gln Val Cys Asn Ser Glu Glu
        595                 600                 605

Cys Pro Gly Thr Tyr Glu Asp Phe Arg Ala Gln Gln Cys Ala Lys Arg
    610                 615                 620

Asn Ser Tyr Tyr Val His Gln Asn Ala Lys His Ser Trp Val Pro Tyr
625                 630                 635                 640

Glu Pro Asp Asp Asp Ala Gln Lys Cys Glu Leu Ile Cys Gln Ser Ala
                645                 650                 655

Asp Thr Gly Asp Val Val Phe Met Asn Gln Val Val His Asp Gly Thr
            660                 665                 670

Arg Cys Ser Tyr Arg Asp Pro Tyr Ser Val Cys Ala Arg Gly Glu Cys
        675                 680                 685

Val Pro Val Gly Cys Asp Lys Glu Val Gly Ser Met Lys Ala Asp Asp
    690                 695                 700

Lys Cys Gly Val Cys Gly Gly Asp Asn Ser His Cys Arg Thr Val Lys
705                 710                 715                 720

Gly Thr Leu Gly Lys Ala Ser Lys Gln Ala Gly Ala Leu Lys Leu Val
```

```
                725                 730                 735

Gln Ile Pro Ala Gly Ala Arg His Ile Gln Ile Glu Ala Leu Glu Lys
            740                 745                 750

Ser Pro His Arg Ile Val Val Lys Asn Gln Val Thr Gly Ser Phe Ile
        755                 760                 765

Leu Asn Pro Lys Gly Lys Glu Ala Thr Ser Arg Thr Phe Thr Ala Met
    770                 775                 780

Gly Leu Glu Trp Glu Asp Ala Val Glu Asp Ala Lys Glu Ser Leu Lys
785                 790                 795                 800

Thr Ser Gly Pro Leu Pro Glu Ala Ile Ala Ile Leu Ala Leu Pro Pro
                805                 810                 815

Thr Glu Gly Gly Pro Arg Ser Ser Leu Ala Tyr Lys Tyr Val Ile His
            820                 825                 830

Glu Asp Leu Leu Pro Leu Ile Gly Ser Asn Asn Val Leu Leu Glu Glu
        835                 840                 845

Met Asp Thr Tyr Glu Trp Ala Leu Lys Ser Trp Ala Pro Cys Ser Lys
    850                 855                 860

Ala Cys Gly Gly Gly Ile Gln Phe Thr Lys Tyr Gly Cys Arg Arg Arg
865                 870                 875                 880

Arg Asp His His Met Val Gln Arg His Leu Cys Asp His Lys Lys Arg
                885                 890                 895

Pro Lys Pro Ile Arg Arg Arg Cys Asn Gln His Pro Cys Ser Gln Pro
            900                 905                 910

Val Trp Val Thr Glu Glu Trp Gly Ala Cys Ser Arg Ser Cys Gly Lys
        915                 920                 925

Leu Gly Val Gln Thr Arg Gly Ile Gln Cys Leu Leu Pro Leu Ser Asn
    930                 935                 940

Gly Thr His Lys Val Met Pro Ala Lys Ala Cys Ala Gly Asp Arg Pro
945                 950                 955                 960
```

```
Glu Ala Arg Arg Pro Cys Leu Arg Val Pro Cys Pro Ala Gln Trp Arg
                965                 970                 975

Leu Gly Ala Trp Ser Gln Cys Ser Ala Thr Cys Gly Glu Gly Ile Gln
            980                 985                 990

Gln Arg Gln Val Val Cys Arg Thr  Asn Ala Asn Ser Leu  Gly His
Cys
        995                 1000                1005

Glu Gly  Asp Arg Pro Asp Thr  Val Gln Val Cys Ser  Leu Pro Ala
    1010                1015                1020

Cys Gly  Gly Asn His Gln Asn  Ser Thr Val Arg Ala  Asp Val Trp
    1025                1030                1035

Glu Leu  Gly Thr Pro Glu Gly  Gln Trp Val Pro Gln  Ser Glu Pro
    1040                1045                1050

Leu His  Pro Ile Asn Lys Ile  Ser Ser Thr Glu Pro  Cys Thr Gly
    1055                1060                1065

Asp Arg  Ser Val Phe Cys Gln  Met Glu Val Leu Asp  Arg Tyr Cys
    1070                1075                1080

Ser Ile  Pro Gly Tyr His Arg  Leu Cys Cys Val Ser  Cys Ile Lys
    1085                1090                1095

Lys Ala  Ser Gly Pro Asn Pro  Gly Pro Asp Pro Gly  Pro Thr Ser
    1100                1105                1110

Leu Pro  Pro Phe Ser Thr Pro  Gly Ser Pro Leu Pro  Gly Pro Gln
    1115                1120                1125

Asp Pro  Ala Asp Ala Ala Glu  Pro Pro Gly Lys Pro  Thr Gly Ser
    1130                1135                1140

Glu Asp  His Gln His Gly Arg  Ala Thr Gln Leu Pro  Gly Ala Leu
    1145                1150                1155

Asp Thr  Ser Ser Pro Gly Thr  Gln His Pro Phe Ala  Pro Glu Thr
    1160                1165                1170
```

```
Pro Ile  Pro Gly Ala Ser Trp  Ser Ile Ser Pro Thr  Thr Pro Gly
    1175                1180                1185


Gly Leu  Pro Trp Gly Trp Thr  Gln Thr Pro Thr Pro  Val Pro Glu
    1190                1195                1200


Asp Lys  Gly Gln Pro Gly Glu  Asp Leu Arg His Pro  Gly Thr Ser
    1205                1210                1215


Leu Pro  Ala Ala Ser Pro Val  Thr
    1220                1225


<210> 2282
<211> 950
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 562; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS15; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 15; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TE58; "

<220>
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<223> /note="ENSP ID: ENSP00000299164"

<400> 2282
Met Leu Leu Leu Gly Ile Leu Thr Leu Ala Phe Ala Gly Arg Thr Ala
1               5                  10                  15


Gly Gly Ser Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp
            20                  25                  30


Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
        35                  40                  45
```

```
Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
    50                  55                  60

Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser
65                  70                  75                  80

Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
                85                  90                  95

Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
            100                 105                 110

Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
        115                 120                 125

Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
    130                 135                 140

Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
145                 150                 155                 160

Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
                165                 170                 175

Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
            180                 185                 190

Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
        195                 200                 205

Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
    210                 215                 220

Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
225                 230                 235                 240

Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
                245                 250                 255

Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
            260                 265                 270
```

```
Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
        275                 280                 285

Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
    290                 295                 300

Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
305                 310                 315                 320

Leu Cys Gly Ala Thr Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
                325                 330                 335

Thr Met Cys Asp Pro Lys Arg Ser Cys Ser Val Ile Glu Asp Asp Gly
            340                 345                 350

Leu Pro Ser Ala Phe Thr Thr Ala His Glu Leu Gly His Val Phe Asn
        355                 360                 365

Met Pro His Asp Asn Val Lys Val Cys Glu Glu Val Phe Gly Lys Leu
    370                 375                 380

Arg Ala Asn His Met Met Ser Pro Thr Leu Ile Gln Ile Asp Arg Ala
385                 390                 395                 400

Asn Pro Trp Ser Ala Cys Ser Ala Ala Ile Ile Thr Asp Phe Leu Asp
                405                 410                 415

Ser Gly His Gly Asp Cys Leu Leu Asp Gln Pro Ser Lys Pro Ile Ser
            420                 425                 430

Leu Pro Glu Asp Leu Pro Gly Ala Ser Tyr Thr Leu Ser Gln Gln Cys
        435                 440                 445

Glu Leu Ala Phe Gly Val Gly Ser Lys Pro Cys Pro Tyr Met Gln Tyr
    450                 455                 460

Cys Thr Lys Leu Trp Cys Thr Gly Lys Ala Lys Gly Gln Met Val Cys
465                 470                 475                 480

Gln Thr Arg His Phe Pro Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly
                485                 490                 495

Lys Leu Cys Leu Lys Gly Ala Cys Val Glu Arg His Asn Leu Asn Lys
```

```
            500                 505                 510

His Arg Val Asp Gly Ser Trp Ala Lys Trp Asp Pro Tyr Gly Pro Cys
        515                 520                 525

Ser Arg Thr Cys Gly Gly Gly Val Gln Leu Ala Arg Arg Gln Cys Thr
    530                 535                 540

Asn Pro Thr Pro Ala Asn Gly Gly Lys Tyr Cys Glu Gly Val Arg Val
545                 550                 555                 560

Lys Tyr Arg Ser Cys Asn Leu Glu Pro Cys Pro Ser Ser Ala Ser Gly
                565                 570                 575

Lys Ser Phe Arg Glu Glu Gln Cys Glu Ala Phe Asn Gly Tyr Asn His
            580                 585                 590

Ser Thr Asn Arg Leu Thr Leu Ala Val Ala Trp Val Pro Lys Tyr Ser
        595                 600                 605

Gly Val Ser Pro Arg Asp Lys Cys Lys Leu Ile Cys Arg Ala Asn Gly
    610                 615                 620

Thr Gly Tyr Phe Tyr Val Leu Ala Pro Lys Val Val Asp Gly Thr Leu
625                 630                 635                 640

Cys Ser Pro Asp Ser Thr Ser Val Cys Val Gln Gly Lys Cys Ile Lys
                645                 650                 655

Ala Gly Cys Asp Gly Asn Leu Gly Ser Lys Lys Arg Phe Asp Lys Cys
            660                 665                 670

Gly Val Cys Gly Gly Asp Asn Lys Ser Cys Lys Lys Val Thr Gly Leu
        675                 680                 685

Phe Thr Lys Pro Met His Gly Tyr Asn Phe Val Val Ala Ile Pro Ala
    690                 695                 700

Gly Ala Ser Ser Ile Asp Ile Arg Gln Arg Gly Tyr Lys Gly Leu Ile
705                 710                 715                 720

Gly Asp Asp Asn Tyr Leu Ala Leu Lys Asn Ser Gln Gly Lys Tyr Leu
                725                 730                 735
```

```
Leu Asn Gly His Phe Val Val Ser Ala Val Glu Arg Asp Leu Val Val
            740                 745                 750

Lys Gly Ser Leu Leu Arg Tyr Ser Gly Thr Gly Thr Ala Val Glu Ser
        755                 760                 765

Leu Gln Ala Ser Arg Pro Ile Leu Glu Pro Leu Thr Val Glu Val Leu
    770                 775                 780

Ser Val Gly Lys Met Thr Pro Pro Arg Val Arg Tyr Ser Phe Tyr Leu
785                 790                 795                 800

Pro Lys Glu Pro Arg Glu Asp Lys Ser Ser His Pro Lys Asp Pro Arg
                805                 810                 815

Gly Pro Ser Val Leu His Asn Ser Val Leu Ser Leu Ser Asn Gln Val
            820                 825                 830

Glu Gln Pro Asp Asp Arg Pro Pro Ala Arg Trp Val Ala Gly Ser Trp
        835                 840                 845

Gly Pro Cys Ser Ala Ser Cys Gly Ser Gly Leu Gln Lys Arg Ala Val
    850                 855                 860

Asp Cys Arg Gly Ser Ala Gly Gln Arg Thr Val Pro Ala Cys Asp Ala
865                 870                 875                 880

Ala His Arg Pro Val Glu Thr Gln Ala Cys Gly Glu Pro Cys Pro Thr
                885                 890                 895

Trp Glu Leu Ser Ala Trp Ser Pro Cys Ser Lys Ser Cys Gly Arg Gly
            900                 905                 910

Phe Gln Arg Arg Ser Leu Lys Cys Val Gly His Gly Gly Arg Leu Leu
        915                 920                 925

Ala Arg Asp Gln Cys Asn Leu His Arg Lys Pro Gln Glu Leu Asp Phe
    930                 935                 940

Cys Val Leu Arg Pro Cys
945                 950
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<210> 2283
<211> 1224
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ADAMTS16; "

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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 16; "

<220>
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<223> /note="Uniprot ID: Q8TE57; "

<220>
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<400> 2283
Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
1   5   10   15

Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
            20   25   30

Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro Pro
        35   40   45

Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
    50   55   60

Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
65   70   75   80

His His Gln Arg Arg Arg Arg Ala Val Pro Val Ser Glu Val Glu Ser
                85   90   95

Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Met Asp Leu
            100   105   110

```
Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
        115                 120                 125

Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
    130                 135                 140

Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
145                 150                 155                 160

Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
                165                 170                 175

Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
            180                 185                 190

Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
        195                 200                 205

Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
    210                 215                 220

Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
225                 230                 235                 240

Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
                245                 250                 255

Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
            260                 265                 270

Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
        275                 280                 285

Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
    290                 295                 300

Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
305                 310                 315                 320

Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
                325                 330                 335

Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
```

```
            340                 345                 350

Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
        355                 360                 365

Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
    370                 375                 380

Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
385                 390                 395                 400

Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
                405                 410                 415

Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
            420                 425                 430

His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn
        435                 440                 445

Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly
    450                 455                 460

Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His
465                 470                 475                 480

Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys
                485                 490                 495

Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr
            500                 505                 510

Asp Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu
        515                 520                 525

Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His
    530                 535                 540

Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly
545                 550                 555                 560

Thr Ile Cys Gly His Asp Met Trp Cys Arg Gly Gly Gln Cys Val Lys
                565                 570                 575
```

```
Tyr Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp
            580                 585                 590

Ser Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His
        595                 600                 605

Arg Ser Arg Leu Cys Thr Asn Pro Lys Pro Ser His Gly Gly Lys Phe
    610                 615                 620

Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys
625                 630                 635                 640

Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn
                645                 650                 655

Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Tyr Thr Gln
            660                 665                 670

Val Glu Asp Gln Asp Leu Cys Lys Leu Tyr Cys Ile Ala Glu Gly Phe
        675                 680                 685

Asp Phe Phe Phe Ser Leu Ser Asn Lys Val Lys Asp Gly Thr Pro Cys
    690                 695                 700

Ser Glu Asp Ser Arg Asn Val Cys Ile Asp Gly Ile Cys Glu Arg Val
705                 710                 715                 720

Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val Glu Asp Val Cys Gly
                725                 730                 735

Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile His Arg Gly Leu Tyr
            740                 745                 750

Thr Lys His His His Thr Asn Gln Tyr Tyr His Met Val Thr Ile Pro
        755                 760                 765

Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn Val Ser Thr Ser
    770                 775                 780

Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr Leu Asn Gly His
785                 790                 795                 800
```

```
Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser Gly Thr Thr Phe
                805                 810                 815

Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu Ile Ala Thr Gly
            820                 825                 830

Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe Gln Gly Arg Asn
        835                 840                 845

Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu Gly Thr Glu Lys
    850                 855                 860

Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile Val Arg Ser Glu
865                 870                 875                 880

Cys Ser Val Ser Cys Gly Gly Gly Gln Met Thr Val Arg Glu Gly Cys
                885                 890                 895

Tyr Arg Asp Leu Lys Phe Gln Val Asn Met Ser Phe Cys Asn Pro Lys
            900                 905                 910

Thr Arg Pro Val Thr Gly Leu Val Pro Cys Lys Val Ser Ala Cys Pro
        915                 920                 925

Pro Ser Trp Ser Val Gly Asn Trp Ser Ala Cys Ser Arg Thr Cys Gly
    930                 935                 940

Gly Gly Ala Gln Ser Arg Pro Val Gln Cys Thr Arg Arg Val His Tyr
945                 950                 955                 960

Asp Ser Glu Pro Val Pro Ala Ser Leu Cys Pro Gln Pro Ala Pro Ser
                965                 970                 975

Ser Arg Gln Ala Cys Asn Ser Gln Ser Cys Pro Pro Ala Trp Ser Ala
            980                 985                 990

Gly Pro Trp Ala Glu Cys Ser His  Thr Cys Gly Lys Gly  Trp Arg
Lys
        995                 1000                1005

Arg Ala  Val Ala Cys Lys Ser  Thr Asn Pro Ser Ala  Arg Ala Gln
    1010                1015                1020
```

```
Leu Leu  Pro Asp Ala Val Cys  Thr Ser Glu Pro Lys  Pro Arg Met
    1025                1030                1035

His Glu  Ala Cys Leu Leu Gln  Arg Cys His Lys Pro  Lys Lys Leu
    1040                1045                1050

Gln Trp  Leu Val Ser Ala Trp  Ser Gln Cys Ser Val  Thr Cys Glu
    1055                1060                1065

Arg Gly  Thr Gln Lys Arg Phe  Leu Lys Cys Ala Glu  Lys Tyr Val
    1070                1075                1080

Ser Gly  Lys Tyr Arg Glu Leu  Ala Ser Lys Lys Cys  Ser His Leu
    1085                1090                1095

Pro Lys  Pro Ser Leu Glu Leu  Glu Arg Ala Cys Ala  Pro Leu Pro
    1100                1105                1110

Cys Pro  Arg His Pro Pro Phe  Ala Ala Ala Gly Pro  Ser Arg Gly
    1115                1120                1125

Ser Trp  Phe Ala Ser Pro Trp  Ser Gln Cys Thr Ala  Ser Cys Gly
    1130                1135                1140

Gly Gly  Val Gln Thr Arg Ser  Val Gln Cys Leu Ala  Gly Gly Arg
    1145                1150                1155

Pro Ala  Ser Gly Cys Leu Leu  His Gln Lys Pro Ser  Ala Ser Leu
    1160                1165                1170

Ala Cys  Asn Thr His Phe Cys  Pro Ile Ala Glu Lys  Lys Asp Ala
    1175                1180                1185

Phe Cys  Lys Asp Tyr Phe His  Trp Cys Tyr Leu Val  Pro Gln His
    1190                1195                1200

Gly Met  Cys Ser His Lys Phe  Tyr Gly Lys Gln Cys  Cys Lys Thr
    1205                1210                1215

Cys Ser  Lys Ser Asn Leu
    1220
```

<210> 2284
<211> 570
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 563; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS16; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 16; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000421631"

<400> 2284

```
Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
1               5                  10                  15

Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
            20                  25                  30

Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro Pro
        35                  40                  45

Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
    50                  55                  60

Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
65                  70                  75                  80

His His Gln Arg Arg Arg Arg Ala Val Pro Val Ser Glu Val Glu Ser
                85                  90                  95

Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Met Asp Leu
            100                 105                 110

Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
        115                 120                 125

Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
```

```
    130                 135                 140

Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
145                 150                 155                 160

Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
                165                 170                 175

Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
            180                 185                 190

Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
        195                 200                 205

Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
    210                 215                 220

Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
225                 230                 235                 240

Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
                245                 250                 255

Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
            260                 265                 270

Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
        275                 280                 285

Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
    290                 295                 300

Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
305                 310                 315                 320

Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
                325                 330                 335

Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
            340                 345                 350

Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
        355                 360                 365
```

```
Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
    370                 375                 380

Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
385                 390                 395                 400

Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
                405                 410                 415

Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
            420                 425                 430

His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn
        435                 440                 445

Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly
    450                 455                 460

Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His
465                 470                 475                 480

Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys
                485                 490                 495

Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr
            500                 505                 510

Asp Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu
        515                 520                 525

Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His
    530                 535                 540

Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly
545                 550                 555                 560

Thr Ile Cys Gly His Asp Met Val Arg Ser
                565                 570
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<210> 2285
<211> 1095
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 564; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS17; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 17; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TE56; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000268070"

<400> 2285

Met	Cys	Asp	Gly	Ala	Leu	Leu	Pro	Pro	Leu	Val	Leu	Pro	Val	Leu	Leu
1				5				10					15		
Leu	Leu	Val	Trp	Gly	Leu	Asp	Pro	Gly	Thr	Ala	Val	Gly	Asp	Ala	Ala
		20					25					30			
Ala	Asp	Val	Glu	Val	Val	Leu	Pro	Trp	Arg	Val	Arg	Pro	Asp	Asp	Val
	35					40					45				
His	Leu	Pro	Pro	Leu	Pro	Ala	Ala	Pro	Gly	Pro	Arg	Arg	Arg	Arg	Arg
50					55					60					
Pro	Arg	Thr	Pro	Pro	Ala	Ala	Pro	Arg	Ala	Arg	Pro	Gly	Glu	Arg	Ala
65				70					75					80	
Leu	Leu	Leu	His	Leu	Pro	Ala	Phe	Gly	Arg	Asp	Leu	Tyr	Leu	Gln	Leu
				85					90					95	
Arg	Arg	Asp	Leu	Arg	Phe	Leu	Ser	Arg	Gly	Phe	Glu	Val	Glu	Glu	Ala
		100					105					110			
Gly	Ala	Ala	Arg	Arg	Arg	Gly	Arg	Pro	Ala	Glu	Leu	Cys	Phe	Tyr	Ser
	115					120					125				

```
Gly Arg Val Leu Gly His Pro Gly Ser Leu Val Ser Leu Ser Ala Cys
    130                 135                 140

Gly Ala Ala Gly Gly Leu Val Gly Leu Ile Gln Leu Gly Gln Glu Gln
145                 150                 155                 160

Val Leu Ile Gln Pro Leu Asn Asn Ser Gln Gly Pro Phe Ser Gly Arg
                165                 170                 175

Glu His Leu Ile Arg Arg Lys Trp Ser Leu Thr Pro Ser Pro Ser Ala
            180                 185                 190

Glu Ala Gln Arg Pro Glu Gln Leu Cys Lys Val Leu Thr Glu Lys Lys
        195                 200                 205

Lys Pro Thr Trp Gly Arg Pro Ser Arg Asp Trp Arg Glu Arg Arg Asn
    210                 215                 220

Ala Ile Arg Leu Thr Ser Glu His Thr Val Glu Thr Leu Val Val Ala
225                 230                 235                 240

Asp Ala Asp Met Val Gln Tyr His Gly Ala Glu Ala Ala Gln Arg Phe
                245                 250                 255

Ile Leu Thr Val Met Asn Met Val Tyr Asn Met Phe Gln His Gln Ser
            260                 265                 270

Leu Gly Ile Lys Ile Asn Ile Gln Val Thr Lys Leu Val Leu Leu Arg
        275                 280                 285

Gln Arg Pro Ala Lys Leu Ser Ile Gly His His Gly Glu Arg Ser Leu
    290                 295                 300

Glu Ser Phe Cys His Trp Gln Asn Glu Glu Tyr Gly Gly Ala Arg Tyr
305                 310                 315                 320

Leu Gly Asn Asn Gln Val Pro Gly Gly Lys Asp Asp Pro Pro Leu Val
                325                 330                 335

Asp Ala Ala Val Phe Val Thr Arg Thr Asp Phe Cys Val His Lys Asp
            340                 345                 350

Glu Pro Cys Asp Thr Val Gly Ile Ala Tyr Leu Gly Gly Val Cys Ser
```

```
        355                 360                 365

Ala Lys Arg Lys Cys Val Leu Ala Glu Asp Asn Gly Leu Asn Leu Ala
    370                 375                 380

Phe Thr Ile Ala His Glu Leu Gly His Asn Leu Gly Met Asn His Asp
385                 390                 395                 400

Asp Asp His Ser Ser Cys Ala Gly Arg Ser His Ile Met Ser Gly Glu
                405                 410                 415

Trp Val Lys Gly Arg Asn Pro Ser Asp Leu Ser Trp Ser Ser Cys Ser
            420                 425                 430

Arg Asp Asp Leu Glu Asn Phe Leu Lys Ser Lys Val Ser Thr Cys Leu
        435                 440                 445

Leu Val Thr Asp Pro Arg Ser Gln His Thr Val Arg Leu Pro His Lys
    450                 455                 460

Leu Pro Gly Met His Tyr Ser Ala Asn Glu Gln Cys Gln Ile Leu Phe
465                 470                 475                 480

Gly Met Asn Ala Thr Phe Cys Arg Asn Met Glu His Leu Met Cys Ala
                485                 490                 495

Gly Leu Trp Cys Leu Val Glu Gly Asp Thr Ser Cys Lys Thr Lys Leu
            500                 505                 510

Asp Pro Pro Leu Asp Gly Thr Glu Cys Gly Ala Asp Lys Trp Cys Arg
        515                 520                 525

Ala Gly Glu Cys Val Ser Lys Thr Pro Ile Pro Glu His Val Asp Gly
    530                 535                 540

Asp Trp Ser Pro Trp Gly Ala Trp Ser Met Cys Ser Arg Thr Cys Gly
545                 550                 555                 560

Thr Gly Ala Arg Phe Arg Gln Arg Lys Cys Asp Asn Pro Pro Pro Gly
                565                 570                 575

Pro Gly Gly Thr His Cys Pro Gly Ala Ser Val Glu His Ala Val Cys
            580                 585                 590
```

```
Glu Asn Leu Pro Cys Pro Lys Gly Leu Pro Ser Phe Arg Asp Gln Gln
        595                 600                 605

Cys Gln Ala His Asp Arg Leu Ser Pro Lys Lys Lys Gly Leu Leu Thr
    610                 615                 620

Ala Val Val Val Asp Asp Lys Pro Cys Glu Leu Tyr Cys Ser Pro Leu
625                 630                 635                 640

Gly Lys Glu Ser Pro Leu Leu Val Ala Asp Arg Val Leu Asp Gly Thr
                645                 650                 655

Pro Cys Gly Pro Tyr Glu Thr Asp Leu Cys Val His Gly Lys Cys Gln
            660                 665                 670

Lys Ile Gly Cys Asp Gly Ile Ile Gly Ser Ala Ala Lys Glu Asp Arg
        675                 680                 685

Cys Gly Val Cys Ser Gly Asp Gly Lys Thr Cys His Leu Val Lys Gly
    690                 695                 700

Asp Phe Ser His Ala Arg Gly Thr Ala Leu Lys Asp Ser Gly Lys Gly
705                 710                 715                 720

Ser Ile Asn Ser Asp Trp Lys Ile Glu Leu Pro Gly Glu Phe Gln Ile
                725                 730                 735

Ala Gly Thr Thr Val Arg Tyr Val Arg Arg Gly Leu Trp Glu Lys Ile
            740                 745                 750

Ser Ala Lys Gly Pro Thr Lys Leu Pro Leu His Leu Met Val Leu Leu
        755                 760                 765

Phe His Asp Gln Asp Tyr Gly Ile His Tyr Glu Tyr Thr Val Pro Val
    770                 775                 780

Asn Arg Thr Ala Glu Asn Gln Ser Glu Pro Glu Lys Pro Gln Asp Ser
785                 790                 795                 800

Leu Phe Ile Trp Thr His Ser Gly Trp Glu Gly Cys Ser Val Gln Cys
                805                 810                 815
```

```
Gly Gly Gly Glu Arg Arg Thr Ile Val Ser Cys Thr Arg Ile Val Asn
            820                 825                 830

Lys Thr Thr Thr Leu Val Asn Asp Ser Asp Cys Pro Gln Ala Ser Arg
        835                 840                 845

Pro Glu Pro Gln Val Arg Arg Cys Asn Leu His Pro Cys Gln Ser Arg
    850                 855                 860

Trp Val Ala Gly Pro Trp Ser Pro Cys Ser Ala Thr Cys Glu Lys Gly
865                 870                 875                 880

Phe Gln His Arg Glu Val Thr Cys Val Tyr Gln Leu Gln Asn Gly Thr
                885                 890                 895

His Val Ala Thr Arg Pro Leu Tyr Cys Pro Gly Pro Arg Pro Ala Ala
            900                 905                 910

Val Gln Ser Cys Glu Gly Gln Asp Cys Leu Ser Ile Trp Glu Ala Ser
        915                 920                 925

Glu Trp Ser Gln Cys Ser Ala Ser Cys Gly Lys Gly Val Trp Lys Arg
    930                 935                 940

Thr Val Ala Cys Thr Asn Ser Gln Gly Lys Cys Asp Ala Ser Thr Arg
945                 950                 955                 960

Pro Arg Ala Glu Glu Ala Cys Glu Asp Tyr Ser Gly Cys Tyr Glu Trp
                965                 970                 975

Lys Thr Gly Asp Trp Ser Thr Cys Ser Ser Thr Cys Gly Lys Gly Leu
            980                 985                 990

Gln Ser Arg Val Val Gln Cys Met  His Lys Val Thr Gly  Arg His
Gly
        995                 1000                1005

Ser Glu  Cys Pro Ala Leu Ser  Lys Pro Ala Pro Tyr  Arg Gln Cys
    1010                1015                1020

Tyr Gln  Glu Val Cys Asn Asp  Arg Ile Asn Ala Asn  Thr Ile Thr
    1025                1030                1035
```

```
Ser Pro  Arg Leu Ala Ala Leu  Thr Tyr Lys Cys Thr  Arg Asp Gln
    1040                1045                1050

Trp Thr  Val Tyr Cys Arg Val  Ile Arg Glu Lys Asn  Leu Cys Gln
    1055                1060                1065

Asp Met  Arg Trp Tyr Gln Arg  Cys Cys Gln Thr Cys  Arg Asp Phe
    1070                1075                1080

Tyr Ala  Asn Lys Met Arg Gln  Pro Pro Pro Asn Ser
    1085                1090                1095


<210> 2286
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 564; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS17; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 17; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000453604"

<400> 2286
Met Cys Asp Gly Ala Leu Leu Pro Pro Leu Val Leu Pro Val Leu Leu
1               5                  10                  15

Leu Leu Val Trp Gly Leu Asp Pro Gly Thr Gly Trp Pro His Ser Ala
            20                  25                  30

Trp Ala Gly Ala Gly Ala Asn Pro Ala Pro Gln Gln Leu Pro Gly Pro
        35                  40                  45

Ile Gln Trp Thr Arg Thr Ser Asp Gln Ala Gln Met Val Leu Asp Pro
    50                  55                  60
```

Gln Pro Phe Cys
65

<210> 2287
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 564; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS17; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 17; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456161"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2287
Xaa Glu Leu Tyr Cys Ser Pro Leu Gly Lys Glu Ser Pro Leu Leu Val
1 5 10 15

Ala Asp Arg Val Leu Asp Gly Thr Pro Cys Gly Pro Tyr Glu Thr Asp
20 25 30

Leu Cys Val His Gly Lys Cys Gln Lys Ile Gly Cys Asp Gly Ile Ile
35 40 45

Gly Ser Ala Ala Lys Glu Asp Arg Cys Gly Val Cys Ser Gly Asp Gly
50 55 60

Lys Thr Cys His Leu Val Lys Gly Asp Phe Ser His Ala Arg Gly Thr
65 70 75 80

Gly Tyr Ile Glu Ala Ala Val Ile Pro Ala Gly Ala Arg Arg Ile Arg
85 90 95

```
Val Val Glu Asp Lys Pro Ala His Ser Phe Leu Ala Leu Lys Asp Ser
            100                 105                 110

Gly Lys Gly Ser Ile Asn Ser Asp Trp Lys Ile Glu Leu Pro Gly Glu
        115                 120                 125

Phe Gln Ile Ala Gly Thr Thr Val Arg Tyr Val Arg Arg Gly Leu Trp
    130                 135                 140

Glu Lys Ile Ser Ala Lys Gly Pro Thr Lys Leu Pro Leu His Leu Met
145                 150                 155                 160

Val Leu Leu Phe His Asp Gln Asp Tyr Gly Ile His Tyr Glu Tyr Thr
                165                 170                 175

Val Pro Val Asn Arg Thr Ala Glu Asn Gln Ser Glu Pro Glu Lys Pro
            180                 185                 190

Gln Asp Ser Leu Phe Ile Trp Thr His Ser Gly Trp Glu Gly Cys Ser
        195                 200                 205

Val Gln Cys Gly Gly Gly
    210
```

<210> 2288
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 564; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS17; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 17; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000458005"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2288
Xaa Gly Arg Pro Ala Glu Leu Cys Phe Tyr Ser Gly Arg Val Leu Gly
1   5   10   15

His Pro Gly Ser Leu Val Ser Leu Ser Ala Cys Gly Ala Ala Gly Gly
            20   25   30

Leu Val Gly Leu Ile Gln Leu Gly Gln Glu Gln Val Leu Ile Gln Pro
        35   40   45

Leu Asn Asn Ser Gln Gly Pro Phe Ser Gly Arg Glu His Leu Ile Arg
    50   55   60

Arg Lys Trp Ser Leu Thr Pro Ser Pro Ser Ala Glu Ala Gln Arg Pro
65   70   75   80

Glu Gln Leu Cys Lys Val Leu Thr Val Pro Gln Cys Leu Gly Leu Thr
                85   90   95

Trp Glu Asp Leu Lys Ser Gly Gly Trp Ser Asp Leu Glu Val Pro His
            100   105   110

Ser Cys Val Trp Pro Gly Gly Gly
        115   120

<210> 2289
<211> 1221
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 565; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS18; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 18; "

<220>
<221> source
<223> /note="Uniprot ID: Q8TE60; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000282849"

<400> 2289
Met Glu Cys Ala Leu Leu Leu Ala Cys Ala Phe Pro Ala Ala Gly Ser
1   5   10   15

Gly Pro Pro Arg Gly Leu Ala Gly Leu Gly Arg Val Ala Lys Ala Leu
            20   25   30

Gln Leu Cys Cys Leu Cys Cys Ala Ser Val Ala Ala Ala Leu Ala Ser
        35   40   45

Asp Ser Ser Ser Gly Ala Ser Gly Leu Asn Asp Asp Tyr Val Phe Val
    50   55   60

Thr Pro Val Glu Val Asp Ser Ala Gly Ser Tyr Ile Ser His Asp Ile
65   70   75   80

Leu His Asn Gly Arg Lys Lys Arg Ser Ala Gln Asn Ala Arg Ser Ser
                85   90   95

Leu His Tyr Arg Phe Ser Ala Phe Gly Gln Glu Leu His Leu Glu Leu
            100   105   110

Lys Pro Ser Ala Ile Leu Ser Ser His Phe Ile Val Gln Val Leu Gly
        115   120   125

Lys Asp Gly Ala Ser Glu Thr Gln Lys Pro Glu Val Gln Gln Cys Phe
    130   135   140

Tyr Gln Gly Phe Ile Arg Asn Asp Ser Ser Ser Ser Val Ala Val Ser
145   150   155   160

Thr Cys Ala Gly Leu Ser Gly Leu Ile Arg Thr Arg Lys Asn Glu Phe
                165   170   175

Leu Ile Ser Pro Leu Pro Gln Leu Leu Ala Gln Glu His Asn Tyr Ser
            180   185   190

```
Ser Pro Ala Gly His His Pro His Val Leu Tyr Lys Arg Thr Ala Glu
        195                 200                 205

Glu Lys Ile Gln Arg Tyr Arg Gly Tyr Pro Gly Ser Gly Arg Asn Tyr
    210                 215                 220

Pro Gly Tyr Ser Pro Ser His Ile Pro His Ala Ser Gln Ser Arg Glu
225                 230                 235                 240

Thr Glu Tyr His His Arg Arg Leu Gln Lys Gln His Phe Cys Gly Arg
                245                 250                 255

Arg Lys Lys Tyr Ala Pro Lys Pro Pro Thr Glu Asp Thr Tyr Leu Arg
            260                 265                 270

Phe Asp Glu Tyr Gly Ser Ser Gly Arg Pro Arg Arg Ser Ala Gly Lys
        275                 280                 285

Ser Gln Lys Gly Leu Asn Val Glu Thr Leu Val Val Ala Asp Lys Lys
    290                 295                 300

Met Val Glu Lys His Gly Lys Gly Asn Val Thr Thr Tyr Ile Leu Thr
305                 310                 315                 320

Val Met Asn Met Val Ser Gly Leu Phe Lys Asp Gly Thr Ile Gly Ser
                325                 330                 335

Asp Ile Asn Val Val Val Val Ser Leu Ile Leu Leu Glu Gln Glu Pro
            340                 345                 350

Gly Gly Leu Leu Ile Asn His His Ala Asp Gln Ser Leu Asn Ser Phe
        355                 360                 365

Cys Gln Trp Gln Ser Ala Leu Ile Gly Lys Asn Gly Lys Arg His Asp
    370                 375                 380

His Ala Ile Leu Leu Thr Gly Phe Asp Ile Cys Ser Trp Lys Asn Glu
385                 390                 395                 400

Pro Cys Asp Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys
                405                 410                 415

Tyr Arg Ser Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe
```

```
            420                 425                 430

Thr Ile Ala His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly
        435                 440                 445

Glu Gly Asn Pro Cys Arg Lys Ala Glu Gly Asn Ile Met Ser Pro Thr
    450                 455                 460

Leu Thr Gly Asn Asn Gly Val Phe Ser Trp Ser Ser Cys Ser Arg Gln
465                 470                 475                 480

Tyr Leu Lys Lys Phe Leu Ser Thr Pro Gln Ala Gly Cys Leu Val Asp
                485                 490                 495

Glu Pro Lys Gln Ala Gly Gln Tyr Lys Tyr Pro Asp Lys Leu Pro Gly
            500                 505                 510

Gln Ile Tyr Asp Ala Asp Thr Gln Cys Lys Trp Gln Phe Gly Ala Lys
        515                 520                 525

Ala Lys Leu Cys Ser Leu Gly Phe Val Lys Asp Ile Cys Lys Ser Leu
    530                 535                 540

Trp Cys His Arg Val Gly His Arg Cys Glu Thr Lys Phe Met Pro Ala
545                 550                 555                 560

Ala Glu Gly Thr Val Cys Gly Leu Ser Met Trp Cys Arg Gln Gly Gln
                565                 570                 575

Cys Val Lys Phe Gly Glu Leu Gly Pro Arg Pro Ile His Gly Gln Trp
            580                 585                 590

Ser Ala Trp Ser Lys Trp Ser Glu Cys Ser Arg Thr Cys Gly Gly Gly
        595                 600                 605

Val Lys Phe Gln Glu Arg His Cys Asn Asn Pro Lys Pro Gln Tyr Gly
    610                 615                 620

Gly Leu Phe Cys Pro Gly Ser Ser Arg Ile Tyr Gln Leu Cys Asn Ile
625                 630                 635                 640

Asn Pro Cys Asn Glu Asn Ser Leu Asp Phe Arg Ala Gln Gln Cys Ala
                645                 650                 655
```

```
Glu Tyr Asn Ser Lys Pro Phe Arg Gly Trp Phe Tyr Gln Trp Lys Pro
            660                 665                 670

Tyr Thr Lys Val Glu Glu Glu Asp Arg Cys Lys Leu Tyr Cys Lys Ala
        675                 680                 685

Glu Asn Phe Glu Phe Phe Phe Ala Met Ser Gly Lys Val Lys Asp Gly
    690                 695                 700

Thr Pro Cys Ser Pro Asn Lys Asn Asp Val Cys Ile Asp Gly Val Cys
705                 710                 715                 720

Glu Leu Val Gly Cys Asp His Glu Leu Gly Ser Lys Ala Val Ser Asp
                725                 730                 735

Ala Cys Gly Val Cys Lys Gly Asp Asn Ser Thr Cys Lys Phe Tyr Lys
            740                 745                 750

Gly Leu Tyr Leu Asn Gln His Lys Ala Asn Glu Tyr Tyr Pro Val Val
        755                 760                 765

Leu Ile Pro Ala Gly Ala Arg Ser Ile Glu Ile Gln Glu Leu Gln Val
    770                 775                 780

Ser Ser Ser Tyr Leu Ala Val Arg Ser Leu Ser Gln Lys Tyr Tyr Leu
785                 790                 795                 800

Thr Gly Gly Trp Ser Ile Asp Trp Pro Gly Glu Phe Pro Phe Ala Gly
                805                 810                 815

Thr Thr Phe Glu Tyr Gln Arg Ser Phe Asn Arg Pro Glu Arg Leu Tyr
            820                 825                 830

Ala Pro Gly Pro Thr Asn Glu Thr Leu Val Phe Glu Ile Leu Met Gln
        835                 840                 845

Gly Lys Asn Pro Gly Ile Ala Trp Lys Tyr Ala Leu Pro Lys Val Met
    850                 855                 860

Asn Gly Thr Pro Pro Ala Thr Lys Arg Pro Ala Tyr Thr Trp Ser Ile
865                 870                 875                 880
```

```
Val Gln Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Tyr Ile Asn Val
                885                 890                 895

Lys Ala Ile Cys Leu Arg Asp Gln Asn Thr Gln Val Asn Ser Ser Phe
            900                 905                 910

Cys Ser Ala Lys Thr Lys Pro Val Thr Glu Pro Lys Ile Cys Asn Ala
        915                 920                 925

Phe Ser Cys Pro Ala Tyr Trp Met Pro Gly Glu Trp Ser Thr Cys Ser
    930                 935                 940

Lys Ala Cys Ala Gly Gly Gln Gln Ser Arg Lys Ile Gln Cys Val Gln
945                 950                 955                 960

Lys Lys Pro Phe Gln Lys Glu Glu Ala Val Leu His Ser Leu Cys Pro
                965                 970                 975

Val Ser Thr Pro Thr Gln Val Gln Ala Cys Asn Ser His Ala Cys Pro
            980                 985                 990

Pro Gln Trp Ser Leu Gly Pro Trp  Ser Gln Cys Ser Lys  Thr Cys
Gly
        995                 1000                1005

Arg Gly  Val Arg Lys Arg Glu  Leu Leu Cys Lys Gly  Ser Ala Ala
    1010                1015                1020

Glu Thr  Leu Pro Glu Ser Gln  Cys Thr Ser Leu Pro  Arg Pro Glu
    1025                1030                1035

Leu Gln  Glu Gly Cys Val Leu  Gly Arg Cys Pro Lys  Asn Ser Arg
    1040                1045                1050

Leu Gln  Trp Val Ala Ser Ser  Trp Ser Glu Cys Ser  Ala Thr Cys
    1055                1060                1065

Gly Leu  Gly Val Arg Lys Arg  Glu Met Lys Cys Ser  Glu Lys Gly
    1070                1075                1080

Phe Gln  Gly Lys Leu Ile Thr  Phe Pro Glu Arg Arg  Cys Arg Asn
    1085                1090                1095
```

```
Ile Lys  Lys Pro Asn Leu Asp  Leu Glu Glu Thr Cys  Asn Arg Arg
    1100                1105                1110

Ala Cys  Pro Ala His Pro Val  Tyr Asn Met Val Ala  Gly Trp Tyr
    1115                1120                1125

Ser Leu  Pro Trp Gln Gln Cys  Thr Val Thr Cys Gly  Gly Gly Val
    1130                1135                1140

Gln Thr  Arg Ser Val His Cys  Val Gln Gln Gly Arg  Pro Ser Ser
    1145                1150                1155

Ser Cys  Leu Leu His Gln Lys  Pro Pro Val Leu Arg  Ala Cys Asn
    1160                1165                1170

Thr Asn  Phe Cys Pro Ala Pro  Glu Lys Arg Glu Asp  Pro Ser Cys
    1175                1180                1185

Val Asp  Phe Phe Asn Trp Cys  His Leu Val Pro Gln  His Gly Val
    1190                1195                1200

Cys Asn  His Lys Phe Tyr Gly  Lys Gln Cys Cys Lys  Ser Cys Thr
    1205                1210                1215

Arg Lys  Ile
    1220


<210> 2290
<211> 274
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 565; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS18; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 18; "

<220>
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<221> source
<223> /note="ENSP ID: ENSP00000392540"

<400> 2290
Met Glu Cys Ala Leu Leu Leu Ala Cys Ala Phe Pro Ala Ala Gly Ser
1   5   10   15

Gly Pro Pro Arg Gly Leu Ala Gly Leu Gly Arg Val Ala Lys Ala Leu
            20   25   30

Gln Leu Cys Cys Leu Cys Cys Ala Ser Val Ala Ala Ala Leu Ala Ser
        35   40   45

Asp Ser Ser Ser Gly Ala Ser Gly Leu Asn Asp Asp Tyr Val Phe Val
    50   55   60

Thr Pro Val Glu Val Asp Ser Ala Gly Ser Tyr Ile Ser His Asp Ile
65   70   75   80

Leu His Asn Gly Arg Lys Lys Arg Ser Ala Gln Asn Ala Arg Ser Ser
                85   90   95

Leu His Tyr Arg Phe Ser Ala Phe Gly Gln Glu Leu His Leu Glu Leu
            100   105   110

Lys Pro Ser Ala Ile Leu Ser Ser His Phe Ile Val Gln Val Leu Gly
        115   120   125

Lys Asp Gly Ala Ser Glu Thr Gln Lys Pro Glu Val Gln Gln Cys Phe
    130   135   140

Tyr Gln Gly Phe Ile Arg Asn Asp Ser Ser Ser Ser Val Ala Val Ser
145   150   155   160

Thr Cys Ala Gly Leu Ser Gly Leu Ile Arg Thr Arg Lys Asn Glu Phe
                165   170   175

Leu Ile Ser Pro Leu Pro Gln Leu Leu Ala Gln Glu His Asn Tyr Ser
            180   185   190

Ser Pro Ala Gly His His Pro His Val Leu Tyr Lys Arg Thr Ala Glu
        195   200   205

Glu Lys Ile Gln Arg Tyr Arg Gly Tyr Pro Gly Ser Gly Arg Asn Tyr

```
    210                 215                 220

Pro Gly Tyr Ser Pro Ser His Ile Pro His Ala Ser Gln Ser Arg Glu
225                 230                 235                 240

Thr Glu Tyr His His Arg Arg Leu Gln Lys Gln His Phe Cys Gly Arg
                245                 250                 255

Arg Lys Lys Cys Ile Cys Ser Gln Ala Ser His Arg Gly His Leu Ser
            260                 265                 270

Lys Val
```

<210> 2291
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 565; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS18; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454368"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2291

```
Xaa Gln Gly Arg Pro Ser Ser Ser Cys Leu Leu His Gln Lys Pro Pro
1               5                   10                  15

Val Leu Arg Ala Cys Asn Thr Asn Phe Cys Pro Ala Pro Glu Lys Arg
            20                  25                  30
```

```
Asp Ser Ala Gly Ser Gln Leu Pro Cys Cys Asp Gly Pro Gln Ala Val
        35                  40                  45


His Glu Glu Gly Leu Arg Phe Pro Asp Asn His Trp Ala Met
    50                  55                  60


<210> 2292
<211> 185
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 565; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS18; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 18; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457395"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2292
Xaa Val Asp Ser Ala Gly Ser Tyr Ile Ser His Asp Ile Leu His Asn
1               5                   10                  15


Gly Arg Lys Lys Arg Ser Ala Gln Asn Ala Arg Ser Ser Leu His Tyr
            20                  25                  30


Arg Phe Ser Ala Phe Gly Gln Glu Leu His Leu Glu Leu Lys Pro Ser
        35                  40                  45


Ala Ile Leu Ser Ser His Phe Ile Val Gln Val Leu Gly Lys Asp Gly
    50                  55                  60


Ala Ser Glu Thr Gln Lys Pro Glu Val Gln Gln Cys Phe Tyr Gln Gly
65                  70                  75                  80
```

```
Phe Ile Arg Asn Asp Ser Ser Ser Ser Val Ala Val Ser Thr Cys Ala
                85                  90                  95

Gly Leu Leu Leu Ala Gln Glu His Asn Tyr Ser Ser Pro Ala Gly His
            100                 105                 110

His Pro His Val Leu Tyr Lys Arg Thr Ala Glu Glu Lys Ile Gln Arg
        115                 120                 125

Tyr Arg Gly Tyr Pro Gly Ser Gly Arg Asn Tyr Pro Gly Tyr Ser Pro
    130                 135                 140

Ser His Ile Pro His Ala Ser Gln Ser Arg Glu Thr Glu Tyr His His
145                 150                 155                 160

Arg Arg Leu Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Cys Ile
                165                 170                 175

Cys Ser Gln Ala Ser His Arg Gly His
            180                 185


<210> 2293
<211> 1207
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 566; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS19; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 19; "

<220>
<221> source
<223> /note="Uniprot ID:  Q8TE59; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000274487"

<400> 2293
```

```
Met Arg Leu Thr His Ile Cys Cys Cys Cys Leu Leu Tyr Gln Leu Gly
1               5                  10                  15

Phe Leu Ser Asn Gly Ile Val Ser Glu Leu Gln Phe Ala Pro Asp Arg
            20                  25                  30

Glu Glu Trp Glu Val Val Phe Pro Ala Leu Trp Arg Arg Glu Pro Val
        35                  40                  45

Asp Pro Ala Gly Gly Ser Gly Gly Ser Ala Asp Pro Gly Trp Val Arg
    50                  55                  60

Gly Val Gly Gly Gly Gly Ser Ala Arg Ala Gln Ala Ala Gly Ser Ser
65                  70                  75                  80

Arg Glu Val Arg Ser Val Ala Pro Val Pro Leu Glu Glu Pro Val Glu
                85                  90                  95

Gly Arg Ser Glu Ser Arg Leu Arg Pro Pro Pro Pro Ser Glu Gly Glu
            100                 105                 110

Glu Asp Glu Glu Leu Glu Ser Gln Glu Leu Pro Arg Gly Ser Ser Gly
        115                 120                 125

Ala Ala Ala Leu Ser Pro Gly Ala Pro Ala Ser Trp Gln Pro Pro Pro
    130                 135                 140

Pro Pro Gln Pro Pro Pro Ser Pro Pro Pro Ala Gln His Ala Glu Pro
145                 150                 155                 160

Asp Gly Asp Glu Val Leu Leu Arg Ile Pro Ala Phe Ser Arg Asp Leu
                165                 170                 175

Tyr Leu Leu Leu Arg Arg Asp Gly Arg Phe Leu Ala Pro Arg Phe Ala
            180                 185                 190

Val Glu Gln Arg Pro Asn Pro Gly Pro Gly Pro Thr Gly Ala Ala Ser
        195                 200                 205

Ala Pro Gln Pro Pro Ala Pro Pro Asp Ala Gly Cys Phe Tyr Thr Gly
    210                 215                 220

Ala Val Leu Arg His Pro Gly Ser Leu Ala Ser Phe Ser Thr Cys Gly
```

225 230 235 240

Gly Gly Leu Met Gly Phe Ile Gln Leu Asn Glu Asp Phe Ile Phe Ile
245 250 255

Glu Pro Leu Asn Asp Thr Met Ala Ile Thr Gly His Pro His Arg Val
260 265 270

Tyr Arg Gln Lys Arg Ser Met Glu Glu Lys Val Thr Glu Lys Ser Ala
275 280 285

Leu His Ser His Tyr Cys Gly Ile Ile Ser Asp Lys Gly Arg Pro Arg
290 295 300

Ser Arg Lys Ile Ala Glu Ser Gly Arg Gly Lys Arg Tyr Ser Tyr Lys
305 310 315 320

Leu Pro Gln Glu Tyr Asn Ile Glu Thr Val Val Val Ala Asp Pro Ala
325 330 335

Met Val Ser Tyr His Gly Ala Asp Ala Ala Arg Arg Phe Ile Leu Thr
340 345 350

Ile Leu Asn Met Val Phe Asn Leu Phe Gln His Lys Ser Leu Ser Val
355 360 365

Gln Val Asn Leu Arg Val Ile Lys Leu Ile Leu Leu His Glu Thr Pro
370 375 380

Pro Glu Leu Tyr Ile Gly His His Gly Glu Lys Met Leu Glu Ser Phe
385 390 395 400

Cys Lys Trp Gln His Glu Glu Phe Gly Lys Lys Asn Asp Ile His Leu
405 410 415

Glu Met Ser Thr Asn Trp Gly Glu Asp Met Thr Ser Val Asp Ala Ala
420 425 430

Ile Leu Ile Thr Arg Lys Asp Phe Cys Val His Lys Asp Glu Pro Cys
435 440 445

Asp Thr Val Gly Ile Ala Tyr Leu Ser Gly Met Cys Ser Glu Lys Arg
450 455 460

```
Lys Cys Ile Ile Ala Glu Asp Asn Gly Leu Asn Leu Ala Phe Thr Ile
465                 470                 475                 480

Ala His Glu Met Gly His Asn Met Gly Ile Asn His Asp Asn Asp His
                485                 490                 495

Pro Ser Cys Ala Asp Gly Leu His Ile Met Ser Gly Glu Trp Ile Lys
            500                 505                 510

Gly Gln Asn Leu Gly Asp Val Ser Trp Ser Arg Cys Ser Lys Glu Asp
        515                 520                 525

Leu Glu Arg Phe Leu Arg Ser Lys Ala Ser Asn Cys Leu Leu Gln Thr
    530                 535                 540

Asn Pro Gln Ser Val Asn Ser Val Met Val Pro Ser Lys Leu Pro Gly
545                 550                 555                 560

Met Thr Tyr Thr Ala Asp Glu Gln Cys Gln Ile Leu Phe Gly Pro Leu
                565                 570                 575

Ala Ser Phe Cys Gln Glu Met Gln His Val Ile Cys Thr Gly Leu Trp
            580                 585                 590

Cys Lys Val Glu Gly Glu Lys Glu Cys Arg Thr Lys Leu Asp Pro Pro
        595                 600                 605

Met Asp Gly Thr Asp Cys Asp Leu Gly Lys Trp Cys Lys Ala Gly Glu
    610                 615                 620

Cys Thr Ser Arg Thr Ser Ala Pro Glu His Leu Ala Gly Glu Trp Ser
625                 630                 635                 640

Leu Trp Ser Pro Cys Ser Arg Thr Cys Ser Ala Gly Ile Ser Ser Arg
                645                 650                 655

Glu Arg Lys Cys Pro Gly Leu Asp Ser Glu Ala Arg Asp Cys Asn Gly
            660                 665                 670

Pro Arg Lys Gln Tyr Arg Ile Cys Glu Asn Pro Pro Cys Pro Ala Gly
        675                 680                 685
```

```
Leu Pro Gly Phe Arg Asp Trp Gln Cys Gln Ala Tyr Ser Val Arg Thr
    690                 695                 700

Ser Ser Pro Lys His Ile Leu Gln Trp Gln Ala Val Leu Asp Glu Glu
705                 710                 715                 720

Lys Pro Cys Ala Leu Phe Cys Ser Pro Val Gly Lys Glu Gln Pro Ile
                725                 730                 735

Leu Leu Ser Glu Lys Val Met Asp Gly Thr Ser Cys Gly Tyr Gln Gly
            740                 745                 750

Leu Asp Ile Cys Ala Asn Gly Arg Cys Gln Lys Val Gly Cys Asp Gly
        755                 760                 765

Leu Leu Gly Ser Leu Ala Arg Glu Asp His Cys Gly Val Cys Asn Gly
    770                 775                 780

Asn Gly Lys Ser Cys Lys Ile Ile Lys Gly Asp Phe Asn His Thr Arg
785                 790                 795                 800

Gly Ala Gly Tyr Val Glu Val Leu Val Ile Pro Ala Gly Ala Arg Arg
                805                 810                 815

Ile Lys Val Val Glu Glu Lys Pro Ala His Ser Tyr Leu Ala Leu Arg
            820                 825                 830

Asp Ala Gly Lys Gln Ser Ile Asn Ser Asp Trp Lys Ile Glu His Ser
        835                 840                 845

Gly Ala Phe Asn Leu Ala Gly Thr Thr Val His Tyr Val Arg Arg Gly
    850                 855                 860

Leu Trp Glu Lys Ile Ser Ala Lys Gly Pro Thr Thr Ala Pro Leu His
865                 870                 875                 880

Leu Leu Val Leu Leu Phe Gln Asp Gln Asn Tyr Gly Leu His Tyr Glu
                885                 890                 895

Tyr Thr Ile Pro Ser Asp Pro Leu Pro Glu Asn Gln Ser Ser Lys Ala
            900                 905                 910
```

```
Pro Glu Pro Leu Phe Met Trp Thr His Thr Ser Trp Glu Asp Cys Asp
        915                 920                 925

Ala Thr Cys Gly Gly Gly Glu Arg Lys Thr Thr Val Ser Cys Thr Lys
    930                 935                 940

Ile Met Ser Lys Asn Ile Ser Ile Val Asp Asn Glu Lys Cys Lys Tyr
945                 950                 955                 960

Leu Thr Lys Pro Glu Pro Gln Ile Arg Lys Cys Asn Glu Gln Pro Cys
                965                 970                 975

Gln Thr Arg Trp Met Met Thr Glu Trp Thr Pro Cys Ser Arg Thr Cys
            980                 985                 990

Gly Lys Gly Met Gln Ser Arg Gln  Val Ala Cys Thr Gln  Gln Leu
Ser
        995                 1000                1005

Asn Gly  Thr Leu Ile Arg Ala  Arg Glu Arg Asp Cys  Ile Gly Pro
    1010                1015                1020

Lys Pro  Ala Ser Ala Gln Arg  Cys Glu Gly Gln Asp  Cys Met Thr
    1025                1030                1035

Val Trp  Glu Ala Gly Val Trp  Ser Glu Cys Ser Val  Lys Cys Gly
    1040                1045                1050

Lys Gly  Ile Arg His Arg Thr  Val Arg Cys Thr Asn  Pro Arg Lys
    1055                1060                1065

Lys Cys  Val Leu Ser Thr Arg  Pro Arg Glu Ala Glu  Asp Cys Glu
    1070                1075                1080

Asp Tyr  Ser Lys Cys Tyr Val  Trp Arg Met Gly Asp  Trp Ser Lys
    1085                1090                1095

Cys Ser  Ile Thr Cys Gly Lys  Gly Met Gln Ser Arg  Val Ile Gln
    1100                1105                1110

Cys Met  His Lys Ile Thr Gly  Arg His Gly Asn Glu  Cys Phe Ser
    1115                1120                1125
```

```
Ser Glu  Lys Pro Ala Ala Tyr  Arg Pro Cys His Leu  Gln Pro Cys
    1130                1135                1140


Asn Glu  Lys Ile Asn Val Asn  Thr Ile Thr Ser Pro  Arg Leu Ala
    1145                1150                1155


Ala Leu  Thr Phe Lys Cys Leu  Gly Asp Gln Trp Pro  Val Tyr Cys
    1160                1165                1170


Arg Val  Ile Arg Glu Lys Asn  Leu Cys Gln Asp Met  Arg Trp Tyr
    1175                1180                1185


Gln Arg  Cys Cys Glu Thr Cys  Arg Asp Phe Tyr Ala  Gln Lys Leu
    1190                1195                1200


Gln Gln  Lys Ser
    1205


<210> 2294
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 566; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS19; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 19; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000422491"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2294
Xaa Asp Ala Gly Cys Phe Tyr Thr Gly Ala Val Leu Arg His Pro Gly
1               5                   10                  15
```

```
Ser Leu Ala Ser Phe Ser Thr Cys Gly Gly Gly Leu Met Gly Phe Ile
            20                  25                  30

Gln Leu Asn Glu Asp Phe Ile Phe Ile Glu Pro Leu Asn Asp Thr Met
        35                  40                  45

Ala Ile Thr Gly His Pro His Arg Val Tyr Arg Gln Lys Arg Ser Met
    50                  55                  60

Glu Glu Lys Val Thr Glu Lys Ser Ala Leu His Ser His Tyr Cys Gly
65                  70                  75                  80

Ile Ile Ser Asp Lys Gly Arg Pro Arg Ser Arg Lys Ile Ala Glu Ser
                85                  90                  95

Gly Arg Gly Lys Arg Tyr Ser Tyr Lys Leu Pro Gln Glu Tyr Asn Ile
            100                 105                 110

Glu Thr Val Val Val Ala Asp Pro Ala Met Val Ser Tyr His Gly Ala
        115                 120                 125

Asp Ala Ala Arg Arg Phe Ile Leu Thr Ile Leu Asn Met Val Gly Lys
    130                 135                 140

Leu
145
```

<210> 2295
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 566; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS19; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 19; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000423537"

<400> 2295
Met Arg Leu Thr His Ile Cys Cys Cys Cys Leu Leu Tyr Gln Leu Gly
1 5 10 15

Phe Leu Ser Asn Gly Ile Val Ser Asp Gly Ile Tyr Thr Ala Gln
            20 25 30

<210> 2296
<211> 1211
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 567; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS2; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 2; "

<220>
<221> source
<223> /note="Uniprot ID: O95450; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000251582"

<400> 2296
Met Asp Pro Pro Ala Gly Ala Ala Arg Arg Leu Leu Cys Pro Ala Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Pro Pro Pro Pro
            20 25 30

Pro Pro Ala Asn Ala Arg Leu Ala Ala Ala Ala Asp Pro Pro Gly Gly
        35 40 45

Pro Leu Gly His Gly Ala Glu Arg Ile Leu Ala Val Pro Val Arg Thr
    50 55 60

Asp Ala Gln Gly Arg Leu Val Ser His Val Val Ser Ala Ala Thr Ser

65 70 75 80

Arg Ala Gly Val Arg Ala Arg Arg Ala Ala Pro Val Arg Thr Pro Ser
85 90 95

Phe Pro Gly Gly Asn Glu Glu Glu Pro Gly Ser His Leu Phe Tyr Asn
100 105 110

Val Thr Val Phe Gly Arg Asp Leu His Leu Arg Leu Arg Pro Asn Ala
115 120 125

Arg Leu Val Ala Pro Gly Ala Thr Met Glu Trp Gln Gly Glu Lys Gly
130 135 140

Thr Thr Arg Val Glu Pro Leu Leu Gly Ser Cys Leu Tyr Val Gly Asp
145 150 155 160

Val Ala Gly Leu Ala Glu Ala Ser Ser Val Ala Leu Ser Asn Cys Asp
165 170 175

Gly Leu Ala Gly Leu Ile Arg Met Glu Glu Glu Glu Phe Phe Ile Glu
180 185 190

Pro Leu Glu Lys Gly Leu Ala Ala Gln Glu Ala Glu Gln Gly Arg Val
195 200 205

His Val Val Tyr Arg Arg Pro Pro Thr Ser Pro Pro Leu Gly Gly Pro
210 215 220

Gln Ala Leu Asp Thr Gly Ala Ser Leu Asp Ser Leu Asp Ser Leu Ser
225 230 235 240

Arg Ala Leu Gly Val Leu Glu Glu His Ala Asn Ser Ser Arg Arg Arg
245 250 255

Ala Arg Arg His Ala Ala Asp Asp Asp Tyr Asn Ile Glu Val Leu Leu
260 265 270

Gly Val Asp Asp Ser Val Val Gln Phe His Gly Lys Glu His Val Gln
275 280 285

Lys Tyr Leu Leu Thr Leu Met Asn Ile Val Asn Glu Ile Tyr His Asp
290 295 300

```
Glu Ser Leu Gly Ala His Ile Asn Val Val Leu Val Arg Ile Ile Leu
305                 310                 315                 320

Leu Ser Tyr Gly Lys Ser Met Ser Leu Ile Glu Ile Gly Asn Pro Ser
                325                 330                 335

Gln Ser Leu Glu Asn Val Cys Arg Trp Ala Tyr Leu Gln Gln Lys Pro
            340                 345                 350

Asp Thr Gly His Asp Glu Tyr His Asp His Ala Ile Phe Leu Thr Arg
        355                 360                 365

Gln Asp Phe Gly Pro Ser Gly Met Gln Gly Tyr Ala Pro Val Thr Gly
    370                 375                 380

Met Cys His Pro Val Arg Ser Cys Thr Leu Asn His Glu Asp Gly Phe
385                 390                 395                 400

Ser Ser Ala Phe Val Val Ala His Glu Thr Gly His Val Leu Gly Met
                405                 410                 415

Glu His Asp Gly Gln Gly Asn Arg Cys Gly Asp Glu Val Arg Leu Gly
            420                 425                 430

Ser Ile Met Ala Pro Leu Val Gln Ala Ala Phe His Arg Phe His Trp
        435                 440                 445

Ser Arg Cys Ser Gln Gln Glu Leu Ser Arg Tyr Leu His Ser Tyr Asp
    450                 455                 460

Cys Leu Leu Asp Asp Pro Phe Ala His Asp Trp Pro Ala Leu Pro Gln
465                 470                 475                 480

Leu Pro Gly Leu His Tyr Ser Met Asn Glu Gln Cys Arg Phe Asp Phe
                485                 490                 495

Gly Leu Gly Tyr Met Met Cys Thr Ala Phe Arg Thr Phe Asp Pro Cys
            500                 505                 510

Lys Gln Leu Trp Cys Ser His Pro Asp Asn Pro Tyr Phe Cys Lys Thr
        515                 520                 525
```

Lys Lys Gly Pro Pro Leu Asp Gly Thr Met Cys Ala Pro Gly Lys His
530 535 540

Cys Phe Lys Gly His Cys Ile Trp Leu Thr Pro Asp Ile Leu Lys Arg
545 550 555 560

Asp Gly Ser Trp Gly Ala Trp Ser Pro Phe Gly Ser Cys Ser Arg Thr
565 570 575

Cys Gly Thr Gly Val Lys Phe Arg Thr Arg Gln Cys Asp Asn Pro His
580 585 590

Pro Ala Asn Gly Gly Arg Thr Cys Ser Gly Leu Ala Tyr Asp Phe Gln
595 600 605

Leu Cys Ser Arg Gln Asp Cys Pro Asp Ser Leu Ala Asp Phe Arg Glu
610 615 620

Glu Gln Cys Arg Gln Trp Asp Leu Tyr Phe Glu His Gly Asp Ala Gln
625 630 635 640

His His Trp Leu Pro His Glu His Arg Asp Ala Lys Glu Arg Cys His
645 650 655

Leu Tyr Cys Glu Ser Arg Glu Thr Gly Glu Val Val Ser Met Lys Arg
660 665 670

Met Val His Asp Gly Thr Arg Cys Ser Tyr Lys Asp Ala Phe Ser Leu
675 680 685

Cys Val Arg Gly Asp Cys Arg Lys Val Gly Cys Asp Gly Val Ile Gly
690 695 700

Ser Ser Lys Gln Glu Asp Lys Cys Gly Val Cys Gly Gly Asp Asn Ser
705 710 715 720

His Cys Lys Val Val Lys Gly Thr Phe Thr Arg Ser Pro Lys Lys His
725 730 735

Gly Tyr Ile Lys Met Phe Glu Ile Pro Ala Gly Ala Arg His Leu Leu
740 745 750

```
Ile Gln Glu Val Asp Ala Thr Ser His His Leu Ala Val Lys Asn Leu
        755                 760                 765

Glu Thr Gly Lys Phe Ile Leu Asn Glu Glu Asn Asp Val Asp Ala Ser
    770                 775                 780

Ser Lys Thr Phe Ile Ala Met Gly Val Glu Trp Glu Tyr Arg Asp Glu
785                 790                 795                 800

Asp Gly Arg Glu Thr Leu Gln Thr Met Gly Pro Leu His Gly Thr Ile
                805                 810                 815

Thr Val Leu Val Ile Pro Val Gly Asp Thr Arg Val Ser Leu Thr Tyr
            820                 825                 830

Lys Tyr Met Ile His Glu Asp Ser Leu Asn Val Asp Asp Asn Asn Val
        835                 840                 845

Leu Glu Glu Asp Ser Val Val Tyr Glu Trp Ala Leu Lys Lys Trp Ser
    850                 855                 860

Pro Cys Ser Lys Pro Cys Gly Gly Gly Ser Gln Phe Thr Lys Tyr Gly
865                 870                 875                 880

Cys Arg Arg Arg Leu Asp His Lys Met Val His Arg Gly Phe Cys Ala
                885                 890                 895

Ala Leu Ser Lys Pro Lys Ala Ile Arg Arg Ala Cys Asn Pro Gln Glu
            900                 905                 910

Cys Ser Gln Pro Val Trp Val Thr Gly Glu Trp Glu Pro Cys Ser Gln
        915                 920                 925

Thr Cys Gly Arg Thr Gly Met Gln Val Arg Ser Val Arg Cys Ile Gln
    930                 935                 940

Pro Leu His Asp Asn Thr Thr Arg Ser Val His Ala Lys His Cys Asn
945                 950                 955                 960

Asp Ala Arg Pro Glu Ser Arg Arg Ala Cys Ser Arg Glu Leu Cys Pro
                965                 970                 975

Gly Arg Trp Arg Ala Gly Pro Trp Ser Gln Cys Ser Val Thr Cys Gly
```

980 985 990

Asn Gly Thr Gln Glu Arg Pro Val Leu Cys Arg Thr Ala Asp Asp Ser
995 1000 1005

Phe Gly Ile Cys Gln Glu Glu Arg Pro Glu Thr Ala Arg Thr Cys
1010 1015 1020

Arg Leu Gly Pro Cys Pro Arg Asn Ile Ser Asp Pro Ser Lys Lys
1025 1030 1035

Ser Tyr Val Val Gln Trp Leu Ser Arg Pro Asp Pro Asp Ser Pro
1040 1045 1050

Ile Arg Lys Ile Ser Ser Lys Gly His Cys Gln Gly Asp Lys Ser
1055 1060 1065

Ile Phe Cys Arg Met Glu Val Leu Ser Arg Tyr Cys Ser Ile Pro
1070 1075 1080

Gly Tyr Asn Lys Leu Cys Cys Lys Ser Cys Asn Leu Tyr Asn Asn
1085 1090 1095

Leu Thr Asn Val Glu Gly Arg Ile Glu Pro Pro Pro Gly Lys His
1100 1105 1110

Asn Asp Ile Asp Val Phe Met Pro Thr Leu Pro Val Pro Thr Val
1115 1120 1125

Ala Met Glu Val Arg Pro Ser Pro Ser Thr Pro Leu Glu Val Pro
1130 1135 1140

Leu Asn Ala Ser Ser Thr Asn Ala Thr Glu Asp His Pro Glu Thr
1145 1150 1155

Asn Ala Val Asp Glu Pro Tyr Lys Ile His Gly Leu Glu Asp Glu
1160 1165 1170

Val Gln Pro Pro Asn Leu Ile Pro Arg Arg Pro Ser Pro Tyr Glu
1175 1180 1185

Lys Thr Arg Asn Gln Arg Ile Gln Glu Leu Ile Asp Glu Met Arg

```
    1190                1195                1200


Lys Lys  Glu Met Leu Gly Lys  Phe
    1205                1210


<210> 2297
<211> 566
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ADAMTS2; "

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<223> /note="Gene Name:
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      motif, 2; "

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<220>
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<400> 2297
Met Asp Pro Pro Ala Gly Ala Ala Arg Arg Leu Leu Cys Pro Ala Leu
1               5                  10                  15


Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Pro Pro Pro Pro
            20                  25                  30


Pro Pro Ala Asn Ala Arg Leu Ala Ala Ala Ala Asp Pro Pro Gly Gly
        35                  40                  45


Pro Leu Gly His Gly Ala Glu Arg Ile Leu Ala Val Pro Val Arg Thr
    50                  55                  60


Asp Ala Gln Gly Arg Leu Val Ser His Val Val Ser Ala Ala Thr Ser
65                  70                  75                  80


Arg Ala Gly Val Arg Ala Arg Arg Ala Ala Pro Val Arg Thr Pro Ser
                85                  90                  95
```

```
Phe Pro Gly Gly Asn Glu Glu Glu Pro Gly Ser His Leu Phe Tyr Asn
            100                 105                 110

Val Thr Val Phe Gly Arg Asp Leu His Leu Arg Leu Arg Pro Asn Ala
        115                 120                 125

Arg Leu Val Ala Pro Gly Ala Thr Met Glu Trp Gln Gly Glu Lys Gly
    130                 135                 140

Thr Thr Arg Val Glu Pro Leu Leu Gly Ser Cys Leu Tyr Val Gly Asp
145                 150                 155                 160

Val Ala Gly Leu Ala Glu Ala Ser Ser Val Ala Leu Ser Asn Cys Asp
                165                 170                 175

Gly Leu Ala Gly Leu Ile Arg Met Glu Glu Glu Glu Phe Phe Ile Glu
            180                 185                 190

Pro Leu Glu Lys Gly Leu Ala Ala Gln Glu Ala Glu Gln Gly Arg Val
        195                 200                 205

His Val Val Tyr Arg Arg Pro Pro Thr Ser Pro Pro Leu Gly Gly Pro
    210                 215                 220

Gln Ala Leu Asp Thr Gly Ala Ser Leu Asp Ser Leu Asp Ser Leu Ser
225                 230                 235                 240

Arg Ala Leu Gly Val Leu Glu Glu His Ala Asn Ser Ser Arg Arg Arg
                245                 250                 255

Ala Arg Arg His Ala Ala Asp Asp Asp Tyr Asn Ile Glu Val Leu Leu
            260                 265                 270

Gly Val Asp Asp Ser Val Val Gln Phe His Gly Lys Glu His Val Gln
        275                 280                 285

Lys Tyr Leu Leu Thr Leu Met Asn Ile Val Asn Glu Ile Tyr His Asp
    290                 295                 300

Glu Ser Leu Gly Ala His Ile Asn Val Val Leu Val Arg Ile Ile Leu
305                 310                 315                 320
```

```
Leu Ser Tyr Gly Lys Ser Met Ser Leu Ile Glu Ile Gly Asn Pro Ser
                325                 330                 335

Gln Ser Leu Glu Asn Val Cys Arg Trp Ala Tyr Leu Gln Gln Lys Pro
            340                 345                 350

Asp Thr Gly His Asp Glu Tyr His Asp His Ala Ile Phe Leu Thr Arg
        355                 360                 365

Gln Asp Phe Gly Pro Ser Gly Met Gln Gly Tyr Ala Pro Val Thr Gly
    370                 375                 380

Met Cys His Pro Val Arg Ser Cys Thr Leu Asn His Glu Asp Gly Phe
385                 390                 395                 400

Ser Ser Ala Phe Val Val Ala His Glu Thr Gly His Val Leu Gly Met
                405                 410                 415

Glu His Asp Gly Gln Gly Asn Arg Cys Gly Asp Glu Val Arg Leu Gly
            420                 425                 430

Ser Ile Met Ala Pro Leu Val Gln Ala Ala Phe His Arg Phe His Trp
        435                 440                 445

Ser Arg Cys Ser Gln Gln Glu Leu Ser Arg Tyr Leu His Ser Tyr Asp
    450                 455                 460

Cys Leu Leu Asp Asp Pro Phe Ala His Asp Trp Pro Ala Leu Pro Gln
465                 470                 475                 480

Leu Pro Gly Leu His Tyr Ser Met Asn Glu Gln Cys Arg Phe Asp Phe
                485                 490                 495

Gly Leu Gly Tyr Met Met Cys Thr Ala Phe Arg Thr Phe Asp Pro Cys
            500                 505                 510

Lys Gln Leu Trp Cys Ser His Pro Asp Asn Pro Tyr Phe Cys Lys Thr
        515                 520                 525

Lys Lys Gly Pro Pro Leu Asp Gly Thr Met Cys Ala Pro Gly Lys Phe
    530                 535                 540
```

```
Arg Pro Gly Ala Val Ala His Ala Cys Tyr Pro Ser Thr Leu Gly Gly
545                 550                 555                 560


Gln Gly Arg Trp Ile Ala
                565


<210> 2298
<211> 1910
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 568; "

<220>
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      ADAM metallopeptidase with thrombospondin type 1
      motif, 20; "

<220>
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<400> 2298
Met Trp Val Ala Lys Trp Leu Thr Gly Leu Leu Tyr His Leu Ser Leu
1               5                   10                  15


Phe Ile Thr Arg Ser Trp Glu Val Asp Phe His Pro Arg Gln Glu Ala
            20                  25                  30


Leu Val Arg Thr Leu Thr Ser Tyr Glu Val Val Ile Pro Glu Arg Val
        35                  40                  45


Asn Glu Phe Gly Glu Val Phe Pro Gln Ser His His Phe Ser Arg Gln
    50                  55                  60


Lys Arg Ser Ser Glu Ala Leu Glu Pro Met Pro Phe Arg Thr His Tyr
65                  70                  75                  80


Arg Phe Thr Ala Tyr Gly Gln Leu Phe Gln Leu Asn Leu Thr Ala Asp
```

```
                85                  90                  95

Ala Ser Phe Leu Ala Ala Gly Tyr Thr Glu Val His Leu Gly Thr Pro
            100                 105                 110

Glu Arg Gly Ala Trp Glu Ser Asp Ala Gly Pro Ser Asp Leu Arg His
        115                 120                 125

Cys Phe Tyr Arg Gly Gln Val Asn Ser Gln Glu Asp Tyr Lys Ala Val
    130                 135                 140

Val Ser Leu Cys Gly Gly Leu Thr Gly Thr Phe Lys Gly Gln Asn Gly
145                 150                 155                 160

Glu Tyr Phe Leu Glu Pro Ile Met Lys Ala Asp Gly Asn Glu Tyr Glu
                165                 170                 175

Asp Gly His Asn Lys Pro His Leu Ile Tyr Arg Gln Asp Leu Asn Asn
            180                 185                 190

Ser Phe Leu Gln Thr Leu Lys Tyr Cys Ser Val Ser Glu Ser Gln Ile
        195                 200                 205

Lys Glu Thr Ser Leu Pro Phe His Thr Tyr Ser Asn Met Asn Glu Asp
    210                 215                 220

Leu Asn Val Met Lys Glu Arg Val Leu Gly His Thr Ser Lys Asn Val
225                 230                 235                 240

Pro Leu Lys Asp Glu Arg Arg His Ser Arg Lys Lys Arg Leu Ile Ser
                245                 250                 255

Tyr Pro Arg Tyr Ile Glu Ile Met Val Thr Ala Asp Ala Lys Val Val
            260                 265                 270

Ser Ala His Gly Ser Asn Leu Gln Asn Tyr Ile Leu Thr Leu Met Ser
        275                 280                 285

Ile Val Ala Thr Ile Tyr Lys Asp Pro Ser Ile Gly Asn Leu Ile His
    290                 295                 300

Ile Val Val Val Lys Leu Val Met Ile His Arg Glu Glu Glu Gly Pro
305                 310                 315                 320
```

```
Val Ile Asn Phe Asp Gly Ala Thr Thr Leu Lys Asn Phe Cys Ser Trp
                325                 330                 335

Gln Gln Thr Gln Asn Asp Leu Asp Asp Val His Pro Ser His His Asp
            340                 345                 350

Thr Ala Val Leu Ile Thr Arg Glu Asp Ile Cys Ser Ser Lys Glu Lys
        355                 360                 365

Cys Asn Met Leu Gly Leu Ser Tyr Leu Gly Thr Ile Cys Asp Pro Leu
    370                 375                 380

Gln Ser Cys Phe Ile Asn Glu Glu Lys Gly Leu Ile Ser Ala Phe Thr
385                 390                 395                 400

Ile Ala His Glu Leu Gly His Thr Leu Gly Val Gln His Asp Asp Asn
                405                 410                 415

Pro Arg Cys Lys Glu Met Lys Val Thr Lys Tyr His Val Met Ala Pro
            420                 425                 430

Ala Leu Ser Phe His Met Ser Pro Trp Ser Trp Ser Asn Cys Ser Arg
        435                 440                 445

Lys Tyr Val Thr Glu Phe Leu Asp Thr Gly Tyr Gly Glu Cys Leu Leu
    450                 455                 460

Asp Lys Pro Asp Glu Glu Ile Tyr Asn Leu Pro Ser Glu Leu Pro Gly
465                 470                 475                 480

Ser Arg Tyr Asp Gly Asn Lys Gln Cys Glu Leu Ala Phe Gly Pro Gly
                485                 490                 495

Ser Gln Met Cys Pro His Ile Asn Ile Cys Met His Leu Trp Cys Thr
            500                 505                 510

Ser Thr Glu Lys Leu His Lys Gly Cys Phe Thr Gln His Val Pro Pro
        515                 520                 525

Ala Asp Gly Thr Asp Cys Gly Pro Gly Met His Cys Arg His Gly Leu
    530                 535                 540
```

```
Cys Val Asn Lys Glu Thr Glu Thr Arg Pro Val Asn Gly Glu Trp Gly
545                 550                 555                 560

Pro Trp Glu Pro Tyr Ser Ser Cys Ser Arg Thr Cys Gly Gly Gly Ile
                565                 570                 575

Glu Ser Ala Thr Arg Arg Cys Asn Arg Pro Glu Pro Arg Asn Gly Gly
            580                 585                 590

Asn Tyr Cys Val Gly Arg Arg Met Lys Phe Arg Ser Cys Asn Thr Asp
        595                 600                 605

Ser Cys Pro Lys Gly Thr Gln Asp Phe Arg Glu Lys Gln Cys Ser Asp
    610                 615                 620

Phe Asn Gly Lys His Leu Asp Ile Ser Gly Ile Pro Ser Asn Val Arg
625                 630                 635                 640

Trp Leu Pro Arg Tyr Ser Gly Ile Gly Thr Lys Asp Arg Cys Lys Leu
                645                 650                 655

Tyr Cys Gln Val Ala Gly Thr Asn Tyr Phe Tyr Leu Leu Lys Asp Met
            660                 665                 670

Val Glu Asp Gly Thr Pro Cys Gly Thr Glu Thr His Asp Ile Cys Val
        675                 680                 685

Gln Gly Gln Cys Met Ala Ala Gly Cys Asp His Val Leu Asn Ser Ser
    690                 695                 700

Ala Lys Ile Asp Lys Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys
705                 710                 715                 720

Lys Thr Ile Thr Gly Val Phe Asn Ser Ser His Tyr Gly Tyr Asn Val
                725                 730                 735

Val Val Lys Ile Pro Ala Gly Ala Thr Asn Val Asp Ile Arg Gln Tyr
            740                 745                 750

Ser Tyr Ser Gly Gln Pro Asp Asp Ser Tyr Leu Ala Leu Ser Asp Ala
        755                 760                 765
```

```
Glu Gly Asn Phe Leu Phe Asn Gly Asn Phe Leu Leu Ser Thr Ser Lys
    770                 775                 780

Lys Glu Ile Asn Val Gln Gly Thr Arg Thr Val Ile Glu Tyr Ser Gly
785                 790                 795                 800

Ser Asn Asn Ala Val Glu Arg Ile Asn Ser Thr Asn Arg Gln Glu Lys
                805                 810                 815

Glu Leu Ile Leu Gln Val Leu Cys Val Gly Asn Leu Tyr Asn Pro Asp
            820                 825                 830

Val His Tyr Ser Phe Asn Ile Pro Leu Glu Glu Arg Ser Asp Met Phe
        835                 840                 845

Thr Trp Asp Pro Tyr Gly Pro Trp Glu Gly Cys Thr Lys Met Cys Gln
    850                 855                 860

Gly Leu Gln Arg Arg Asn Ile Thr Cys Ile His Lys Ser Asp His Ser
865                 870                 875                 880

Val Val Ser Asp Lys Glu Cys Asp His Leu Pro Leu Pro Ser Phe Val
                885                 890                 895

Thr Gln Ser Cys Asn Thr Asp Cys Glu Leu Arg Trp His Val Ile Gly
            900                 905                 910

Lys Ser Glu Cys Ser Ser Gln Cys Gly Gln Gly Tyr Arg Thr Leu Asp
        915                 920                 925

Ile His Cys Met Lys Tyr Ser Ile His Glu Gly Gln Thr Val Gln Val
    930                 935                 940

Asp Asp His Tyr Cys Gly Asp Gln Leu Lys Pro Pro Thr Gln Glu Leu
945                 950                 955                 960

Cys His Gly Asn Cys Val Phe Thr Arg Trp His Tyr Ser Glu Trp Ser
                965                 970                 975

Gln Cys Ser Arg Ser Cys Gly Gly Gly Glu Arg Ser Arg Glu Ser Tyr
            980                 985                 990

Cys Met Asn Asn Phe Gly His Arg  Leu Ala Asp Asn Glu  Cys Gln
```

Glu
995 1000 1005

Leu Ser Arg Val Thr Arg Glu Asn Cys Asn Glu Phe Ser Cys Pro
1010 1015 1020

Ser Trp Ala Ala Ser Glu Trp Ser Glu Cys Leu Val Thr Cys Gly
1025 1030 1035

Lys Gly Thr Lys Gln Arg Gln Val Trp Cys Gln Leu Asn Val Asp
1040 1045 1050

His Leu Ser Asp Gly Phe Cys Asn Ser Ser Thr Lys Pro Glu Ser
1055 1060 1065

Leu Ser Pro Cys Glu Leu His Thr Cys Ala Ser Trp Gln Val Gly
1070 1075 1080

Pro Trp Gly Pro Cys Thr Thr Thr Cys Gly His Gly Tyr Gln Met
1085 1090 1095

Arg Asp Val Lys Cys Val Asn Glu Leu Ala Ser Ala Val Leu Glu
1100 1105 1110

Asp Thr Glu Cys His Glu Ala Ser Arg Pro Ser Asp Arg Gln Ser
1115 1120 1125

Cys Val Leu Thr Pro Cys Ser Phe Ile Ser Lys Leu Glu Thr Ala
1130 1135 1140

Leu Leu Pro Thr Val Leu Ile Lys Lys Met Ala Gln Trp Arg His
1145 1150 1155

Gly Ser Trp Thr Pro Cys Ser Val Ser Cys Gly Arg Gly Thr Gln
1160 1165 1170

Ala Arg Tyr Val Ser Cys Arg Asp Ala Leu Asp Arg Ile Ala Asp
1175 1180 1185

Glu Ser Tyr Cys Ala His Leu Pro Arg Pro Ala Glu Ile Trp Asp
1190 1195 1200

Cys Phe Thr Pro Cys Gly Glu Trp Gln Ala Gly Asp Trp Ser Pro

1205 1210 1215

Cys Ser Ala Ser Cys Gly His Gly Lys Thr Thr Arg Gln Val Leu
1220 1225 1230

Cys Met Asn Tyr His Gln Pro Ile Asp Glu Asn Tyr Cys Asp Pro
1235 1240 1245

Glu Val Arg Pro Leu Met Glu Gln Glu Cys Ser Leu Ala Ala Cys
1250 1255 1260

Pro Pro Ala His Ser His Phe Pro Ser Ser Pro Val Gln Pro Ser
1265 1270 1275

Tyr Tyr Leu Ser Thr Asn Leu Pro Leu Thr Gln Lys Leu Glu Asp
1280 1285 1290

Asn Glu Asn Gln Val Val His Pro Ser Val Arg Gly Asn Gln Trp
1295 1300 1305

Arg Thr Gly Pro Trp Gly Ser Cys Ser Ser Ser Cys Ser Gly Gly
1310 1315 1320

Leu Gln His Arg Ala Val Val Cys Gln Asp Glu Asn Gly Gln Ser
1325 1330 1335

Ala Ser Tyr Cys Asp Ala Ala Ser Lys Pro Pro Glu Leu Gln Gln
1340 1345 1350

Cys Gly Pro Gly Pro Cys Pro Gln Trp Asn Tyr Gly Asn Trp Gly
1355 1360 1365

Glu Cys Ser Gln Thr Cys Gly Gly Gly Ile Lys Ser Arg Leu Val
1370 1375 1380

Ile Cys Gln Phe Pro Asn Gly Gln Ile Leu Glu Asp His Asn Cys
1385 1390 1395

Glu Ile Val Asn Lys Pro Pro Ser Val Ile Gln Cys His Met His
1400 1405 1410

Ala Cys Pro Ala Asp Val Ser Trp His Gln Glu Pro Trp Thr Ser
1415 1420 1425

```
Cys Ser  Ala Ser Cys Gly Lys  Gly Arg Lys Tyr Arg  Glu Val Phe
    1430                1435                1440

Cys Ile  Asp Gln Phe Gln Arg  Lys Leu Glu Asp Thr  Asn Cys Ser
    1445                1450                1455

Gln Val  Gln Lys Pro Pro Thr  His Lys Ala Cys Arg  Ser Val Arg
    1460                1465                1470

Cys Pro  Ser Trp Lys Ala Asn  Ser Trp Asn Glu Cys  Ser Val Thr
    1475                1480                1485

Cys Gly  Ser Gly Val Gln Gln  Arg Asp Val Tyr Cys  Arg Leu Lys
    1490                1495                1500

Gly Val  Gly Gln Val Val Glu  Glu Met Cys Asp Gln  Ser Thr Arg
    1505                1510                1515

Pro Cys  Ser Gln Arg Arg Cys  Trp Ser Gln Asp Cys  Val Gln His
    1520                1525                1530

Lys Gly  Met Glu Arg Gly Arg  Leu Asn Cys Ser Thr  Ser Cys Glu
    1535                1540                1545

Arg Lys  Asp Ser His Gln Arg  Met Glu Cys Thr Asp  Asn Gln Ile
    1550                1555                1560

Arg Gln  Val Asn Glu Ile Val  Tyr Asn Ser Ser Thr  Ile Ser Leu
    1565                1570                1575

Thr Ser  Lys Asn Cys Arg Asn  Pro Pro Cys Asn Tyr  Ile Val Val
    1580                1585                1590

Thr Ala  Asp Ser Ser Gln Cys  Ala Asn Asn Cys Gly  Phe Ser Tyr
    1595                1600                1605

Arg Gln  Arg Ile Thr Tyr Cys  Thr Glu Ile Pro Ser  Thr Lys Lys
    1610                1615                1620

His Lys  Leu His Arg Leu Arg  Pro Ile Val Tyr Gln  Glu Cys Pro
    1625                1630                1635
```

```
Val Val  Pro Ser Ser Gln Val  Tyr Gln Cys Ile Asn  Ser Cys Leu
    1640                1645                1650

His Leu  Ala Thr Trp Lys Val  Gly Lys Trp Ser Lys  Cys Ser Val
    1655                1660                1665

Thr Cys  Gly Ile Gly Ile Met  Lys Arg Gln Val Lys  Cys Ile Thr
    1670                1675                1680

Lys His  Gly Leu Ser Ser Asp  Leu Cys Leu Asn His  Leu Lys Pro
    1685                1690                1695

Gly Ala  Gln Lys Lys Cys Tyr  Ala Asn Asp Cys Lys  Ser Phe Thr
    1700                1705                1710

Thr Cys  Lys Glu Ile Gln Val  Lys Asn His Ile Arg  Lys Asp Gly
    1715                1720                1725

Asp Tyr  Tyr Leu Asn Ile Lys  Gly Arg Ile Ile Lys  Ile Tyr Cys
    1730                1735                1740

Ala Asp  Met Tyr Leu Glu Asn  Pro Lys Glu Tyr Leu  Thr Leu Val
    1745                1750                1755

Gln Gly  Glu Glu Asn Phe Ser  Glu Val Tyr Gly Phe  Arg Leu Lys
    1760                1765                1770

Asn Pro  Tyr Gln Cys Pro Phe  Asn Gly Ser Arg Arg  Glu Asp Cys
    1775                1780                1785

Glu Cys  Asp Asn Gly His Leu  Ala Ala Gly Tyr Thr  Val Phe Ser
    1790                1795                1800

Lys Ile  Arg Ile Asp Leu Thr  Ser Met Gln Ile Lys  Thr Thr Asp
    1805                1810                1815

Leu Leu  Phe Ser Lys Thr Ile  Phe Gly Asn Ala Val  Pro Phe Ala
    1820                1825                1830

Thr Ala  Gly Asp Cys Tyr Ser  Ala Phe Arg Cys Pro  Gln Gly Gln
    1835                1840                1845
```

```
Phe Ser  Ile Asn Leu Ser Gly  Thr Gly Met Lys Ile  Ser Ser Thr
    1850                 1855                 1860


Ala Lys  Trp Leu Thr Gln Gly  Ser Tyr Thr Ser Val  Ser Ile Arg
    1865                 1870                 1875


Arg Ser  Glu Asp Gly Thr Arg  Phe Phe Gly Lys Cys  Gly Gly Tyr
    1880                 1885                 1890


Cys Gly  Lys Cys Leu Pro His  Met Thr Thr Gly Leu  Pro Ile Gln
    1895                 1900                 1905


Val Ile
    1910


<210> 2299
<211> 1504
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 568; "

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<223> /note="Gene Symbol: ADAMTS20; "

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      ADAM metallopeptidase with thrombospondin type 1
      motif, 20; "

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<400> 2299
Met Trp Val Ala Lys Trp Leu Thr Gly Leu Leu Tyr His Leu Ser Leu
1               5                  10                  15


Phe Ile Thr Arg Ser Trp Glu Val Asp Phe His Pro Arg Gln Glu Ala
            20                  25                  30


Leu Val Arg Thr Leu Thr Ser Tyr Glu Val Val Ile Pro Glu Arg Val
        35                  40                  45


Asn Glu Phe Gly Glu Val Phe Pro Gln Ser His His Phe Ser Arg Gln
```

```
    50                  55                  60

Lys Arg Ser Ser Glu Ala Leu Glu Pro Met Pro Phe Arg Thr His Tyr
65                  70                  75                  80

Arg Phe Thr Ala Tyr Gly Gln Leu Phe Gln Leu Asn Leu Thr Ala Asp
                85                  90                  95

Ala Ser Phe Leu Ala Ala Gly Tyr Thr Glu Val His Leu Gly Thr Pro
            100                 105                 110

Glu Arg Gly Ala Trp Glu Ser Asp Ala Gly Pro Ser Asp Leu Arg His
        115                 120                 125

Cys Phe Tyr Arg Gly Gln Val Asn Ser Gln Glu Asp Tyr Lys Ala Val
    130                 135                 140

Val Ser Leu Cys Gly Gly Leu Val Gly Thr Phe Lys Gly Gln Asn Gly
145                 150                 155                 160

Glu Tyr Phe Leu Glu Pro Ile Met Lys Ala Asp Gly Asn Glu Tyr Glu
                165                 170                 175

Asp Gly His Asn Lys Pro His Leu Ile Tyr Arg Gln Asp Leu Asn Asn
            180                 185                 190

Ser Phe Leu Gln Thr Leu Lys Tyr Cys Ser Val Ser Glu Ser Gln Ile
        195                 200                 205

Lys Glu Thr Ser Leu Pro Phe His Thr Tyr Ser Asn Met Asn Glu Asp
    210                 215                 220

Leu Asn Val Met Lys Glu Arg Val Leu Gly His Thr Ser Lys Asn Val
225                 230                 235                 240

Pro Leu Lys Asp Glu Arg Arg His Ser Arg Lys Lys Arg Leu Ile Ser
                245                 250                 255

Tyr Pro Arg Tyr Ile Glu Ile Met Val Thr Ala Asp Ala Lys Val Val
            260                 265                 270

Ser Ala His Gly Ser Asn Leu Gln Asn Tyr Ile Leu Thr Leu Met Ser
        275                 280                 285
```

```
Ile Val Ala Thr Ile Tyr Lys Asp Pro Ser Ile Gly Asn Leu Ile His
    290                 295                 300

Ile Val Val Val Lys Leu Val Met Ile His Arg Glu Glu Glu Gly Pro
305                 310                 315                 320

Val Ile Asn Phe Asp Gly Ala Thr Thr Leu Lys Asn Phe Cys Ser Trp
                325                 330                 335

Gln Gln Thr Gln Asn Asp Leu Asp Asp Val His Pro Ser His His Asp
            340                 345                 350

Thr Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Ser Ser Lys Glu Lys
        355                 360                 365

Cys Asn Met Leu Gly Leu Ser Tyr Leu Gly Thr Ile Cys Asp Pro Leu
    370                 375                 380

Gln Ser Cys Phe Ile Asn Glu Glu Lys Gly Leu Ile Ser Ala Phe Thr
385                 390                 395                 400

Ile Ala His Glu Leu Gly His Thr Leu Gly Val Gln His Asp Asp Asn
                405                 410                 415

Pro Arg Cys Lys Glu Met Lys Val Thr Lys Tyr His Val Met Ala Pro
            420                 425                 430

Ala Leu Ser Phe His Met Ser Pro Trp Ser Trp Ser Asn Cys Ser Arg
        435                 440                 445

Lys Tyr Val Thr Glu Phe Leu Asp Thr Gly Tyr Gly Glu Cys Leu Leu
    450                 455                 460

Asp Lys Pro Asp Glu Glu Ile Tyr Asn Leu Pro Ser Glu Leu Pro Gly
465                 470                 475                 480

Ser Arg Tyr Asp Gly Asn Lys Gln Cys Glu Leu Ala Phe Gly Pro Gly
                485                 490                 495

Ser Gln Met Cys Pro His Ile Asn Ile Cys Met His Leu Trp Cys Thr
            500                 505                 510
```

Ser Thr Glu Lys Leu His Lys Gly Cys Phe Thr Gln His Val Pro Pro
515 520 525

Ala Asp Gly Thr Asp Cys Gly Pro Gly Met His Cys Arg His Gly Leu
530 535 540

Cys Val Asn Lys Glu Thr Glu Thr Arg Pro Val Asn Gly Glu Trp Gly
545 550 555 560

Pro Trp Glu Pro Tyr Ser Ser Cys Ser Arg Thr Cys Gly Gly Gly Ile
565 570 575

Glu Ser Ala Thr Arg Arg Cys Asn Arg Pro Glu Pro Arg Asn Gly Gly
580 585 590

Asn Tyr Cys Val Gly Arg Arg Met Lys Phe Arg Ser Cys Asn Thr Asp
595 600 605

Ser Cys Pro Lys Gly Thr Gln Asp Phe Arg Glu Lys Gln Cys Ser Asp
610 615 620

Phe Asn Gly Lys His Leu Asp Ile Ser Gly Ile Pro Ser Asn Val Arg
625 630 635 640

Trp Leu Pro Arg Tyr Ser Gly Ile Gly Thr Lys Asp Arg Cys Lys Leu
645 650 655

Tyr Cys Gln Val Ala Gly Thr Asn Tyr Phe Tyr Leu Leu Lys Asp Met
660 665 670

Val Glu Asp Gly Thr Pro Cys Gly Thr His Ser Tyr Asn Ile Asp Cys
675 680 685

Asn Cys Val Leu Lys Ala Ala Gly Cys Asp His Val Leu Asn Ser Ser
690 695 700

Ala Lys Ile Asp Lys Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys
705 710 715 720

Lys Thr Ile Thr Gly Val Phe Asn Ser Ser His Tyr Gly Tyr Asn Val
725 730 735

```
Val Val Lys Ile Pro Ala Gly Ala Thr Asn Val Asp Ile Arg Gln Tyr
            740                 745                 750

Ser Tyr Ser Gly Gln Pro Asp Asp Ser Tyr Leu Ala Leu Ser Asp Ala
        755                 760                 765

Glu Gly Asn Phe Leu Phe Asn Gly Asn Phe Leu Leu Ser Thr Ser Lys
    770                 775                 780

Lys Glu Ile Asn Val Gln Gly Thr Arg Thr Val Ile Glu Tyr Ser Gly
785                 790                 795                 800

Ser Asn Asn Ala Val Glu Arg Ile Asn Ser Thr Asn Arg Gln Glu Lys
                805                 810                 815

Glu Ile Leu Ile Glu Val Leu Cys Val Gly Asn Leu Tyr Asn Pro Asp
            820                 825                 830

Val His Tyr Ser Phe Asn Ile Pro Leu Glu Glu Arg Ser Asp Met Phe
        835                 840                 845

Thr Trp Asp Pro Tyr Gly Pro Trp Glu Gly Cys Thr Lys Met Cys Gln
    850                 855                 860

Gly Leu Gln Arg Arg Asn Ile Thr Cys Ile His Lys Ser Asp His Ser
865                 870                 875                 880

Val Val Ser Asp Lys Glu Cys Asp His Leu Pro Leu Pro Ser Phe Val
                885                 890                 895

Thr Gln Ser Cys Asn Thr Asp Cys Glu Leu Arg Trp His Val Ile Gly
            900                 905                 910

Lys Ser Glu Cys Ser Ser Gln Cys Gly Gln Gly Tyr Arg Thr Leu Asp
        915                 920                 925

Ile His Cys Met Lys Tyr Ser Ile His Glu Gly Gln Thr Val Gln Val
    930                 935                 940

Asp Asp His Tyr Cys Gly Asp Gln Leu Lys Pro Pro Thr Gln Glu Leu
945                 950                 955                 960

Cys His Gly Asn Cys Val Phe Thr Arg Trp His Tyr Ser Glu Trp Ser
```

965 970 975

Gln Cys Ser Arg Ser Cys Gly Gly Gly Glu Arg Ser Arg Glu Ser Tyr
980 985 990

Cys Met Asn Asn Phe Gly His Arg Leu Ala Asp Asn Glu Cys Gln Glu
995 1000 1005

Leu Ser Arg Val Thr Arg Glu Asn Cys Asn Glu Phe Ser Cys Pro
1010 1015 1020

Ser Trp Ala Ala Ser Glu Trp Ser Glu Cys Leu Val Thr Cys Gly
1025 1030 1035

Lys Gly Thr Lys Gln Arg Gln Val Trp Cys Gln Leu Asn Val Asp
1040 1045 1050

His Leu Ser Asp Gly Phe Cys Asn Ser Ser Thr Lys Pro Glu Ser
1055 1060 1065

Leu Ser Pro Cys Glu Leu His Thr Cys Ala Ser Trp Gln Val Gly
1070 1075 1080

Pro Trp Gly Pro Cys Thr Thr Thr Cys Gly His Gly Tyr Gln Met
1085 1090 1095

Arg Asp Val Lys Cys Val Asn Glu Leu Ala Ser Ala Val Leu Glu
1100 1105 1110

Asp Thr Glu Cys His Glu Ala Ser Arg Pro Ser Asp Arg Gln Ser
1115 1120 1125

Cys Val Leu Thr Pro Cys Ser Phe Ile Ser Lys Leu Glu Thr Ala
1130 1135 1140

Leu Leu Pro Thr Val Leu Ile Lys Lys Met Ala Gln Trp Arg His
1145 1150 1155

Gly Ser Trp Thr Pro Cys Ser Val Ser Cys Gly Arg Gly Thr Gln
1160 1165 1170

Ala Arg Tyr Val Ser Cys Arg Asp Ala Leu Asp Arg Ile Ala Asp

1175 1180 1185

Glu Ser Tyr Cys Ala His Leu Pro Arg Pro Ala Glu Ile Trp Asp
1190 1195 1200

Cys Phe Thr Pro Cys Gly Glu Trp Gln Ala Gly Asp Trp Ser Pro
1205 1210 1215

Cys Ser Ala Ser Cys Gly His Gly Lys Thr Thr Arg Gln Val Leu
1220 1225 1230

Cys Met Asn Tyr His Gln Pro Ile Asp Glu Asn Tyr Cys Asp Pro
1235 1240 1245

Glu Val Arg Pro Leu Met Glu Gln Glu Cys Ser Leu Ala Ala Cys
1250 1255 1260

Pro Pro Ala His Ser His Phe Pro Ser Ser Pro Val Gln Pro Ser
1265 1270 1275

Tyr Tyr Leu Ser Thr Asn Leu Pro Leu Thr Gln Lys Leu Glu Asp
1280 1285 1290

Asn Glu Asn Gln Val Val His Pro Ser Val Arg Gly Asn Gln Trp
1295 1300 1305

Arg Thr Gly Pro Trp Gly Gln Cys Ser Ser Ser Cys Ser Gly Gly
1310 1315 1320

Leu Gln His Arg Ala Val Val Cys Gln Asp Glu Asn Gly Gln Ser
1325 1330 1335

Ala Ser Tyr Cys Asp Ala Ala Ser Lys Pro Pro Glu Leu Gln Gln
1340 1345 1350

Cys Gly Pro Gly Pro Cys Pro Gln Trp Asn Tyr Gly Asn Trp Gly
1355 1360 1365

Glu Cys Ser Gln Thr Cys Gly Gly Gly Ile Lys Ser Arg Leu Val
1370 1375 1380

Ile Cys Gln Phe Pro Asn Gly Gln Ile Leu Glu Asp His Asn Cys
1385 1390 1395

```
Glu Ile  Val Asn Lys Pro Pro  Ser Val Ile Gln Cys  His Met His
    1400                1405                1410

Ala Cys  Pro Ala Asp Val Ser  Trp His Gln Glu Pro  Trp Thr Ser
    1415                1420                1425

Glu Asp  Leu Lys Val Lys Leu  Leu Pro Gln Arg Thr  Ile Ile Leu
    1430                1435                1440

Trp Glu  Leu Met Lys Asn Ile  Phe Cys His Gly Lys  His Ser His
    1445                1450                1455

Met Tyr  Leu Ile Asn Val Val  Thr Asp His Leu Leu  Tyr Pro Arg
    1460                1465                1470

His Cys  Asp Pro Glu Thr Ile  Glu Thr Tyr Phe Leu  Ser Leu Trp
    1475                1480                1485

Ser Leu  Gln Phe Thr Trp Gly  Asp Leu Lys Tyr Tyr  Lys Asn Ser
    1490                1495                1500

Leu
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<210> 2300
<211> 634
<212> PRT
<213> Homo sapiens

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<220>
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<223> /note="Gene Symbol: ADAMTS20; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 20; "

<220>
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<223> /note="ENSP ID: ENSP00000447427"

<400> 2300
Tyr Ser Phe Asn Ile Pro Leu Glu Glu Arg Ser Asp Met Phe Thr Trp
1 5 10 15

Asp Pro Tyr Gly Pro Trp Glu Gly Cys Thr Lys Met Cys Gln Gly Leu
20 25 30

Gln Arg Arg Asn Ile Thr Cys Ile His Lys Ser Asp His Ser Val Val
35 40 45

Ser Asp Lys Glu Cys Asp His Leu Pro Leu Pro Ser Phe Val Thr Gln
50 55 60

Ser Cys Asn Thr Asp Cys Glu Leu Arg Trp His Val Ile Gly Lys Ser
65 70 75 80

Glu Cys Ser Ser Gln Cys Gly Gln Gly Tyr Arg Thr Leu Asp Ile His
85 90 95

Cys Met Lys Tyr Ser Ile His Glu Gly Gln Thr Val Gln Val Asp Asp
100 105 110

His Tyr Cys Gly Asp Gln Leu Lys Pro Pro Thr Gln Glu Leu Cys His
115 120 125

Gly Asn Cys Val Phe Thr Arg Trp His Tyr Ser Glu Trp Ser Gln Cys
130 135 140

Ser Arg Ser Cys Gly Gly Gly Glu Arg Ser Arg Glu Ser Tyr Cys Met
145 150 155 160

Asn Asn Phe Gly His Arg Leu Ala Asp Asn Glu Cys Gln Glu Leu Ser
165 170 175

Arg Val Thr Arg Glu Asn Cys Asn Glu Phe Ser Cys Pro Ser Trp Ala
180 185 190

Ala Ser Glu Trp Ser Glu Cys Leu Val Thr Cys Gly Lys Gly Thr Lys
195 200 205

Gln Arg Gln Val Trp Cys Gln Leu Asn Val Asp His Leu Ser Asp Gly
210 215 220

```
Phe Cys Asn Ser Ser Thr Lys Pro Glu Ser Leu Ser Pro Cys Glu Leu
225                 230                 235                 240

His Thr Cys Ala Ser Trp Gln Val Gly Pro Trp Gly Pro Cys Thr Thr
                245                 250                 255

Thr Cys Gly His Gly Tyr Gln Met Arg Asp Val Lys Cys Val Asn Glu
            260                 265                 270

Leu Ala Ser Ala Val Leu Glu Asp Thr Glu Cys His Glu Ala Ser Arg
        275                 280                 285

Pro Ser Asp Arg Gln Cys Ser Val Ser Cys Gly Arg Gly Thr Gln Ala
    290                 295                 300

Arg Tyr Val Ser Cys Arg Asp Ala Leu Asp Arg Ile Ala Asp Glu Ser
305                 310                 315                 320

Tyr Cys Ala His Leu Pro Arg Pro Ala Glu Ile Trp Asp Cys Phe Thr
                325                 330                 335

Pro Cys Gly Glu Trp Gln Ala Gly Asp Trp Ser Pro Cys Ser Ala Ser
            340                 345                 350

Cys Gly His Gly Lys Thr Thr Arg Gln Val Leu Cys Met Asn Tyr His
        355                 360                 365

Gln Pro Ile Asp Glu Asn Tyr Cys Asp Pro Glu Val Arg Pro Leu Met
    370                 375                 380

Glu Gln Glu Cys Ser Leu Ala Ala Cys Pro Pro Ala His Ser His Phe
385                 390                 395                 400

Pro Ser Ser Pro Val Gln Pro Ser Tyr Tyr Leu Ser Thr Asn Leu Pro
                405                 410                 415

Leu Thr Gln Lys Leu Glu Asp Asn Glu Asn Gln Val Val His Pro Ser
            420                 425                 430

Val Arg Gly Asn Gln Trp Arg Thr Gly Pro Trp Gly Ser Cys Ser Ser
        435                 440                 445

Ser Cys Ser Gly Gly Leu Gln His Arg Ala Val Val Cys Gln Asp Glu
```

```
    450                 455                 460

Asn Gly Gln Ser Ala Ser Tyr Cys Asp Ala Ala Ser Lys Pro Pro Glu
465                 470                 475                 480

Leu Gln Gln Cys Gly Pro Gly Pro Cys Pro Gln Trp Asn Tyr Gly Asn
                485                 490                 495

Trp Gly Glu Cys Ser Gln Thr Cys Gly Gly Gly Ile Lys Ser Arg Leu
            500                 505                 510

Val Ile Cys Gln Phe Pro Asn Gly Gln Ile Leu Glu Asp His Asn Cys
        515                 520                 525

Glu Ile Val Asn Lys Pro Pro Ser Val Ile Gln Cys His Met His Ala
    530                 535                 540

Cys Pro Ala Asp Val Ser Trp His Gln Glu Pro Trp Thr Ser Glu Asp
545                 550                 555                 560

Leu Lys Val Lys Leu Leu Pro Gln Arg Thr Ile Ile Leu Trp Glu Leu
                565                 570                 575

Met Lys Asn Ile Phe Cys His Gly Lys His Ser His Met Tyr Leu Ile
            580                 585                 590

Asn Val Val Thr Asp His Leu Leu Tyr Pro Arg His Cys Asp Pro Glu
        595                 600                 605

Thr Ile Glu Thr Tyr Phe Leu Ser Leu Trp Ser Leu Gln Phe Thr Trp
    610                 615                 620

Gly Asp Leu Lys Tyr Tyr Lys Asn Ser Leu
625                 630


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ADAM metallopeptidase with thrombospondin type 1
motif, 20; "

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<400> 2301

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Met Trp Val Ala Lys Trp Leu Thr Gly Leu Leu Tyr His Leu Ser Leu
1               5                  10                  15

Phe Ile Thr Arg Ser Trp Glu Val Asp Phe His Pro Arg Gln Glu Ala
            20                  25                  30

Leu Val Arg Thr Leu Thr Ser Tyr Glu Val Val Ile Pro Glu Arg Val
        35                  40                  45

Asn Glu Phe Gly Glu Val Phe Pro Gln Ser His His Phe Ser Arg Gln
    50                  55                  60

Lys Arg Ser Ser Glu Ala Leu Glu Pro Met Pro Phe Arg Thr His Tyr
65                  70                  75                  80

Arg Phe Thr Ala Tyr Gly Gln Leu Phe Gln Leu Asn Leu Thr Ala Asp
                85                  90                  95

Ala Ser Phe Leu Ala Ala Gly Tyr Thr Glu Val His Leu Gly Thr Pro
            100                 105                 110

Glu Arg Gly Ala Trp Glu Ser Asp Ala Gly Pro Ser Asp Leu Arg His
        115                 120                 125

Cys Phe Tyr Arg Gly Gln Val Asn Ser Gln Glu Asp Tyr Lys Ala Val
    130                 135                 140

Val Ser Leu Cys Gly Gly Leu Thr Gly Thr Phe Lys Gly Gln Asn Gly
145                 150                 155                 160

Glu Tyr Phe Leu Glu Pro Ile Met Lys Ala Asp Gly Asn Glu Tyr Glu
                165                 170                 175
```

```
Asp Gly His Asn Lys Pro His Leu Ile Tyr Arg Gln Asp Leu Asn Asn
            180                 185                 190

Ser Phe Leu Gln Thr Leu Lys Tyr Cys Ser Val Ser Glu Ser Gln Ile
        195                 200                 205

Lys Glu Thr Ser Leu Pro Phe His Thr Tyr Ser Asn Met Asn Glu Asp
    210                 215                 220

Leu Asn Val Met Lys Glu Arg Val Leu Gly His Thr Ser Lys Asn Val
225                 230                 235                 240

Pro Leu Lys Asp Glu Arg Arg His Ser Arg Lys Lys Arg Leu Ile Ser
                245                 250                 255

Tyr Pro Arg Tyr Ile Glu Ile Met Val Thr Ala Asp Ala Lys Val Val
            260                 265                 270

Ser Ala His Gly Ser Asn Leu Gln Asn Tyr Ile Leu Thr Leu Met Ser
        275                 280                 285

Ile Val Ala Thr Ile Tyr Lys Asp Pro Ser Ile Gly Asn Leu Ile His
    290                 295                 300

Ile Val Val Val Lys Leu Val Met Ile His Arg Glu Glu Glu Gly Pro
305                 310                 315                 320

Val Ile Asn Phe Asp Gly Ala Thr Thr Leu Lys Asn Phe Cys Ser Trp
                325                 330                 335

Gln Gln Thr Gln Asn Asp Leu Asp Asp Val His Pro Ser His His Asp
            340                 345                 350

Thr Ala Val Leu Ile Thr Arg Glu Asp Ile Cys Ser Ser Lys Glu Lys
        355                 360                 365

Cys Asn Met Leu Gly Leu Ser Tyr Leu Gly Thr Ile Cys Asp Pro Leu
    370                 375                 380

Gln Ser Cys Phe Ile Asn Glu Glu Lys Gly Leu Ile Ser Ala Phe Thr
385                 390                 395                 400
```

```
Ile Ala His Glu Leu Gly His Thr Leu Gly Val Gln His Asp Asp Asn
                405                 410                 415

Pro Arg Cys Lys Glu Met Lys Val Thr Lys Tyr His Val Met Ala Pro
            420                 425                 430

Ala Leu Ser Phe His Met Ser Pro Trp Ser Trp Ser Asn Cys Ser Arg
        435                 440                 445

Lys Tyr Val Thr Glu Phe Leu Asp Thr Gly Tyr Gly Glu Cys Leu Leu
    450                 455                 460

Asp Lys Pro Asp Glu Glu Ile Tyr Asn Leu Pro Ser Glu Leu Pro Gly
465                 470                 475                 480

Ser Arg Tyr Asp Gly Asn Lys Gln Cys Glu Leu Ala Phe Gly Pro Gly
                485                 490                 495

Ser Gln Met Cys Pro His Ile Asn Ile Cys Met His Leu Trp Cys Thr
            500                 505                 510

Ser Thr Glu Lys Leu His Lys Gly Cys Phe Thr Gln His Val Pro Pro
        515                 520                 525

Ala Asp Gly Thr Asp Cys Gly Pro Gly Met His Cys Arg His Gly Leu
    530                 535                 540

Cys Val Asn Lys Glu Thr Glu Thr Arg Pro Val Asn Gly Glu Trp Gly
545                 550                 555                 560

Pro Trp Glu Pro Tyr Ser Ser Cys Ser Arg Thr Cys Gly Gly Gly Ile
                565                 570                 575

Glu Ser Ala Thr Arg Arg Cys Asn Arg Pro Glu Pro Arg Asn Gly Gly
            580                 585                 590

Asn Tyr Cys Val Gly Arg Arg Met Lys Phe Arg Ser Cys Asn Thr Asp
        595                 600                 605

Ser Cys Pro Lys Gly Thr Gln Asp Phe Arg Glu Lys Gln Cys Ser Asp
    610                 615                 620

Phe Asn Gly Lys His Leu Asp Ile Ser Gly Ile Pro Ser Asn Val Arg
```

625 630 635 640

Trp Leu Pro Arg Tyr Ser Gly Ile Gly Thr Lys Asp Arg Cys Lys Leu
645 650 655

Tyr Cys Gln Val Ala Gly Thr Asn Tyr Phe Tyr Leu Leu Lys Asp Met
660 665 670

Val Glu Asp Gly Thr Pro Cys Gly Thr Glu Thr His Asp Ile Cys Val
675 680 685

Gln Gly Gln Cys Met Ala Ala Gly Cys Asp His Val Leu Asn Ser Ser
690 695 700

Ala Lys Ile Asp Lys Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys
705 710 715 720

Lys Thr Ile Thr Gly Val Phe Asn Ser Ser His Tyr Gly Tyr Asn Val
725 730 735

Val Val Lys Ile Pro Ala Gly Ala Thr Asn Val Asp Ile Arg Gln Tyr
740 745 750

Ser Tyr Ser Gly Gln Pro Asp Asp Ser Tyr Leu Ala Leu Ser Asp Ala
755 760 765

Glu Gly Asn Phe Leu Phe Asn Gly Asn Phe Leu Leu Ser Thr Ser Lys
770 775 780

Lys Glu Ile Asn Val Gln Gly Thr Arg Thr Val Ile Glu Tyr Ser Gly
785 790 795 800

Ser Asn Asn Ala Val Glu Arg Ile Asn Ser Thr Asn Arg Gln Glu Lys
805 810 815

Glu Leu Ile Leu Gln Val Leu Cys Val Gly Asn Leu Tyr Asn Pro Asp
820 825 830

Val His Tyr Ser Phe Asn Ile Pro Leu Glu Glu Arg Ser Asp Met Phe
835 840 845

Thr Trp Asp Pro Tyr Gly Pro Trp Glu Gly Cys Thr Lys Met Cys Gln
850 855 860

```
Gly Leu Gln Arg Arg Asn Ile Thr Cys Ile His Lys Ser Asp His Ser
865                 870                 875                 880

Val Val Ser Asp Lys Glu Cys Asp His Leu Pro Leu Pro Ser Phe Val
                885                 890                 895

Thr Gln Ser Cys Asn Thr Asp Cys Glu Leu Arg Trp His Val Ile Gly
            900                 905                 910

Lys Ser Glu Cys Ser Ser Gln Cys Gly Gln Gly Tyr Arg Thr Leu Asp
        915                 920                 925

Ile His Cys Met Lys Tyr Ser Ile His Glu Gly Gln Thr Val Gln Val
    930                 935                 940

Asp Asp His Tyr Cys Gly Asp Gln Leu Lys Pro Pro Thr Gln Glu Leu
945                 950                 955                 960

Cys His Gly Asn Cys Val Phe Thr Arg Trp His Tyr Ser Glu Trp Ser
                965                 970                 975

Gln Cys Ser Arg Ser Cys Gly Gly Gly Glu Arg Ser Arg Glu Ser Tyr
            980                 985                 990

Cys Met Asn Asn Phe Gly His Arg  Leu Ala Asp Asn Glu  Cys Gln
Glu
        995                 1000                1005

Leu Ser  Arg Val Thr Arg Glu  Asn Cys Asn Glu Phe  Ser Cys Pro
    1010                1015                1020

Ser Trp  Ala Ala Ser Glu Trp  Ser Glu Cys Leu Val  Thr Cys Gly
    1025                1030                1035

Lys Gly  Thr Lys Gln Arg Gln  Val Trp Cys Gln Leu  Asn Val Asp
    1040                1045                1050

His Leu  Ser Asp Gly Phe Cys  Asn Ser Ser Thr Lys  Pro Glu Ser
    1055                1060                1065

Leu Ser  Pro Cys Glu Leu His  Thr Cys Ala Ser Trp  Gln Val Gly
    1070                1075                1080
```

```
Pro Trp  Gly Pro Cys Thr Thr  Thr Cys Gly His Gly  Tyr Gln Met
    1085                1090                1095

Arg Asp  Val Lys Cys Val Asn  Glu Leu Ala Ser Ala  Val Leu Glu
    1100                1105                1110

Asp Thr  Glu Cys His Glu Ala  Ser Arg Pro Ser Asp  Arg Gln Ser
    1115                1120                1125

Cys Val  Leu Thr Pro Cys Ser  Phe Ile Ser Lys Leu  Glu Thr Ala
    1130                1135                1140

Leu Leu  Pro Thr Val Leu Ile  Lys Lys Met Ala Gln  Trp Arg His
    1145                1150                1155

Gly Ser  Trp Thr Pro Cys Ser  Val Ser Cys Gly Arg  Gly Thr Gln
    1160                1165                1170

Ala Arg  Tyr Val Ser Cys Arg  Asp Ala Leu Asp Arg  Ile Ala Asp
    1175                1180                1185

Glu Ser  Tyr Cys Ala His Leu  Pro Arg Pro Ala Glu  Ile Trp Asp
    1190                1195                1200

Cys Phe  Thr Pro Cys Gly Glu  Trp Gln Ala Gly Asp  Trp Ser Pro
    1205                1210                1215

Cys Ser  Ala Ser Cys Gly His  Gly Lys Thr Thr Arg  Gln Val Leu
    1220                1225                1230

Cys Met  Asn Tyr His Gln Pro  Ile Asp Glu Asn Tyr  Cys Asp Pro
    1235                1240                1245

Glu Val  Arg Pro Leu Met Glu  Gln Glu Cys Ser Leu  Ala Ala Cys
    1250                1255                1260

Pro Pro  Ala His Ser His Phe  Pro Ser Ser Pro Val  Gln Pro Ser
    1265                1270                1275

Tyr Tyr  Leu Ser Thr Asn Leu  Pro Leu Thr Gln Lys  Leu Glu Asp
    1280                1285                1290
```

```
Asn Glu  Asn Gln Val Val His  Pro Ser Val Arg Gly  Asn Gln Trp
    1295                1300                1305

Arg Thr  Gly Pro Trp Gly Ser  Cys Ser Ser Ser Cys  Ser Gly Gly
    1310                1315                1320

Leu Gln  His Arg Ala Val Val  Cys Gln Asp Glu Asn  Gly Gln Ser
    1325                1330                1335

Ala Ser  Tyr Cys Asp Ala Ala  Ser Lys Pro Pro Glu  Leu Gln Gln
    1340                1345                1350

Cys Gly  Pro Gly Pro Cys Pro  Gln Trp Asn Tyr Gly  Asn Trp Gly
    1355                1360                1365

Glu Cys  Ser Gln Thr Cys Gly  Gly Gly Ile Lys Ser  Arg Leu Val
    1370                1375                1380

Ile Cys  Gln Phe Pro Asn Gly  Gln Ile Leu Glu Asp  His Asn Cys
    1385                1390                1395

Glu Ile  Val Asn Lys Pro Pro  Ser Val Ile Gln Cys  His Met His
    1400                1405                1410

Ala Cys  Pro Ala Asp Val Ser  Trp His Gln Glu Pro  Trp Thr Ser
    1415                1420                1425

Glu Asp  Leu Lys Val Lys Leu  Leu Pro Gln Arg Thr  Ile Ile Leu
    1430                1435                1440

Trp Glu  Leu Met Lys Asn Ile  Phe Cys His Gly Lys  His Ser His
    1445                1450                1455

Met Tyr  Leu Ile Asn Val Val  Thr Asp His Leu Leu  Tyr Pro Arg
    1460                1465                1470

His Cys  Asp Pro Glu Thr Ile  Glu Thr Tyr Phe Leu  Ser Leu Trp
    1475                1480                1485

Ser Leu  Gln Phe Thr Trp Gly  Asp Leu Lys Tyr Tyr  Lys Asn Ser
    1490                1495                1500
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Leu

<210> 2302
<211> 1205
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ADAM metallopeptidase with thrombospondin type 1
motif, 3; "

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Met Val Leu Leu Ser Leu Trp Leu Ile Ala Ala Ala Leu Val Glu Val
1   5   10   15

Arg Thr Ser Ala Asp Gly Gln Ala Gly Asn Glu Glu Met Val Gln Ile
            20   25   30

Asp Leu Pro Ile Lys Arg Tyr Arg Glu Tyr Glu Leu Val Thr Pro Val
        35   40   45

Ser Thr Asn Leu Glu Gly Arg Tyr Leu Ser His Thr Leu Ser Ala Ser
    50   55   60

His Lys Lys Arg Ser Ala Arg Asp Val Ser Ser Asn Pro Glu Gln Leu
65   70   75   80

Phe Phe Asn Ile Thr Ala Phe Gly Lys Asp Phe His Leu Arg Leu Lys
                85   90   95

Pro Asn Thr Gln Leu Val Ala Pro Gly Ala Val Val Glu Trp His Glu

```
            100                 105                 110

Thr Ser Leu Val Pro Gly Asn Ile Thr Asp Pro Ile Asn Asn His Gln
        115                 120                 125

Pro Gly Ser Ala Thr Tyr Arg Ile Arg Arg Thr Glu Pro Leu Gln Thr
    130                 135                 140

Asn Cys Ala Tyr Val Gly Asp Ile Val Asp Ile Pro Gly Thr Ser Val
145                 150                 155                 160

Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly Met Ile Lys Ser Asp Asn
                165                 170                 175

Glu Glu Tyr Phe Ile Glu Pro Leu Glu Arg Gly Lys Gln Met Glu Glu
            180                 185                 190

Glu Lys Gly Arg Ile His Val Val Tyr Lys Arg Ser Ala Val Glu Gln
        195                 200                 205

Ala Pro Ile Asp Met Ser Lys Asp Phe His Tyr Arg Glu Ser Asp Leu
    210                 215                 220

Glu Gly Leu Asp Asp Leu Gly Thr Val Tyr Gly Asn Ile His Gln Gln
225                 230                 235                 240

Leu Asn Glu Thr Met Arg Arg Arg Arg His Ala Gly Glu Asn Asp Tyr
                245                 250                 255

Asn Ile Glu Val Leu Leu Gly Val Asp Asp Ser Val Val Arg Phe His
            260                 265                 270

Gly Lys Glu His Val Gln Asn Tyr Leu Leu Thr Leu Met Asn Ile Val
        275                 280                 285

Asn Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile Asn Val Val
    290                 295                 300

Leu Val Arg Met Ile Met Leu Gly Tyr Ala Lys Ser Ile Ser Leu Ile
305                 310                 315                 320

Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Asn Val Cys Arg Trp Ala
                325                 330                 335
```

```
Ser Gln Gln Gln Arg Ser Asp Leu Asn His Ser Glu His His Asp His
            340                 345                 350

Ala Ile Phe Leu Thr Arg Gln Asp Phe Gly Pro Ala Gly Met Gln Gly
        355                 360                 365

Tyr Ala Pro Val Thr Gly Met Cys His Pro Val Arg Ser Cys Thr Leu
    370                 375                 380

Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Val Ala His Glu Thr
385                 390                 395                 400

Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Arg Cys Gly
                405                 410                 415

Asp Glu Thr Ala Met Gly Ser Val Met Ala Pro Leu Val Gln Ala Ala
            420                 425                 430

Phe His Arg Tyr His Trp Ser Arg Cys Ser Gly Gln Glu Leu Lys Arg
        435                 440                 445

Tyr Ile His Ser Tyr Asp Cys Leu Leu Asp Asp Pro Phe Asp His Asp
    450                 455                 460

Trp Pro Lys Leu Pro Glu Leu Pro Gly Ile Asn Tyr Ser Met Asp Glu
465                 470                 475                 480

Gln Cys Arg Phe Asp Phe Gly Val Gly Tyr Lys Met Cys Thr Ala Phe
                485                 490                 495

Arg Thr Phe Asp Pro Cys Lys Gln Leu Trp Cys Ser His Pro Asp Asn
            500                 505                 510

Pro Tyr Phe Cys Lys Thr Lys Lys Gly Pro Pro Leu Asp Gly Thr Glu
        515                 520                 525

Cys Ala Ala Gly Lys Trp Cys Tyr Lys Gly His Cys Met Trp Lys Asn
    530                 535                 540

Ala Asn Gln Gln Lys Gln Asp Gly Asn Trp Gly Ser Trp Thr Lys Phe
545                 550                 555                 560
```

```
Gly Ser Cys Ser Arg Thr Cys Gly Thr Gly Val Arg Phe Arg Thr Arg
                565                 570                 575

Gln Cys Asn Asn Pro Met Pro Ile Asn Gly Gly Gln Asp Cys Pro Gly
            580                 585                 590

Val Asn Phe Glu Tyr Gln Leu Cys Asn Thr Glu Glu Cys Gln Lys His
        595                 600                 605

Phe Glu Asp Phe Arg Ala Gln Gln Cys Gln Gln Arg Asn Ser His Phe
    610                 615                 620

Glu Tyr Gln Asn Thr Lys His His Trp Leu Pro Tyr Glu His Pro Asp
625                 630                 635                 640

Pro Lys Lys Arg Cys His Leu Tyr Cys Gln Ser Lys Glu Thr Gly Asp
                645                 650                 655

Val Ala Tyr Met Lys Gln Leu Val His Asp Gly Thr His Cys Ser Tyr
            660                 665                 670

Lys Asp Pro Tyr Ser Ile Cys Val Arg Gly Glu Cys Val Lys Val Gly
        675                 680                 685

Cys Asp Lys Glu Ile Gly Ser Asn Lys Val Glu Asp Lys Cys Gly Val
    690                 695                 700

Cys Gly Gly Asp Asn Ser His Cys Arg Thr Val Lys Gly Thr Phe Thr
705                 710                 715                 720

Arg Thr Pro Arg Lys Leu Gly Tyr Leu Lys Met Phe Asp Ile Pro Pro
                725                 730                 735

Gly Ala Arg His Val Leu Ile Gln Glu Asp Glu Ala Ser Pro His Ile
            740                 745                 750

Leu Ala Ile Lys Asn Gln Ala Thr Gly His Tyr Ile Leu Asn Gly Lys
        755                 760                 765

Gly Glu Glu Ala Lys Ser Arg Thr Phe Ile Asp Leu Gly Val Glu Trp
    770                 775                 780
```

```
Asp Tyr Asn Ile Glu Asp Asp Ile Glu Ser Leu His Thr Asp Gly Pro
785                 790                 795                 800

Leu His Asp Pro Val Ile Val Leu Ile Ile Pro Gln Glu Asn Asp Thr
                805                 810                 815

Arg Ser Ser Leu Thr Tyr Lys Tyr Ile Ile His Glu Asp Ser Val Pro
            820                 825                 830

Thr Ile Asn Ser Asn Asn Val Ile Gln Glu Glu Leu Asp Thr Phe Glu
        835                 840                 845

Trp Ala Leu Lys Ser Trp Ser Gln Cys Ser Lys Pro Cys Gly Gly Gly
    850                 855                 860

Phe Gln Tyr Thr Lys Tyr Gly Cys Arg Arg Lys Ser Asp Asn Lys Met
865                 870                 875                 880

Val His Arg Ser Phe Cys Glu Ala Asn Lys Lys Pro Lys Pro Ile Arg
                885                 890                 895

Arg Met Cys Asn Ile Gln Glu Cys Thr His Pro Leu Trp Val Ala Glu
            900                 905                 910

Glu Trp Glu His Cys Thr Lys Thr Cys Gly Ser Ser Gly Tyr Gln Leu
        915                 920                 925

Arg Thr Val Arg Cys Leu Gln Pro Leu Leu Asp Gly Thr Asn Arg Ser
    930                 935                 940

Val His Ser Lys Tyr Cys Met Gly Asp Arg Pro Glu Ser Arg Arg Pro
945                 950                 955                 960

Cys Asn Arg Val Pro Cys Pro Ala Gln Trp Lys Thr Gly Pro Trp Ser
                965                 970                 975

Glu Cys Ser Val Thr Cys Gly Glu Gly Thr Glu Val Arg Gln Val Leu
            980                 985                 990

Cys Arg Ala Gly Asp His Cys Asp  Gly Glu Lys Pro Glu  Ser Val
Arg
        995                 1000                1005
```

```
Ala Cys  Gln Leu Pro Pro Cys  Asn Asp Glu Pro Cys  Leu Gly Asp
    1010                1015                1020

Lys Ser  Ile Phe Cys Gln Met  Glu Val Leu Ala Arg  Tyr Cys Ser
    1025                1030                1035

Ile Pro  Gly Tyr Asn Lys Leu  Cys Cys Glu Ser Cys  Ser Lys Arg
    1040                1045                1050

Ser Ser  Thr Leu Pro Pro Pro  Tyr Leu Leu Glu Ala  Ala Glu Thr
    1055                1060                1065

His Asp  Asp Val Ile Ser Asn  Pro Ser Asp Leu Pro  Arg Ser Leu
    1070                1075                1080

Val Met  Pro Thr Ser Leu Val  Pro Tyr His Ser Glu  Thr Pro Ala
    1085                1090                1095

Lys Lys  Met Ser Leu Ser Ser  Ile Ser Ser Val Gly  Gly Pro Asn
    1100                1105                1110

Ala Tyr  Ala Ala Phe Arg Pro  Asn Ser Lys Pro Asp  Gly Ala Asn
    1115                1120                1125

Leu Arg  Gln Arg Ser Ala Gln  Gln Ala Gly Ser Lys  Thr Val Arg
    1130                1135                1140

Leu Val  Thr Val Pro Ser Ser  Pro Pro Thr Lys Arg  Val His Leu
    1145                1150                1155

Ser Ser  Ala Ser Gln Met Ala  Ala Ala Ser Phe Phe  Ala Ala Ser
    1160                1165                1170

Asp Ser  Ile Gly Ala Ser Ser  Gln Ala Arg Thr Ser  Lys Lys Asp
    1175                1180                1185

Gly Lys  Ile Ile Asp Asn Arg  Arg Pro Thr Arg Ser  Ser Thr Leu
    1190                1195                1200

Glu Arg
    1205
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<210> 2303

<211> 1205
<212> PRT
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<220>
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<220>
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ADAM metallopeptidase with thrombospondin type 1
motif, 3; "

<220>
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<220>
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<400> 2303

Met	Val	Leu	Leu	Ser	Leu	Trp	Leu	Ile	Ala	Ala	Ala	Leu	Val	Glu	Val
1				5				10						15	
Arg	Thr	Ser	Ala	Asp	Gly	Gln	Ala	Gly	Asn	Glu	Glu	Met	Val	Gln	Ile
			20					25					30		
Asp	Leu	Pro	Ile	Lys	Arg	Tyr	Arg	Glu	Tyr	Glu	Leu	Val	Thr	Pro	Val
		35					40					45			
Ser	Thr	Asn	Leu	Glu	Gly	Arg	Tyr	Leu	Ser	His	Thr	Leu	Ser	Ala	Ser
	50					55					60				
His	Lys	Lys	Arg	Ser	Ala	Arg	Asp	Val	Ser	Ser	Asn	Pro	Glu	Gln	Leu
65					70					75					80
Phe	Phe	Asn	Ile	Thr	Ala	Phe	Gly	Lys	Asp	Phe	His	Leu	Arg	Leu	Lys
				85					90					95	
Pro	Asn	Thr	Gln	Leu	Val	Ala	Pro	Gly	Ala	Val	Val	Glu	Trp	His	Glu
			100					105					110		
Thr	Ser	Leu	Val	Pro	Gly	Asn	Ile	Thr	Asp	Pro	Ile	Asn	Asn	His	Gln
		115					120					125			

```
Pro Gly Ser Ala Thr Tyr Arg Ile Arg Arg Thr Glu Pro Leu Gln Thr
    130                 135                 140

Asn Cys Ala Tyr Val Gly Asp Ile Val Asp Ile Pro Gly Thr Ser Val
145                 150                 155                 160

Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly Met Ile Lys Ser Asp Asn
                165                 170                 175

Glu Glu Tyr Phe Ile Glu Pro Leu Glu Arg Gly Lys Gln Met Glu Glu
            180                 185                 190

Glu Lys Gly Arg Ile His Val Val Tyr Lys Arg Ser Ala Val Glu Gln
        195                 200                 205

Ala Pro Ile Asp Met Ser Lys Asp Phe His Tyr Arg Glu Ser Asp Leu
    210                 215                 220

Glu Gly Leu Asp Asp Leu Gly Thr Val Tyr Gly Asn Ile His Gln Gln
225                 230                 235                 240

Leu Asn Glu Thr Met Arg Arg Arg Arg His Ala Gly Glu Asn Asp Tyr
                245                 250                 255

Asn Ile Glu Val Leu Leu Gly Val Asp Asp Ser Val Val Arg Phe His
            260                 265                 270

Gly Lys Glu His Val Gln Asn Tyr Leu Leu Thr Leu Met Asn Ile Val
        275                 280                 285

Asn Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile Asn Val Val
    290                 295                 300

Leu Val Arg Met Ile Met Leu Gly Tyr Ala Lys Ser Ile Ser Leu Ile
305                 310                 315                 320

Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Asn Val Cys Arg Trp Ala
                325                 330                 335

Ser Gln Gln Gln Arg Ser Asp Leu Asn His Ser Glu His His Asp His
            340                 345                 350
```

```
Ala Ile Phe Leu Thr Arg Gln Asp Phe Gly Pro Ala Gly Met Gln Gly
        355                 360                 365

Tyr Ala Pro Val Thr Gly Met Cys His Pro Val Arg Ser Cys Thr Leu
    370                 375                 380

Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Val Ala His Glu Thr
385                 390                 395                 400

Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Arg Cys Gly
                405                 410                 415

Asp Glu Thr Ala Met Gly Ser Val Met Ala Pro Leu Val Gln Ala Ala
            420                 425                 430

Phe His Arg Tyr His Trp Ser Arg Cys Ser Gly Gln Glu Leu Lys Arg
        435                 440                 445

Tyr Ile His Ser Tyr Asp Cys Leu Leu Asp Asp Pro Phe Asp His Asp
    450                 455                 460

Trp Pro Lys Leu Pro Glu Leu Pro Gly Ile Asn Tyr Ser Met Asp Glu
465                 470                 475                 480

Gln Cys Arg Phe Asp Phe Gly Val Gly Tyr Lys Met Cys Thr Ala Phe
                485                 490                 495

Arg Thr Phe Asp Pro Cys Lys Gln Leu Trp Cys Ser His Pro Asp Asn
            500                 505                 510

Pro Tyr Phe Cys Lys Thr Lys Lys Gly Pro Pro Leu Asp Gly Thr Glu
        515                 520                 525

Cys Ala Ala Gly Lys Trp Cys Tyr Lys Gly His Cys Met Trp Lys Asn
    530                 535                 540

Ala Asn Gln Gln Lys Gln Asp Gly Asn Trp Gly Ser Trp Thr Lys Phe
545                 550                 555                 560

Gly Ser Cys Ser Arg Thr Cys Gly Thr Gly Val Arg Phe Arg Thr Arg
                565                 570                 575
```

```
Gln Cys Asn Asn Pro Met Pro Ile Asn Gly Gly Gln Asp Cys Pro Gly
            580                 585                 590

Val Asn Phe Glu Tyr Gln Leu Cys Asn Thr Glu Glu Cys Gln Lys His
        595                 600                 605

Phe Glu Asp Phe Arg Ala Gln Gln Cys Gln Gln Arg Asn Ser His Phe
    610                 615                 620

Glu Tyr Gln Asn Thr Lys His His Trp Leu Pro Tyr Glu His Pro Asp
625                 630                 635                 640

Pro Lys Lys Arg Cys His Leu Tyr Cys Gln Ser Lys Glu Thr Gly Asp
                645                 650                 655

Val Ala Tyr Met Lys Gln Leu Val His Asp Gly Thr His Cys Ser Tyr
            660                 665                 670

Lys Asp Pro Tyr Ser Ile Cys Val Arg Gly Glu Cys Val Lys Val Gly
        675                 680                 685

Cys Asp Lys Glu Ile Gly Ser Asn Lys Val Glu Asp Lys Cys Gly Val
    690                 695                 700

Cys Gly Gly Asp Asn Ser His Cys Arg Thr Val Lys Gly Thr Phe Thr
705                 710                 715                 720

Arg Thr Pro Arg Lys Leu Gly Tyr Leu Lys Met Phe Asp Ile Pro Pro
                725                 730                 735

Gly Ala Arg His Val Leu Ile Gln Glu Asp Glu Ala Ser Pro His Ile
            740                 745                 750

Leu Ala Ile Lys Asn Gln Ala Thr Gly His Tyr Ile Leu Asn Gly Lys
        755                 760                 765

Gly Glu Glu Ala Lys Ser Arg Thr Phe Ile Asp Leu Gly Val Glu Trp
    770                 775                 780

Asp Tyr Asn Ile Glu Asp Asp Ile Glu Ser Leu His Thr Asp Gly Pro
785                 790                 795                 800

Leu His Asp Pro Val Ile Val Leu Ile Ile Pro Gln Glu Asn Asp Thr
```

805 810 815

Arg Ser Ser Leu Thr Tyr Lys Tyr Ile Ile His Glu Asp Ser Val Pro
820 825 830

Thr Ile Asn Ser Asn Asn Val Ile Gln Glu Glu Leu Asp Thr Phe Glu
835 840 845

Trp Ala Leu Lys Ser Trp Ser Gln Cys Ser Lys Pro Cys Gly Gly Gly
850 855 860

Phe Gln Tyr Thr Lys Tyr Gly Cys Arg Arg Lys Ser Asp Asn Lys Met
865 870 875 880

Val His Arg Ser Phe Cys Glu Ala Asn Lys Lys Pro Lys Pro Ile Arg
885 890 895

Arg Met Cys Asn Ile Gln Glu Cys Thr His Pro Leu Trp Val Ala Glu
900 905 910

Glu Trp Glu His Cys Thr Lys Thr Cys Gly Ser Ser Gly Tyr Gln Leu
915 920 925

Arg Thr Val Arg Cys Leu Gln Pro Leu Leu Asp Gly Thr Asn Arg Ser
930 935 940

Val His Ser Lys Tyr Cys Met Gly Asp Arg Pro Glu Ser Arg Arg Pro
945 950 955 960

Cys Asn Arg Val Pro Cys Pro Ala Gln Trp Lys Thr Gly Pro Trp Ser
965 970 975

Glu Cys Ser Val Thr Cys Gly Glu Gly Thr Glu Val Arg Gln Val Leu
980 985 990

Cys Arg Ala Gly Asp His Cys Asp Gly Glu Lys Pro Glu Ser Val
Arg
995 1000 1005

Ala Cys Gln Leu Pro Pro Cys Asn Asp Glu Pro Cys Leu Gly Asp
1010 1015 1020

Lys Ser Ile Phe Cys Gln Met Glu Val Leu Ala Arg Tyr Cys Ser

1025 1030 1035

Ile Pro Gly Tyr Asn Lys Leu Cys Cys Glu Ser Cys Ser Lys Arg
1040 1045 1050

Ser Ser Thr Leu Pro Pro Pro Tyr Leu Leu Glu Ala Ala Glu Thr
1055 1060 1065

His Asp Asp Val Ile Ser Asn Pro Ser Asp Leu Pro Arg Ser Leu
1070 1075 1080

Val Met Pro Thr Ser Leu Val Pro Tyr His Ser Glu Thr Pro Ala
1085 1090 1095

Lys Lys Met Ser Leu Ser Ser Ile Ser Ser Val Gly Gly Pro Asn
1100 1105 1110

Ala Tyr Ala Ala Phe Arg Pro Asn Ser Lys Pro Asp Gly Ala Asn
1115 1120 1125

Leu Arg Gln Arg Ser Ala Gln Gln Ala Gly Ser Lys Thr Val Arg
1130 1135 1140

Leu Val Thr Val Pro Ser Ser Pro Pro Thr Lys Arg Val His Leu
1145 1150 1155

Ser Ser Ala Ser Gln Met Ala Ala Ala Ser Phe Phe Ala Ala Ser
1160 1165 1170

Asp Ser Ile Gly Ala Ser Ser Gln Ala Arg Thr Ser Lys Lys Asp
1175 1180 1185

Gly Lys Ile Ile Asp Asn Arg Arg Pro Thr Arg Ser Ser Thr Leu
1190 1195 1200

Glu Arg
1205

<210> 2304
<211> 339
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 570; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS4; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356974"

<400> 2304

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg	Trp
1				5				10						15	
Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro	Leu	Ser
			20					25					30		
Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	Leu	Pro	Ser
		35					40					45			
Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	Ile	Val	Phe	Pro
	50					55					60				
Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	Gly	Ala	Pro	Ala	Arg
65					70					75					80
Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	Thr	Leu	Leu	Leu	Glu	Leu
				85					90					95	
Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	Gly	Leu	Thr	Val	Gln	Tyr	Leu
			100					105					110		
Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu
		115					120					125			
Thr	Gly	Thr	Ile	Asn	Gly	Asp	Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp
	130					135					140				
Asp	Gly	Gly	Ala	Leu	Leu	Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu
145					150					155					160

```
His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro
                165                 170                 175

Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro
            180                 185                 190

Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg
        195                 200                 205

Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val
    210                 215                 220

Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
225                 230                 235                 240

Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro
                245                 250                 255

Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu
            260                 265                 270

Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr
        275                 280                 285

Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp
    290                 295                 300

Ser Asp Pro Asp His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Val
305                 310                 315                 320

Arg Pro Gln Ser Ala Pro Gln Ala Met His Cys Thr Ile Leu Arg Ser
                325                 330                 335

Ala Thr Thr
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<210> 2305
<211> 837
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 570; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS4; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 4; "

<220>
<221> source
<223> /note="Uniprot ID: O75173; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000356975"

<400> 2305
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp
1   5   10   15

Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro Leu Ser
            20   25   30

Trp Leu Val Trp Leu Leu Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser
        35   40   45

Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro
    50   55   60

Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg
65   70   75   80

Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu Thr Leu Leu Leu Glu Leu
                85   90   95

Glu Gln Asp Ser Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu
            100   105   110

Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu
        115   120   125

Thr Gly Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp
    130   135   140

Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu

145 150 155 160

His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro
165 170 175

Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro
180 185 190

Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg
195 200 205

Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val
210 215 220

Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
225 230 235 240

Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro
245 250 255

Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu
260 265 270

Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr
275 280 285

Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp
290 295 300

Ser Asp Pro Asp His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
305 310 315 320

Leu Cys Gly Val Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
325 330 335

Thr Val Cys Asp Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly
340 345 350

Leu Gln Ser Ala Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn
355 360 365

Met Leu His Asp Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu
370 375 380

```
Ser Thr Ser Arg His Val Met Ala Pro Val Met Ala His Val Asp Pro
385                 390                 395                 400

Glu Glu Pro Trp Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu
                405                 410                 415

Asp Asn Gly Tyr Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu
            420                 425                 430

His Leu Pro Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln
        435                 440                 445

Cys Gln Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro
    450                 455                 460

Pro Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
465                 470                 475                 480

Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys Gly
                485                 490                 495

Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp Gln Leu
            500                 505                 510

Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro Trp Gly Pro
        515                 520                 525

Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Gln Phe Ser Ser
    530                 535                 540

Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly Gly Lys Tyr Cys Glu
545                 550                 555                 560

Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn Thr Glu Asp Cys Pro Thr
                565                 570                 575

Gly Ser Ala Leu Thr Phe Arg Glu Glu Gln Cys Ala Ala Tyr Asn His
            580                 585                 590

Arg Thr Asp Leu Phe Lys Ser Phe Pro Gly Pro Met Asp Trp Val Pro
        595                 600                 605
```

```
Arg Tyr Thr Gly Val Ala Pro Gln Asp Gln Cys Lys Leu Thr Cys Gln
    610                 615                 620

Ala Gln Ala Leu Gly Tyr Tyr Tyr Val Leu Glu Pro Arg Val Val Asp
625                 630                 635                 640

Gly Thr Pro Cys Ser Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg
                645                 650                 655

Cys Ile His Ala Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe
            660                 665                 670

Asp Lys Cys Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln
        675                 680                 685

Ser Gly Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr
    690                 695                 700

Ile Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
705                 710                 715                 720

Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser Tyr
                725                 730                 735

Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp Val Val
            740                 745                 750

Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr Ala Ala Ser
        755                 760                 765

Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro Leu Thr Leu Gln
    770                 775                 780

Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe
785                 790                 795                 800

Phe Val Pro Arg Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp
                805                 810                 815

Trp Leu His Arg Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Arg Pro
            820                 825                 830
```

Trp Ala Gly Arg Lys
835

<210> 2306
<211> 930
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 571; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS5; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 5; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UNA0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000284987"

<400> 2306
Met Leu Leu Gly Trp Ala Ser Leu Leu Leu Cys Ala Phe Arg Leu Pro
1 5 10 15

Leu Ala Ala Val Gly Pro Ala Ala Thr Pro Ala Gln Asp Lys Ala Gly
20 25 30

Gln Pro Pro Thr Ala Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly
35 40 45

Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu
50 55 60

Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu
65 70 75 80

Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg
85 90 95

Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly

```
            100                 105                 110

Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser
        115                 120                 125

His Cys Phe Tyr Arg Gly Thr Val Asp Gly Ser Pro Arg Ser Leu Ala
    130                 135                 140

Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His
145                 150                 155                 160

Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu
                165                 170                 175

Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val
            180                 185                 190

Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser
        195                 200                 205

Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala
    210                 215                 220

His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp
225                 230                 235                 240

Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp
                245                 250                 255

Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu
            260                 265                 270

Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln
        275                 280                 285

His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His
    290                 295                 300

Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val
305                 310                 315                 320

Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr
                325                 330                 335
```

```
Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly
            340                 345                 350

Asp Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu
        355                 360                 365

Asp Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val
    370                 375                 380

Gly Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp
385                 390                 395                 400

Gly Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu
                405                 410                 415

Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser
            420                 425                 430

Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala
        435                 440                 445

Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu
    450                 455                 460

Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile
465                 470                 475                 480

Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln
                485                 490                 495

Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp
            500                 505                 510

Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val
        515                 520                 525

Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys
    530                 535                 540

Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys
545                 550                 555                 560
```

Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp
565 570 575

Gly Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg
580 585 590

His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly
595 600 605

Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn
610 615 620

Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln
625 630 635 640

Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr
645 650 655

Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys
660 665 670

Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr
675 680 685

Glu Cys Arg Leu Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val
690 695 700

Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys
705 710 715 720

Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly
725 730 735

Thr Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro
740 745 750

Glu Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln
755 760 765

Thr Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr
770 775 780

```
Leu Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp
785                 790                 795                 800

Ile Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp
                805                 810                 815

Phe Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val
            820                 825                 830

Gln Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser
        835                 840                 845

Phe Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser
    850                 855                 860

His Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val
865                 870                 875                 880

Thr Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His
                885                 890                 895

Thr Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly
            900                 905                 910

Cys Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys
        915                 920                 925

Lys Cys
    930


<210> 2307
<211> 1117
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 572; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS6; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
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motif, 6; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKP5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000370443"

<400> 2307
Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
1   5   10   15

Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
            20   25   30

Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
        35   40   45

Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
    50   55   60

Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
65   70   75   80

Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
                85   90   95

His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
            100   105   110

Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
        115   120   125

Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
    130   135   140

Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
145   150   155   160

Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
                165   170   175

Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
            180   185   190

```
Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
        195                 200                 205

Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
    210                 215                 220

Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
225                 230                 235                 240

Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
                245                 250                 255

Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
            260                 265                 270

His Tyr Ile Leu Ser Val Met Asn Ile Val Ala Lys Leu Tyr Arg Asp
        275                 280                 285

Ser Ser Leu Gly Asn Val Val Asn Ile Ile Val Ala Arg Leu Ile Val
    290                 295                 300

Leu Thr Glu Asp Gln Pro Asn Leu Glu Ile Asn His His Ala Asp Lys
305                 310                 315                 320

Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser Ile Leu Ser His Gln
                325                 330                 335

Ser Asp Gly Asn Thr Ile Pro Glu Asn Gly Ile Ala His His Asp Asn
            340                 345                 350

Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Thr Tyr Lys Asn Lys Pro
        355                 360                 365

Cys Gly Thr Leu Gly Leu Ala Ser Val Ala Gly Met Cys Glu Pro Glu
    370                 375                 380

Arg Ser Cys Ser Ile Asn Glu Asp Ile Gly Leu Gly Ser Ala Phe Thr
385                 390                 395                 400

Ile Ala His Glu Ile Gly His Asn Phe Gly Met Asn His Asp Gly Ile
                405                 410                 415
```

```
Gly Asn Ser Cys Gly Thr Lys Gly His Glu Ala Ala Lys Leu Met Ala
            420                 425                 430

Ala His Ile Thr Ala Asn Thr Asn Pro Phe Ser Trp Ser Ala Cys Ser
        435                 440                 445

Arg Asp Tyr Ile Thr Ser Phe Leu Asp Ser Gly Arg Gly Thr Cys Leu
    450                 455                 460

Asp Asn Glu Pro Pro Lys Arg Asp Phe Leu Tyr Pro Ala Val Ala Pro
465                 470                 475                 480

Gly Gln Val Tyr Asp Ala Asp Glu Gln Cys Arg Phe Gln Tyr Gly Ala
                485                 490                 495

Thr Ser Arg Gln Cys Lys Tyr Gly Glu Val Cys Arg Glu Leu Trp Cys
            500                 505                 510

Leu Ser Lys Ser Asn Arg Cys Val Thr Asn Ser Ile Pro Ala Ala Glu
        515                 520                 525

Gly Thr Leu Cys Gln Thr Gly Asn Ile Glu Lys Gly Trp Cys Tyr Gln
    530                 535                 540

Gly Asp Cys Val Pro Phe Gly Thr Trp Pro Gln Ser Ile Asp Gly Gly
545                 550                 555                 560

Trp Gly Pro Trp Ser Leu Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
                565                 570                 575

Gly Val Ser Ser Ser Leu Arg His Cys Asp Ser Pro Ala Pro Ser Gly
            580                 585                 590

Gly Gly Lys Tyr Cys Leu Gly Glu Arg Lys Arg Tyr Arg Ser Cys Asn
        595                 600                 605

Thr Asp Pro Cys Pro Leu Gly Ser Arg Asp Phe Arg Glu Lys Gln Cys
    610                 615                 620

Ala Asp Phe Asp Asn Met Pro Phe Arg Gly Lys Tyr Tyr Asn Trp Lys
625                 630                 635                 640
```

```
Pro Tyr Thr Gly Gly Gly Val Lys Pro Cys Ala Leu Asn Cys Leu Ala
                645                 650                 655

Glu Gly Tyr Asn Phe Tyr Thr Glu Arg Ala Pro Ala Val Ile Asp Gly
            660                 665                 670

Thr Gln Cys Asn Ala Asp Ser Leu Asp Ile Cys Ile Asn Gly Glu Cys
        675                 680                 685

Lys His Val Gly Cys Asp Asn Ile Leu Gly Ser Asp Ala Arg Glu Asp
    690                 695                 700

Arg Cys Arg Val Cys Gly Gly Asp Gly Ser Thr Cys Asp Ala Ile Glu
705                 710                 715                 720

Gly Phe Phe Asn Asp Ser Leu Pro Arg Gly Gly Tyr Met Glu Val Val
                725                 730                 735

Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met
            740                 745                 750

Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile
        755                 760                 765

Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly
    770                 775                 780

Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu
785                 790                 795                 800

Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln
                805                 810                 815

Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg
            820                 825                 830

Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro
        835                 840                 845

Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Val Gln Arg Gln Glu
    850                 855                 860

Val Val Cys Lys Arg Leu Asp Asp Asn Ser Ile Val Gln Asn Asn Tyr
```

865 870 875 880

Cys Asp Pro Asp Ser Lys Pro Pro Glu Asn Gln Arg Ala Cys Asn Thr
885 890 895

Glu Pro Cys Pro Pro Glu Trp Phe Ile Gly Asp Trp Leu Glu Cys Ser
900 905 910

Lys Thr Cys Asp Gly Gly Met Arg Thr Arg Ala Val Leu Cys Ile Arg
915 920 925

Lys Ile Gly Pro Ser Glu Glu Glu Thr Leu Asp Tyr Ser Gly Cys Leu
930 935 940

Thr His Arg Pro Val Glu Lys Glu Pro Cys Asn Asn Gln Ser Cys Pro
945 950 955 960

Pro Gln Trp Val Ala Leu Asp Trp Ser Glu Cys Thr Pro Lys Cys Gly
965 970 975

Pro Gly Phe Lys His Arg Ile Val Leu Cys Lys Ser Ser Asp Leu Ser
980 985 990

Lys Thr Phe Pro Ala Ala Gln Cys Pro Glu Glu Ser Lys Pro Pro
Val
995 1000 1005

Arg Ile Arg Cys Ser Leu Gly Arg Cys Pro Pro Pro Arg Trp Val
1010 1015 1020

Thr Gly Asp Trp Gly Gln Cys Ser Ala Gln Cys Gly Leu Gly Gln
1025 1030 1035

Gln Met Arg Thr Val Gln Cys Leu Ser Tyr Thr Gly Gln Ala Ser
1040 1045 1050

Ser Asp Cys Leu Glu Thr Val Arg Pro Pro Ser Met Gln Gln Cys
1055 1060 1065

Glu Ser Lys Cys Asp Ser Thr Pro Ile Ser Asn Thr Glu Glu Cys
1070 1075 1080

Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val Leu Lys Phe

1085 1090 1095

Lys Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys Thr
1100 1105 1110

Cys Gln Gly His
1115

<210> 2308
<211> 292
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ADAMTS6; "

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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 6; "

<220>
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<223> /note="Uniprot ID: Q9UKP5; "

<220>
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<400> 2308
Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
1 5 10 15

Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
20 25 30

Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
35 40 45

Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
50 55 60

Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
65 70 75 80

```
Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
                85                  90                  95

His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
            100                 105                 110

Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
        115                 120                 125

Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
    130                 135                 140

Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
145                 150                 155                 160

Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
                165                 170                 175

Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
            180                 185                 190

Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
        195                 200                 205

Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
    210                 215                 220

Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
225                 230                 235                 240

Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
                245                 250                 255

Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
            260                 265                 270

His Tyr Ile Leu Ser Val Met Asn Ile Val Arg Leu Pro Asn Phe Thr
        275                 280                 285

Val Ile Pro Ala
    290
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<210> 2309
<211> 1686
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ADAMTS7; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 7; "

<220>
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<223> /note="Uniprot ID: Q9UKP4; "

<220>
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<223> /note="ENSP ID: ENSP00000373472"

<400> 2309

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Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro
1               5                  10                  15


Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala
            20                  25                  30


Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro
        35                  40                  45


Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro
    50                  55                  60


Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala
65                  70                  75                  80


Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr
                85                  90                  95


Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg
            100                 105                 110
```

```
Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys
        115                 120                 125

His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala
    130                 135                 140

Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn
145                 150                 155                 160

Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly
                165                 170                 175

His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu
            180                 185                 190

Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val
        195                 200                 205

Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln
    210                 215                 220

Trp Arg Arg Pro Arg Leu Arg Arg Leu His Gln Arg Ser Val Ser Lys
225                 230                 235                 240

Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys Met Val Glu
                245                 250                 255

Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr Ile Met Asn
            260                 265                 270

Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn Pro Ile His
        275                 280                 285

Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu Glu Asp Leu
    290                 295                 300

Lys Ile Thr His His Ala Asp Asn Thr Leu Lys Ser Phe Cys Lys Trp
305                 310                 315                 320

Gln Lys Ser Ile Asn Met Lys Gly Asp Ala His Pro Leu His His Asp
                325                 330                 335

Thr Ala Ile Leu Leu Thr Arg Lys Asp Leu Cys Ala Ala Met Asn Arg
```

```
            340                 345                 350

Pro Cys Glu Thr Leu Gly Leu Ser His Val Ala Gly Met Cys Gln Pro
        355                 360                 365

His Arg Ser Cys Ser Ile Asn Glu Asp Thr Gly Leu Pro Leu Ala Phe
    370                 375                 380

Thr Val Ala His Glu Leu Gly His Ser Phe Gly Ile Gln His Asp Gly
385                 390                 395                 400

Ser Gly Asn Asp Cys Glu Pro Val Gly Lys Arg Pro Phe Ile Met Ser
                405                 410                 415

Pro Gln Leu Leu Tyr Asp Ala Ala Pro Leu Thr Trp Ser Arg Cys Ser
            420                 425                 430

Arg Gln Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp Gly Leu Cys Leu
        435                 440                 445

Asp Asp Pro Pro Ala Lys Asp Ile Ile Asp Phe Pro Ser Val Pro Pro
    450                 455                 460

Gly Val Leu Tyr Asp Val Ser His Gln Cys Arg Leu Gln Tyr Gly Ala
465                 470                 475                 480

Tyr Ser Ala Phe Cys Glu Asp Met Asp Asn Val Cys His Thr Leu Trp
                485                 490                 495

Cys Ser Val Gly Thr Thr Cys His Ser Lys Leu Asp Ala Ala Val Asp
            500                 505                 510

Gly Thr Arg Cys Gly Glu Asn Lys Trp Cys Leu Ser Gly Glu Cys Val
        515                 520                 525

Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp Ser Gly Trp
    530                 535                 540

Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly Val Gln Ser
545                 550                 555                 560

Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys Gly Arg Tyr
                565                 570                 575
```

```
Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu Gln Ala Cys
            580                 585                 590

Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser His Phe Asp
        595                 600                 605

Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn
    610                 615                 620

Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe
625                 630                 635                 640

Ala Glu Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln
                645                 650                 655

Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val
            660                 665                 670

Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly
        675                 680                 685

Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe
    690                 695                 700

Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala
705                 710                 715                 720

Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe
                725                 730                 735

Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly
            740                 745                 750

Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe
        755                 760                 765

Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro
    770                 775                 780

Thr Lys Glu Pro Val Trp Ile Gln Leu Leu Phe Gln Glu Ser Asn Pro
785                 790                 795                 800
```

```
Gly Val His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp
                805                 810                 815

Glu Val Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys
            820                 825                 830

Cys Thr Val Thr Cys Gly Arg Gly Val Gln Arg Gln Asn Val Tyr Cys
        835                 840                 845

Leu Glu Arg Gln Ala Gly Pro Val Asp Glu Glu His Cys Asp Pro Leu
    850                 855                 860

Gly Arg Pro Asp Asp Gln Gln Arg Lys Cys Ser Glu Gln Pro Cys Pro
865                 870                 875                 880

Ala Arg Trp Trp Ala Gly Glu Trp Gln Leu Cys Ser Ser Ser Cys Gly
                885                 890                 895

Pro Gly Gly Leu Ser Arg Arg Ala Val Leu Cys Ile Arg Ser Val Gly
            900                 905                 910

Leu Asp Glu Gln Ser Ala Leu Glu Pro Pro Ala Cys Glu His Leu Pro
        915                 920                 925

Arg Pro Pro Thr Glu Thr Pro Cys Asn Arg His Val Pro Cys Pro Ala
    930                 935                 940

Thr Trp Ala Val Gly Asn Trp Ser Gln Cys Ser Val Thr Cys Gly Glu
945                 950                 955                 960

Gly Thr Gln Arg Arg Asn Val Leu Cys Thr Asn Asp Thr Gly Val Pro
                965                 970                 975

Cys Asp Glu Ala Gln Gln Pro Ala Ser Glu Val Thr Cys Ser Leu Pro
            980                 985                 990

Leu Cys Arg Trp Pro Leu Gly Thr  Leu Gly Pro Glu Gly  Ser Gly
Ser
        995                 1000                1005

Gly Ser  Ser Ser His Glu Leu  Phe Asn Glu Ala Asp  Phe Ile Pro
    1010                1015                1020
```

```
His His  Leu Ala Pro Arg Pro  Ser Pro Ala Ser Ser  Pro Lys Pro
    1025                1030                1035

Gly Thr  Met Gly Asn Ala Ile  Glu Glu Glu Ala Pro  Glu Leu Asp
    1040                1045                1050

Leu Pro  Gly Pro Val Phe Val  Asp Asp Phe Tyr Tyr  Asp Tyr Asn
    1055                1060                1065

Phe Ile  Asn Phe His Glu Asp  Leu Ser Tyr Gly Pro  Ser Glu Glu
    1070                1075                1080

Pro Asp  Leu Asp Leu Ala Gly  Thr Gly Asp Arg Thr  Pro Pro Pro
    1085                1090                1095

His Ser  His Pro Ala Ala Pro  Ser Thr Gly Ser Pro  Val Pro Ala
    1100                1105                1110

Thr Glu  Pro Pro Ala Ala Lys  Glu Glu Gly Val Leu  Gly Pro Trp
    1115                1120                1125

Ser Pro  Ser Pro Trp Pro Ser  Gln Ala Gly Arg Ser  Pro Pro Pro
    1130                1135                1140

Pro Ser  Glu Gln Thr Pro Gly  Asn Pro Leu Ile Asn  Phe Leu Pro
    1145                1150                1155

Glu Glu  Asp Thr Pro Ile Gly  Ala Pro Asp Leu Gly  Leu Pro Ser
    1160                1165                1170

Leu Ser  Trp Pro Arg Val Ser  Thr Asp Gly Leu Gln  Thr Pro Ala
    1175                1180                1185

Thr Pro  Glu Ser Gln Asn Asp  Phe Pro Val Gly Lys  Asp Ser Gln
    1190                1195                1200

Ser Gln  Leu Pro Pro Pro Trp  Arg Asp Arg Thr Asn  Glu Val Phe
    1205                1210                1215

Lys Asp  Asp Glu Glu Pro Lys  Gly Arg Gly Ala Pro  His Leu Pro
    1220                1225                1230
```

```
Pro Arg  Pro Ser Ser Thr Leu  Pro Pro Leu Ser Pro  Val Gly Ser
    1235                1240                1245

Thr His  Ser Ser Pro Ser Pro  Asp Val Ala Glu Leu  Trp Thr Gly
    1250                1255                1260

Gly Thr  Val Ala Trp Glu Pro  Ala Leu Glu Gly Gly  Leu Gly Pro
    1265                1270                1275

Val Asp  Ser Glu Leu Trp Pro  Thr Val Gly Val Ala  Ser Leu Leu
    1280                1285                1290

Pro Pro  Pro Ile Ala Pro Leu  Pro Glu Met Lys Val  Arg Asp Ser
    1295                1300                1305

Ser Leu  Glu Pro Gly Thr Pro  Ser Phe Pro Thr Pro  Gly Pro Gly
    1310                1315                1320

Ser Trp  Asp Leu Gln Thr Val  Ala Val Trp Gly Thr  Phe Leu Pro
    1325                1330                1335

Thr Thr  Leu Thr Gly Leu Gly  His Met Pro Glu Pro  Ala Leu Asn
    1340                1345                1350

Pro Gly  Pro Lys Gly Gln Pro  Glu Ser Leu Ser Pro  Glu Val Pro
    1355                1360                1365

Leu Ser  Ser Arg Leu Leu Ser  Thr Pro Ala Trp Asp  Ser Pro Ala
    1370                1375                1380

Asn Ser  His Arg Val Pro Glu  Thr Gln Pro Leu Ala  Pro Ser Leu
    1385                1390                1395

Ala Glu  Ala Gly Pro Pro Ala  Asp Pro Leu Val Val  Arg Asn Ala
    1400                1405                1410

Gly Trp  Gln Ala Gly Asn Trp  Ser Glu Cys Ser Thr  Thr Cys Gly
    1415                1420                1425

Leu Gly  Ala Val Trp Arg Pro  Val Arg Cys Ser Ser  Gly Arg Asp
    1430                1435                1440

Glu Asp  Cys Ala Pro Ala Gly  Arg Pro Gln Pro Ala  Arg Arg Cys
```

1445 1450 1455

His Leu Arg Pro Cys Ala Thr Trp His Ser Gly Asn Trp Ser Lys
1460 1465 1470

Cys Ser Arg Ser Cys Gly Gly Gly Ser Ser Val Arg Asp Val Gln
1475 1480 1485

Cys Val Asp Thr Arg Asp Leu Arg Pro Leu Arg Pro Phe His Cys
1490 1495 1500

Gln Pro Gly Pro Ala Lys Pro Pro Ala His Arg Pro Cys Gly Ala
1505 1510 1515

Gln Pro Cys Leu Ser Trp Tyr Thr Ser Ser Trp Arg Glu Cys Ser
1520 1525 1530

Glu Ala Cys Gly Gly Gly Glu Gln Gln Arg Leu Val Thr Cys Pro
1535 1540 1545

Glu Pro Gly Leu Cys Glu Glu Ala Leu Arg Pro Asn Thr Thr Arg
1550 1555 1560

Pro Cys Asn Thr His Pro Cys Thr Gln Trp Val Val Gly Pro Trp
1565 1570 1575

Gly Gln Cys Ser Gly Pro Cys Gly Gly Gly Val Gln Arg Arg Leu
1580 1585 1590

Val Lys Cys Val Asn Thr Gln Thr Gly Leu Pro Glu Glu Asp Ser
1595 1600 1605

Asp Gln Cys Gly His Glu Ala Trp Pro Glu Ser Ser Arg Pro Cys
1610 1615 1620

Gly Thr Glu Asp Cys Glu Pro Val Glu Pro Pro Arg Cys Glu Arg
1625 1630 1635

Asp Arg Leu Ser Phe Gly Phe Cys Glu Thr Leu Arg Leu Leu Gly
1640 1645 1650

Arg Cys Gln Leu Pro Thr Ile Arg Thr Gln Cys Cys Arg Ser Cys
1655 1660 1665

```
Ser Pro  Pro Ser His Gly Ala  Pro Ser Arg Gly His  Gln Arg Val
    1670                1675                1680


Ala Arg  Arg
    1685


<210> 2310
<211> 889
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ADAMTS8; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 8; "

<220>
<221> source
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<220>
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Met Leu Pro Ala Pro Ala Ala Pro Arg Trp Pro Pro Leu Leu Leu Leu
1               5                  10                  15


Leu Leu Leu Leu Leu Pro Leu Ala Arg Gly Ala Pro Ala Arg Pro Ala
            20                  25                  30


Ala Gly Gly Gln Ala Ser Glu Leu Val Val Pro Thr Arg Leu Pro Gly
        35                  40                  45


Ser Ala Gly Glu Leu Ala Leu His Leu Ser Ala Phe Gly Lys Gly Phe
    50                  55                  60


Val Leu Arg Leu Ala Pro Asp Asp Ser Phe Leu Ala Pro Glu Phe Lys
65                  70                  75                  80
```

```
Ile Glu Arg Leu Gly Gly Ser Gly Arg Ala Thr Gly Gly Glu Arg Gly
                85                  90                  95

Leu Arg Gly Cys Phe Phe Ser Gly Thr Val Asn Gly Glu Pro Glu Ser
            100                 105                 110

Leu Ala Ala Val Ser Leu Cys Arg Gly Leu Ser Gly Ser Phe Leu Leu
        115                 120                 125

Asp Gly Glu Glu Phe Thr Ile Gln Pro Gln Gly Ala Gly Gly Ser Leu
    130                 135                 140

Ala Gln Pro His Arg Leu Gln Arg Trp Gly Pro Ala Gly Ala Arg Pro
145                 150                 155                 160

Leu Pro Arg Gly Pro Glu Trp Glu Val Glu Thr Gly Glu Gly Gln Arg
                165                 170                 175

Gln Glu Arg Gly Asp His Gln Glu Asp Ser Glu Glu Glu Ser Gln Glu
            180                 185                 190

Glu Glu Ala Glu Gly Ala Ser Glu Pro Pro Pro Pro Leu Gly Ala Thr
        195                 200                 205

Ser Arg Thr Lys Arg Phe Val Ser Glu Ala Arg Phe Val Glu Thr Leu
    210                 215                 220

Leu Val Ala Asp Ala Ser Met Ala Ala Phe Tyr Gly Ala Asp Leu Gln
225                 230                 235                 240

Asn His Ile Leu Thr Leu Met Ser Val Ala Ala Arg Ile Tyr Lys His
                245                 250                 255

Pro Ser Ile Lys Asn Ser Ile Asn Leu Met Val Val Lys Val Leu Ile
            260                 265                 270

Val Glu Asp Glu Lys Trp Gly Pro Glu Val Ser Asp Asn Gly Gly Leu
        275                 280                 285

Thr Leu Arg Asn Phe Cys Asn Trp Gln Arg Arg Phe Asn Gln Pro Ser
    290                 295                 300
```

```
Asp Arg His Pro Glu His Tyr Asp Thr Ala Ile Leu Leu Thr Arg Gln
305                 310                 315                 320

Asn Phe Cys Gly Gln Glu Gly Leu Cys Asp Thr Leu Gly Val Ala Asp
                325                 330                 335

Ile Gly Thr Ile Cys Asp Pro Asn Lys Ser Cys Ser Val Ile Glu Asp
            340                 345                 350

Glu Gly Leu Gln Ala Ala His Thr Leu Ala His Glu Leu Gly His Val
        355                 360                 365

Leu Ser Met Pro His Asp Asp Ser Lys Pro Cys Thr Arg Leu Phe Gly
    370                 375                 380

Pro Met Gly Lys His His Val Met Ala Pro Leu Phe Val His Leu Asn
385                 390                 395                 400

Gln Thr Leu Pro Trp Ser Pro Cys Ser Ala Met Tyr Leu Thr Glu Leu
                405                 410                 415

Leu Asp Gly Gly His Gly Asp Cys Leu Leu Asp Ala Pro Ala Ala Ala
            420                 425                 430

Leu Pro Leu Pro Thr Gly Leu Pro Gly Arg Met Ala Leu Tyr Gln Leu
        435                 440                 445

Asp Gln Gln Cys Arg Gln Ile Phe Gly Pro Asp Phe Arg His Cys Pro
    450                 455                 460

Asn Thr Ser Ala Gln Asp Val Cys Ala Gln Leu Trp Cys His Thr Asp
465                 470                 475                 480

Gly Ala Glu Pro Leu Cys His Thr Lys Asn Gly Ser Leu Pro Trp Ala
                485                 490                 495

Asp Gly Thr Pro Cys Gly Pro Gly His Leu Cys Ser Glu Gly Ser Cys
            500                 505                 510

Leu Pro Glu Glu Glu Val Glu Arg Pro Lys Pro Val Ala Asp Gly Gly
        515                 520                 525

Trp Ala Pro Trp Gly Pro Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
```

```
    530                 535                 540

Gly Val Gln Phe Ser His Arg Glu Cys Lys Asp Pro Glu Pro Gln Asn
545                 550                 555                 560

Gly Gly Arg Tyr Cys Leu Gly Arg Arg Ala Lys Tyr Gln Ser Cys His
                565                 570                 575

Thr Glu Glu Cys Pro Pro Asp Gly Lys Ser Phe Arg Glu Gln Gln Cys
            580                 585                 590

Glu Lys Tyr Asn Ala Tyr Asn Tyr Thr Asp Met Asp Gly Asn Leu Leu
        595                 600                 605

Gln Trp Val Pro Lys Tyr Ala Gly Val Ser Pro Arg Asp Arg Cys Lys
    610                 615                 620

Leu Phe Cys Arg Ala Arg Gly Arg Ser Glu Phe Lys Val Phe Glu Ala
625                 630                 635                 640

Lys Val Ile Asp Gly Thr Leu Cys Gly Pro Glu Thr Leu Ala Ile Cys
                645                 650                 655

Val Arg Gly Gln Cys Val Lys Ala Gly Cys Asp His Val Val Asp Ser
            660                 665                 670

Pro Arg Lys Leu Asp Lys Cys Gly Val Cys Gly Gly Lys Gly Asn Ser
        675                 680                 685

Cys Arg Lys Val Ser Gly Ser Leu Thr Pro Thr Asn Tyr Gly Tyr Asn
    690                 695                 700

Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile Asp Val Lys Gln
705                 710                 715                 720

Arg Ser His Pro Gly Val Gln Asn Asp Gly Asn Tyr Leu Ala Leu Lys
                725                 730                 735

Thr Ala Asp Gly Gln Tyr Leu Leu Asn Gly Asn Leu Ala Ile Ser Ala
            740                 745                 750

Ile Glu Gln Asp Ile Leu Val Lys Gly Thr Ile Leu Lys Tyr Ser Gly
        755                 760                 765
```

```
Ser Ile Ala Thr Leu Glu Arg Leu Gln Ser Phe Arg Pro Leu Pro Glu
    770                 775                 780

Pro Leu Thr Val Gln Leu Leu Thr Val Pro Gly Glu Val Phe Pro Pro
785                 790                 795                 800

Lys Val Lys Tyr Thr Phe Phe Val Pro Asn Asp Val Asp Phe Ser Met
                805                 810                 815

Gln Ser Ser Lys Glu Arg Ala Thr Thr Asn Ile Ile Gln Pro Leu Leu
            820                 825                 830

His Ala Gln Trp Val Leu Gly Asp Trp Ser Glu Cys Ser Ser Thr Cys
        835                 840                 845

Gly Ala Gly Trp Gln Arg Arg Thr Val Glu Cys Arg Asp Pro Ser Gly
    850                 855                 860

Gln Ala Ser Ala Thr Cys Asn Lys Ala Leu Lys Pro Glu Asp Ala Lys
865                 870                 875                 880

Pro Cys Glu Ser Gln Leu Cys Pro Leu
                885

<210> 2311
<211> 1907
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: ADAMTS9; "

<220>
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<223> /note="Gene Name:
      ADAM metallopeptidase with thrombospondin type 1
      motif, 9; "

<220>
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<223> /note="Uniprot ID:  Q9P2N4; "
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<220>
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<223> /note="ENSP ID: ENSP00000295903"

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Met Gln Phe Val Ser Trp Ala Thr Leu Leu Thr Leu Leu Val Arg Asp
1 5 10 15

Leu Ala Glu Met Gly Ser Pro Asp Ala Ala Ala Ala Val Arg Lys Asp
20 25 30

Arg Leu His Pro Arg Gln Val Lys Leu Leu Glu Thr Leu Ser Glu Tyr
35 40 45

Glu Ile Val Ser Pro Ile Arg Val Asn Ala Leu Gly Glu Pro Phe Pro
50 55 60

Thr Asn Val His Phe Lys Arg Thr Arg Arg Ser Ile Asn Ser Ala Thr
65 70 75 80

Asp Pro Trp Pro Ala Phe Ala Ser Ser Ser Ser Ser Ser Thr Ser Ser
85 90 95

Gln Ala His Tyr Arg Leu Ser Ala Phe Gly Gln Gln Phe Leu Phe Asn
100 105 110

Leu Thr Ala Asn Ala Gly Phe Ile Ala Pro Leu Phe Thr Val Thr Leu
115 120 125

Leu Gly Thr Pro Gly Val Asn Gln Thr Lys Phe Tyr Ser Glu Glu Glu
130 135 140

Ala Glu Leu Lys His Cys Phe Tyr Lys Gly Tyr Val Asn Thr Asn Ser
145 150 155 160

Glu His Thr Ala Val Ile Ser Leu Cys Ser Gly Met Leu Gly Thr Phe
165 170 175

Arg Ser His Asp Gly Asp Tyr Phe Ile Glu Pro Leu Gln Ser Met Asp
180 185 190

Glu Gln Glu Asp Glu Glu Glu Gln Asn Lys Pro His Ile Ile Tyr Arg
195 200 205

```
Arg Ser Ala Pro Gln Arg Glu Pro Ser Thr Gly Arg His Ala Cys Asp
    210                 215                 220

Thr Ser Glu His Lys Asn Arg His Ser Lys Asp Lys Lys Lys Thr Arg
225                 230                 235                 240

Ala Arg Lys Trp Gly Glu Arg Ile Asn Leu Ala Gly Asp Val Ala Ala
                245                 250                 255

Leu Asn Ser Gly Leu Ala Thr Glu Ala Phe Ser Ala Tyr Gly Asn Lys
            260                 265                 270

Thr Asp Asn Thr Arg Glu Lys Arg Thr His Arg Arg Thr Lys Arg Phe
        275                 280                 285

Leu Ser Tyr Pro Arg Phe Val Glu Val Leu Val Val Ala Asp Asn Arg
    290                 295                 300

Met Val Ser Tyr His Gly Glu Asn Leu Gln His Tyr Ile Leu Thr Leu
305                 310                 315                 320

Met Ser Ile Asp Gly Pro Ser Ile Ser Phe Asn Ala Gln Thr Thr Leu
                325                 330                 335

Lys Asn Phe Cys Gln Trp Gln His Ser Lys Asn Ser Pro Gly Gly Ile
            340                 345                 350

His His Asp Thr Ala Val Leu Leu Thr Arg Gln Asp Ile Cys Arg Ala
        355                 360                 365

His Asp Lys Cys Asp Thr Leu Gly Leu Ala Glu Leu Gly Thr Ile Cys
    370                 375                 380

Asp Pro Tyr Arg Ser Cys Ser Ile Ser Glu Asp Ser Gly Leu Ser Thr
385                 390                 395                 400

Ala Phe Thr Ile Ala His Glu Leu Gly His Val Phe Asn Met Pro His
                405                 410                 415

Asp Asp Asn Asn Lys Cys Lys Glu Glu Gly Val Lys Ser Pro Gln His
            420                 425                 430

Val Met Ala Pro Thr Leu Asn Phe Tyr Thr Asn Pro Trp Met Trp Ser
```

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        435                 440                 445

Lys Cys Ser Arg Lys Tyr Ile Thr Glu Phe Leu Asp Thr Gly Tyr Gly
    450                 455                 460

Glu Cys Leu Leu Asn Glu Pro Glu Ser Arg Pro Tyr Pro Leu Pro Val
465                 470                 475                 480

Gln Leu Pro Gly Ile Leu Tyr Asn Val Asn Lys Gln Cys Glu Leu Ile
                485                 490                 495

Phe Gly Pro Gly Ser Gln Val Cys Pro Tyr Met Met Gln Cys Arg Arg
            500                 505                 510

Leu Trp Cys Asn Asn Val Asn Gly Val His Lys Gly Cys Arg Thr Gln
        515                 520                 525

His Thr Pro Trp Ala Asp Gly Thr Glu Cys Glu Pro Gly Lys His Cys
    530                 535                 540

Lys Tyr Gly Phe Cys Val Pro Lys Glu Met Asp Val Pro Val Thr Asp
545                 550                 555                 560

Gly Ser Trp Gly Ser Trp Ser Pro Phe Gly Thr Cys Ser Arg Thr Cys
                565                 570                 575

Gly Gly Gly Ile Lys Thr Ala Ile Arg Glu Cys Asn Arg Pro Glu Pro
            580                 585                 590

Lys Asn Gly Gly Lys Tyr Cys Val Gly Arg Arg Met Lys Phe Lys Ser
        595                 600                 605

Cys Asn Thr Glu Pro Cys Leu Lys Gln Lys Arg Asp Phe Arg Asp Glu
    610                 615                 620

Gln Cys Ala His Phe Asp Gly Lys His Phe Asn Ile Asn Gly Leu Leu
625                 630                 635                 640

Pro Asn Val Arg Trp Val Pro Lys Tyr Ser Gly Ile Leu Met Lys Asp
                645                 650                 655

Arg Cys Lys Leu Phe Cys Arg Val Ala Gly Asn Thr Ala Tyr Tyr Gln
            660                 665                 670
```

```
Leu Arg Asp Arg Val Ile Asp Gly Thr Pro Cys Gly Gln Asp Thr Asn
        675                 680                 685

Asp Ile Cys Val Gln Gly Leu Cys Arg Gln Ala Gly Cys Asp His Val
    690                 695                 700

Leu Asn Ser Lys Ala Arg Arg Asp Lys Cys Gly Val Cys Gly Gly Asp
705                 710                 715                 720

Asn Ser Ser Cys Lys Thr Val Ala Gly Thr Phe Asn Thr Val His Tyr
                725                 730                 735

Gly Tyr Asn Thr Val Val Arg Ile Pro Ala Gly Ala Thr Asn Ile Asp
            740                 745                 750

Val Arg Gln His Ser Phe Ser Gly Glu Thr Asp Asp Asp Asn Tyr Leu
        755                 760                 765

Ala Leu Ser Ser Ser Lys Gly Glu Phe Leu Leu Asn Gly Asn Phe Val
    770                 775                 780

Val Thr Met Ala Lys Arg Glu Ile Arg Ile Gly Asn Ala Val Val Glu
785                 790                 795                 800

Tyr Ser Gly Ser Glu Thr Ala Val Glu Arg Ile Asn Ser Thr Asp Arg
                805                 810                 815

Ile Glu Gln Glu Leu Leu Leu Gln Val Leu Ser Val Gly Lys Leu Tyr
            820                 825                 830

Asn Pro Asp Val Arg Tyr Ser Phe Asn Ile Pro Ile Glu Asp Lys Pro
        835                 840                 845

Gln Gln Phe Tyr Trp Asn Ser His Gly Pro Trp Gln Ala Cys Ser Lys
    850                 855                 860

Pro Cys Gln Gly Glu Arg Lys Arg Lys Leu Val Cys Thr Arg Glu Ser
865                 870                 875                 880

Asp Gln Leu Thr Val Ser Asp Gln Arg Cys Asp Arg Leu Pro Gln Pro
                885                 890                 895
```

```
Gly His Ile Thr Glu Pro Cys Gly Thr Asp Cys Asp Leu Arg Trp His
            900                 905                 910

Val Ala Ser Arg Ser Glu Cys Ser Ala Gln Cys Gly Leu Gly Tyr Arg
        915                 920                 925

Thr Leu Asp Ile Tyr Cys Ala Lys Tyr Ser Arg Leu Asp Gly Lys Thr
    930                 935                 940

Glu Lys Val Asp Asp Gly Phe Cys Ser Ser His Pro Lys Pro Ser Asn
945                 950                 955                 960

Arg Glu Lys Cys Ser Gly Glu Cys Asn Thr Gly Gly Trp Arg Tyr Ser
                965                 970                 975

Ala Trp Thr Glu Cys Ser Lys Ser Cys Asp Gly Gly Thr Gln Arg Arg
            980                 985                 990

Arg Ala Ile Cys Val Asn Thr Arg  Asn Asp Val Leu Asp  Asp Ser
Lys
        995                 1000                1005

Cys Thr  His Gln Glu Lys Val  Thr Ile Gln Arg Cys  Ser Glu Phe
    1010                1015                1020

Pro Cys  Pro Gln Trp Lys Ser  Gly Asp Trp Ser Glu  Cys Leu Val
    1025                1030                1035

Thr Cys  Gly Lys Gly His Lys  His Arg Gln Val Trp  Cys Gln Phe
    1040                1045                1050

Gly Glu  Asp Arg Leu Asn Asp  Arg Met Cys Asp Pro  Glu Thr Lys
    1055                1060                1065

Pro Thr  Ser Met Gln Thr Cys  Gln Gln Pro Glu Cys  Ala Ser Trp
    1070                1075                1080

Gln Ala  Gly Pro Trp Gly Gln  Cys Ser Val Thr Cys  Gly Gln Gly
    1085                1090                1095

Tyr Gln  Leu Arg Ala Val Lys  Cys Ile Ile Gly Thr  Tyr Met Ser
    1100                1105                1110
```

```
Val Val  Asp Asp Asn Asp Cys  Asn Ala Ala Thr Arg  Pro Thr Asp
    1115                1120                1125

Thr Gln  Asp Cys Glu Leu Pro  Ser Cys His Pro Pro  Pro Ala Ala
    1130                1135                1140

Pro Glu  Thr Arg Arg Ser Thr  Tyr Ser Ala Pro Arg  Thr Gln Trp
    1145                1150                1155

Arg Phe  Gly Ser Trp Thr Pro  Cys Ser Ala Thr Cys  Gly Lys Gly
    1160                1165                1170

Thr Arg  Met Arg Tyr Val Ser  Cys Arg Asp Glu Asn  Gly Ser Val
    1175                1180                1185

Ala Asp  Glu Ser Ala Cys Ala  Thr Leu Pro Arg Pro  Val Ala Lys
    1190                1195                1200

Glu Glu  Cys Ser Val Thr Pro  Cys Gly Gln Trp Lys  Ala Leu Asp
    1205                1210                1215

Trp Ser  Ser Cys Ser Val Thr  Cys Gly Gln Gly Arg  Ala Thr Arg
    1220                1225                1230

Gln Val  Met Cys Val Asn Tyr  Ser Asp His Val Ile  Asp Arg Ser
    1235                1240                1245

Glu Cys  Asp Gln Asp Tyr Ile  Pro Glu Thr Asp Gln  Asp Cys Ser
    1250                1255                1260

Met Ser  Pro Cys Pro Gln Arg  Thr Pro Asp Ser Gly  Leu Ala Gln
    1265                1270                1275

His Pro  Phe Gln Asn Glu Asp  Tyr Arg Pro Arg Ser  Ala Ser Pro
    1280                1285                1290

Ser Arg  Thr His Val Leu Gly  Gly Asn Gln Trp Arg  Thr Gly Pro
    1295                1300                1305

Trp Gly  Ala Cys Ser Ser Thr  Cys Ala Gly Gly Ser  Gln Arg Arg
    1310                1315                1320
```

Val Val Val Cys Gln Asp Glu Asn Gly Tyr Thr Ala Asn Asp Cys
1325 1330 1335

Val Glu Arg Ile Lys Pro Asp Glu Gln Arg Ala Cys Glu Ser Gly
1340 1345 1350

Pro Cys Pro Gln Trp Ala Tyr Gly Asn Trp Gly Glu Cys Thr Lys
1355 1360 1365

Leu Cys Gly Gly Gly Ile Arg Thr Arg Leu Val Val Cys Gln Arg
1370 1375 1380

Ser Asn Gly Glu Arg Phe Pro Asp Leu Ser Cys Glu Ile Leu Asp
1385 1390 1395

Lys Pro Pro Asp Arg Glu Gln Cys Asn Thr His Ala Cys Pro His
1400 1405 1410

Asp Ala Ala Trp Ser Thr Gly Pro Trp Ser Ser Cys Ser Val Ser
1415 1420 1425

Cys Gly Arg Gly His Lys Gln Arg Asn Val Tyr Cys Met Ala Lys
1430 1435 1440

Asp Gly Ser His Leu Glu Ser Asp Tyr Cys Lys His Leu Ala Lys
1445 1450 1455

Pro His Gly His Arg Lys Cys Arg Gly Gly Arg Cys Pro Lys Trp
1460 1465 1470

Lys Ala Gly Ala Trp Ser Gln Cys Ser Val Ser Cys Gly Arg Gly
1475 1480 1485

Val Gln Gln Arg His Val Gly Cys Gln Ile Gly Thr His Lys Ile
1490 1495 1500

Ala Arg Glu Thr Glu Cys Asn Pro Tyr Thr Arg Pro Glu Ser Glu
1505 1510 1515

Arg Asp Cys Gln Gly Pro Arg Cys Pro Leu Tyr Thr Trp Arg Ala
1520 1525 1530

Glu Glu Trp Gln Glu Cys Thr Lys Thr Cys Gly Glu Gly Ser Arg

1535 1540 1545

Tyr Arg Lys Val Val Cys Val Asp Asp Asn Lys Asn Glu Val His
1550 1555 1560

Gly Ala Arg Cys Asp Val Ser Lys Arg Pro Val Asp Arg Glu Ser
1565 1570 1575

Cys Ser Leu Gln Pro Cys Glu Tyr Val Trp Ile Thr Gly Glu Trp
1580 1585 1590

Ser Glu Cys Ser Val Thr Cys Gly Lys Gly Tyr Lys Gln Arg Leu
1595 1600 1605

Val Ser Cys Ser Glu Ile Tyr Thr Gly Lys Glu Asn Tyr Glu Tyr
1610 1615 1620

Ser Tyr Gln Thr Thr Ile Asn Cys Pro Gly Thr Gln Pro Pro Ser
1625 1630 1635

Val His Pro Cys Tyr Leu Arg Asp Cys Pro Val Ser Ala Thr Trp
1640 1645 1650

Arg Val Gly Asn Trp Gly Ser Cys Ser Val Ser Cys Gly Val Gly
1655 1660 1665

Val Met Gln Arg Ser Val Gln Cys Leu Thr Asn Glu Asp Gln Pro
1670 1675 1680

Ser His Leu Cys His Thr Asp Leu Lys Pro Glu Glu Arg Lys Thr
1685 1690 1695

Cys Arg Asn Val Tyr Asn Cys Glu Leu Pro Gln Asn Cys Lys Glu
1700 1705 1710

Val Lys Arg Leu Lys Gly Ala Ser Glu Asp Gly Glu Tyr Phe Leu
1715 1720 1725

Met Ile Arg Gly Lys Leu Leu Lys Ile Phe Cys Ala Gly Met His
1730 1735 1740

Ser Asp His Pro Lys Glu Tyr Val Thr Leu Val His Gly Asp Ser
1745 1750 1755

```
Glu Asn  Phe Ser Glu Val Tyr  Gly His Arg Leu His  Asn Pro Thr
    1760                1765                1770

Glu Cys  Pro Tyr Asn Gly Ser  Arg Arg Asp Asp Cys  Gln Cys Arg
    1775                1780                1785

Lys Asp  Tyr Thr Ala Ala Gly  Phe Ser Ser Phe Gln  Lys Ile Arg
    1790                1795                1800

Ile Asp  Leu Thr Ser Met Gln  Ile Ile Thr Thr Asp  Leu Gln Phe
    1805                1810                1815

Ala Arg  Thr Ser Glu Gly His  Pro Val Pro Phe Ala  Thr Ala Gly
    1820                1825                1830

Asp Cys  Tyr Ser Ala Ala Lys  Cys Pro Gln Gly Arg  Phe Ser Ile
    1835                1840                1845

Asn Leu  Tyr Gly Thr Gly Leu  Ser Leu Thr Glu Ser  Ala Arg Trp
    1850                1855                1860

Ile Ser  Gln Gly Asn Tyr Ala  Val Ser Asp Ile Lys  Lys Ser Pro
    1865                1870                1875

Asp Gly  Thr Arg Val Val Gly  Lys Cys Gly Gly Tyr  Cys Gly Lys
    1880                1885                1890

Cys Thr  Pro Ser Ser Gly Thr  Gly Leu Glu Val Arg  Val Leu
    1895                1900                1905


<210> 2312
<211> 991
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<223> /note="Gene Symbol: ADAMTS9; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 9; "

<220>
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<222> (1)..(1)
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<400> 2312

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Xaa Glu Cys Ser Ala Gln Cys Gly Leu Gly Tyr Arg Thr Leu Asp Ile
1               5                  10                  15

Tyr Cys Ala Lys Tyr Ser Arg Leu Asp Gly Lys Thr Glu Lys Val Asp
            20                  25                  30

Asp Gly Phe Cys Ser Ser His Pro Lys Pro Ser Asn Arg Glu Lys Cys
        35                  40                  45

Ser Gly Glu Cys Asn Thr Gly Gly Trp Arg Tyr Ser Ala Trp Thr Glu
    50                  55                  60

Cys Ser Lys Ser Cys Asp Gly Gly Thr Gln Arg Arg Arg Ala Ile Cys
65                  70                  75                  80

Val Asn Thr Arg Asn Asp Val Leu Asp Asp Ser Lys Cys Thr His Gln
                85                  90                  95

Glu Lys Val Thr Ile Gln Arg Cys Ser Glu Phe Pro Cys Pro Gln Trp
            100                 105                 110

Lys Ser Gly Asp Trp Ser Glu Cys Leu Val Thr Cys Gly Lys Gly His
        115                 120                 125

Lys His Arg Gln Val Trp Cys Gln Phe Gly Glu Asp Arg Leu Asn Asp
    130                 135                 140

Arg Met Cys Asp Pro Glu Thr Lys Pro Thr Ser Met Gln Thr Cys Gln
145                 150                 155                 160

Gln Pro Glu Cys Ala Ser Trp Gln Ala Gly Pro Trp Gly Gln Cys Ser
                165                 170                 175
```

```
Val Thr Cys Gly Gln Gly Tyr Gln Leu Arg Ala Val Lys Cys Ile Ile
            180                 185                 190

Gly Thr Tyr Met Ser Val Val Asp Asp Asn Asp Cys Asn Ala Ala Thr
        195                 200                 205

Arg Pro Thr Asp Thr Gln Asp Cys Glu Leu Pro Ser Cys His Pro Pro
    210                 215                 220

Pro Ala Ala Pro Glu Thr Arg Arg Ser Thr Tyr Ser Ala Pro Arg Thr
225                 230                 235                 240

Gln Trp Arg Phe Gly Ser Trp Thr Pro Cys Ser Ala Thr Cys Gly Lys
                245                 250                 255

Gly Thr Arg Met Arg Tyr Val Ser Cys Arg Asp Glu Asn Gly Ser Val
            260                 265                 270

Ala Asp Glu Ser Ala Cys Ala Thr Leu Pro Arg Pro Val Ala Lys Glu
        275                 280                 285

Glu Cys Ser Val Thr Pro Cys Gly Gln Trp Lys Ala Leu Asp Trp Ser
    290                 295                 300

Ser Cys Ser Val Thr Cys Gly Gln Gly Arg Ala Thr Arg Gln Val Met
305                 310                 315                 320

Cys Val Asn Tyr Ser Asp His Val Ile Asp Arg Ser Glu Cys Asp Gln
                325                 330                 335

Asp Tyr Ile Pro Glu Thr Asp Gln Asp Cys Ser Met Ser Pro Cys Pro
            340                 345                 350

Gln Arg Thr Pro Asp Ser Gly Leu Ala Gln His Pro Phe Gln Asn Glu
        355                 360                 365

Asp Tyr Arg Pro Arg Ser Ala Ser Pro Ser Arg Thr His Val Leu Gly
    370                 375                 380

Gly Asn Gln Trp Arg Thr Gly Pro Trp Gly Ala Cys Ser Ser Thr Cys
385                 390                 395                 400
```

```
Ala Gly Gly Ser Gln Arg Arg Val Val Val Cys Gln Asp Glu Asn Gly
                405                 410                 415

Tyr Thr Ala Asn Asp Cys Val Glu Arg Ile Lys Pro Asp Glu Gln Arg
            420                 425                 430

Ala Cys Glu Ser Gly Pro Cys Pro Gln Trp Ala Tyr Gly Asn Trp Gly
        435                 440                 445

Glu Cys Thr Lys Leu Cys Gly Gly Gly Ile Arg Thr Arg Leu Val Val
    450                 455                 460

Cys Gln Arg Ser Asn Gly Glu Arg Phe Pro Asp Leu Ser Cys Glu Ile
465                 470                 475                 480

Leu Asp Lys Pro Pro Asp Arg Glu Gln Cys Asn Thr His Ala Cys Pro
                485                 490                 495

His Asp Ala Ala Trp Ser Thr Gly Pro Trp Ser Ser Cys Ser Val Ser
            500                 505                 510

Cys Gly Arg Gly His Lys Gln Arg Asn Val Tyr Cys Met Ala Lys Asp
        515                 520                 525

Gly Ser His Leu Glu Ser Asp Tyr Cys Lys His Leu Ala Lys Pro His
    530                 535                 540

Gly His Arg Lys Cys Arg Gly Gly Arg Cys Pro Lys Trp Lys Ala Gly
545                 550                 555                 560

Ala Trp Ser Gln Cys Ser Val Ser Cys Gly Arg Gly Val Gln Gln Arg
                565                 570                 575

His Val Gly Cys Gln Ile Gly Thr His Lys Ile Ala Arg Glu Thr Glu
            580                 585                 590

Cys Asn Pro Tyr Thr Arg Pro Glu Ser Glu Arg Asp Cys Gln Gly Pro
        595                 600                 605

Arg Cys Pro Leu Tyr Thr Trp Arg Ala Glu Glu Trp Gln Glu Cys Thr
    610                 615                 620
```

```
Lys Thr Cys Gly Glu Gly Ser Arg Tyr Arg Lys Val Val Cys Val Asp
625                 630                 635                 640

Asp Asn Lys Asn Glu Val His Gly Ala Arg Cys Asp Val Ser Lys Arg
                645                 650                 655

Pro Val Asp Arg Glu Ser Cys Ser Leu Gln Pro Cys Glu Tyr Val Trp
            660                 665                 670

Ile Thr Gly Glu Trp Ser Glu Cys Ser Val Thr Cys Gly Lys Gly Tyr
        675                 680                 685

Lys Gln Arg Leu Val Ser Cys Ser Glu Ile Tyr Thr Gly Lys Glu Asn
    690                 695                 700

Tyr Glu Tyr Ser Tyr Gln Thr Thr Ile Asn Cys Pro Gly Thr Gln Pro
705                 710                 715                 720

Pro Ser Val His Pro Cys Tyr Leu Arg Asp Cys Pro Val Ser Ala Thr
                725                 730                 735

Trp Arg Val Gly Asn Trp Gly Ser Cys Ser Val Ser Cys Gly Val Gly
            740                 745                 750

Val Met Gln Arg Ser Val Gln Cys Leu Thr Asn Glu Asp Gln Pro Ser
        755                 760                 765

His Leu Cys His Thr Asp Leu Lys Pro Glu Glu Arg Lys Thr Cys Arg
    770                 775                 780

Asn Val Tyr Asn Cys Glu Leu Pro Gln Asn Cys Lys Glu Val Lys Arg
785                 790                 795                 800

Leu Lys Gly Ala Ser Glu Asp Gly Glu Tyr Phe Leu Met Ile Arg Gly
                805                 810                 815

Lys Leu Leu Lys Ile Phe Cys Ala Gly Met His Ser Asp His Pro Lys
            820                 825                 830

Glu Tyr Val Thr Leu Val His Gly Asp Ser Glu Asn Phe Ser Glu Val
        835                 840                 845

Tyr Gly His Arg Leu His Asn Pro Thr Glu Cys Pro Tyr Asn Gly Ser
```

```
    850                 855                 860

Arg Arg Asp Asp Cys Gln Cys Arg Lys Asp Tyr Thr Ala Ala Gly Phe
865                 870                 875                 880

Ser Ser Phe Gln Lys Ile Arg Ile Asp Leu Thr Ser Met Gln Ile Ile
                885                 890                 895

Thr Thr Asp Leu Gln Phe Ala Arg Thr Ser Glu Gly His Pro Val Pro
            900                 905                 910

Phe Ala Thr Ala Gly Asp Cys Tyr Ser Ala Ala Lys Cys Pro Gln Gly
        915                 920                 925

Arg Phe Ser Ile Asn Leu Tyr Gly Thr Gly Leu Ser Leu Thr Glu Ser
    930                 935                 940

Ala Arg Trp Ile Ser Gln Gly Asn Tyr Ala Val Ser Asp Ile Lys Lys
945                 950                 955                 960

Ser Pro Asp Gly Thr Arg Val Val Gly Lys Cys Gly Gly Tyr Cys Gly
                965                 970                 975

Lys Cys Thr Pro Ser Ser Gly Thr Gly Leu Glu Val Arg Val Leu
            980                 985                 990


<210> 2313
<211> 1935
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<220>
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      ADAM metallopeptidase with thrombospondin type 1
      motif, 9; "

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Met Gln Phe Val Ser Trp Ala Thr Leu Leu Thr Leu Leu Val Arg Asp
1   5   10   15

Leu Ala Glu Met Gly Ser Pro Asp Ala Ala Ala Ala Val Arg Lys Asp
            20   25   30

Arg Leu His Pro Arg Gln Val Lys Leu Leu Glu Thr Leu Ser Glu Tyr
        35   40   45

Glu Ile Val Ser Pro Ile Arg Val Asn Ala Leu Gly Glu Pro Phe Pro
    50   55   60

Thr Asn Val His Phe Lys Arg Thr Arg Arg Ser Ile Asn Ser Ala Thr
65   70   75   80

Asp Pro Trp Pro Ala Phe Ala Ser Ser Ser Ser Ser Ser Thr Ser Ser
                85   90   95

Gln Ala His Tyr Arg Leu Ser Ala Phe Gly Gln Gln Phe Leu Phe Asn
            100   105   110

Leu Thr Ala Asn Ala Gly Phe Ile Ala Pro Leu Phe Thr Val Thr Leu
        115   120   125

Leu Gly Thr Pro Gly Val Asn Gln Thr Lys Phe Tyr Ser Glu Glu Glu
    130   135   140

Ala Glu Leu Lys His Cys Phe Tyr Lys Gly Tyr Val Asn Thr Asn Ser
145   150   155   160

Glu His Thr Ala Val Ile Ser Leu Cys Ser Gly Met Leu Gly Thr Phe
                165   170   175

Arg Ser His Asp Gly Asp Tyr Phe Ile Glu Pro Leu Gln Ser Met Asp
            180   185   190

Glu Gln Glu Asp Glu Glu Glu Gln Asn Lys Pro His Ile Ile Tyr Arg
        195   200   205

```
Arg Ser Ala Pro Gln Arg Glu Pro Ser Thr Gly Arg His Ala Cys Asp
    210                 215                 220

Thr Ser Glu His Lys Asn Arg His Ser Lys Asp Lys Lys Lys Thr Arg
225                 230                 235                 240

Ala Arg Lys Trp Gly Glu Arg Ile Asn Leu Ala Gly Asp Val Ala Ala
                245                 250                 255

Leu Asn Ser Gly Leu Ala Thr Glu Ala Phe Ser Ala Tyr Gly Asn Lys
            260                 265                 270

Thr Asp Asn Thr Arg Glu Lys Arg Thr His Arg Arg Thr Lys Arg Phe
        275                 280                 285

Leu Ser Tyr Pro Arg Phe Val Glu Val Leu Val Val Ala Asp Asn Arg
    290                 295                 300

Met Val Ser Tyr His Gly Glu Asn Leu Gln His Tyr Ile Leu Thr Leu
305                 310                 315                 320

Met Ser Ile Val Ala Ser Ile Tyr Lys Asp Pro Ser Ile Gly Asn Leu
                325                 330                 335

Ile Asn Ile Val Ile Val Asn Leu Ile Val Ile His Asn Glu Gln Asp
            340                 345                 350

Gly Pro Ser Ile Ser Phe Asn Ala Gln Thr Thr Leu Lys Asn Phe Cys
        355                 360                 365

Gln Trp Gln His Ser Lys Asn Ser Pro Gly Gly Ile His His Asp Thr
    370                 375                 380

Ala Val Leu Leu Thr Arg Gln Asp Ile Cys Arg Ala His Asp Lys Cys
385                 390                 395                 400

Asp Thr Leu Gly Leu Ala Glu Leu Gly Thr Ile Cys Asp Pro Tyr Arg
                405                 410                 415

Ser Cys Ser Ile Ser Glu Asp Ser Gly Leu Ser Thr Ala Phe Thr Ile
            420                 425                 430
```

```
Ala His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Asn Asn
        435                 440                 445

Lys Cys Lys Glu Glu Gly Val Lys Ser Pro Gln His Val Met Ala Pro
    450                 455                 460

Thr Leu Asn Phe Tyr Thr Asn Pro Trp Met Trp Ser Lys Cys Ser Arg
465                 470                 475                 480

Lys Tyr Ile Thr Glu Phe Leu Asp Thr Gly Tyr Gly Glu Cys Leu Leu
                485                 490                 495

Asn Glu Pro Glu Ser Arg Pro Tyr Pro Leu Pro Val Gln Leu Pro Gly
            500                 505                 510

Ile Leu Tyr Asn Val Asn Lys Gln Cys Glu Leu Ile Phe Gly Pro Gly
        515                 520                 525

Ser Gln Val Cys Pro Tyr Met Met Gln Cys Arg Arg Leu Trp Cys Asn
    530                 535                 540

Asn Val Asn Gly Val His Lys Gly Cys Arg Thr Gln His Thr Pro Trp
545                 550                 555                 560

Ala Asp Gly Thr Glu Cys Glu Pro Gly Lys His Cys Lys Tyr Gly Phe
                565                 570                 575

Cys Val Pro Lys Glu Met Asp Val Pro Val Thr Asp Gly Ser Trp Gly
            580                 585                 590

Ser Trp Ser Pro Phe Gly Thr Cys Ser Arg Thr Cys Gly Gly Gly Ile
        595                 600                 605

Lys Thr Ala Ile Arg Glu Cys Asn Arg Pro Glu Pro Lys Asn Gly Gly
    610                 615                 620

Lys Tyr Cys Val Gly Arg Arg Met Lys Phe Lys Ser Cys Asn Thr Glu
625                 630                 635                 640

Pro Cys Leu Lys Gln Lys Arg Asp Phe Arg Asp Glu Gln Cys Ala His
                645                 650                 655

Phe Asp Gly Lys His Phe Asn Ile Asn Gly Leu Leu Pro Asn Val Arg
```

660 665 670

Trp Val Pro Lys Tyr Ser Gly Ile Leu Met Lys Asp Arg Cys Lys Leu
675 680 685

Phe Cys Arg Val Ala Gly Asn Thr Ala Tyr Tyr Gln Leu Arg Asp Arg
690 695 700

Val Ile Asp Gly Thr Pro Cys Gly Gln Asp Thr Asn Asp Ile Cys Val
705 710 715 720

Gln Gly Leu Cys Arg Gln Ala Gly Cys Asp His Val Leu Asn Ser Lys
725 730 735

Ala Arg Arg Asp Lys Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys
740 745 750

Lys Thr Val Ala Gly Thr Phe Asn Thr Val His Tyr Gly Tyr Asn Thr
755 760 765

Val Val Arg Ile Pro Ala Gly Ala Thr Asn Ile Asp Val Arg Gln His
770 775 780

Ser Phe Ser Gly Glu Thr Asp Asp Asp Asn Tyr Leu Ala Leu Ser Ser
785 790 795 800

Ser Lys Gly Glu Phe Leu Leu Asn Gly Asn Phe Val Val Thr Met Ala
805 810 815

Lys Arg Glu Ile Arg Ile Gly Asn Ala Val Val Glu Tyr Ser Gly Ser
820 825 830

Glu Thr Ala Val Glu Arg Ile Asn Ser Thr Asp Arg Ile Glu Gln Glu
835 840 845

Leu Leu Leu Gln Val Leu Ser Val Gly Lys Leu Tyr Asn Pro Asp Val
850 855 860

Arg Tyr Ser Phe Asn Ile Pro Ile Glu Asp Lys Pro Gln Gln Phe Tyr
865 870 875 880

Trp Asn Ser His Gly Pro Trp Gln Ala Cys Ser Lys Pro Cys Gln Gly
885 890 895

```
Glu Arg Lys Arg Lys Leu Val Cys Thr Arg Glu Ser Asp Gln Leu Thr
            900                 905                 910

Val Ser Asp Gln Arg Cys Asp Arg Leu Pro Gln Pro Gly His Ile Thr
        915                 920                 925

Glu Pro Cys Gly Thr Asp Cys Asp Leu Arg Trp His Val Ala Ser Arg
    930                 935                 940

Ser Glu Cys Ser Ala Gln Cys Gly Leu Gly Tyr Arg Thr Leu Asp Ile
945                 950                 955                 960

Tyr Cys Ala Lys Tyr Ser Arg Leu Asp Gly Lys Thr Glu Lys Val Asp
                965                 970                 975

Asp Gly Phe Cys Ser Ser His Pro Lys Pro Ser Asn Arg Glu Lys Cys
            980                 985                 990

Ser Gly Glu Cys Asn Thr Gly Gly  Trp Arg Tyr Ser Ala  Trp Thr
Glu
        995                 1000                1005

Cys Ser  Lys Ser Cys Asp Gly  Gly Thr Gln Arg Arg  Arg Ala Ile
    1010                1015                1020

Cys Val  Asn Thr Arg Asn Asp  Val Leu Asp Asp Ser  Lys Cys Thr
    1025                1030                1035

His Gln  Glu Lys Val Thr Ile  Gln Arg Cys Ser Glu  Phe Pro Cys
    1040                1045                1050

Pro Gln  Trp Lys Ser Gly Asp  Trp Ser Glu Cys Leu  Val Thr Cys
    1055                1060                1065

Gly Lys  Gly His Lys His Arg  Gln Val Trp Cys Gln  Phe Gly Glu
    1070                1075                1080

Asp Arg  Leu Asn Asp Arg Met  Cys Asp Pro Glu Thr  Lys Pro Thr
    1085                1090                1095

Ser Met  Gln Thr Cys Gln Gln  Pro Glu Cys Ala Ser  Trp Gln Ala
    1100                1105                1110
```

```
Gly Pro  Trp Gly Gln Cys Ser  Val Thr Cys Gly Gln  Gly Tyr Gln
    1115                1120                1125

Leu Arg  Ala Val Lys Cys Ile  Ile Gly Thr Tyr Met  Ser Val Val
    1130                1135                1140

Asp Asp  Asn Asp Cys Asn Ala  Ala Thr Arg Pro Thr  Asp Thr Gln
    1145                1150                1155

Asp Cys  Glu Leu Pro Ser Cys  His Pro Pro Pro Ala  Ala Pro Glu
    1160                1165                1170

Thr Arg  Arg Ser Thr Tyr Ser  Ala Pro Arg Thr Gln  Trp Arg Phe
    1175                1180                1185

Gly Ser  Trp Thr Pro Cys Ser  Ala Thr Cys Gly Lys  Gly Thr Arg
    1190                1195                1200

Met Arg  Tyr Val Ser Cys Arg  Asp Glu Asn Gly Ser  Val Ala Asp
    1205                1210                1215

Glu Ser  Ala Cys Ala Thr Leu  Pro Arg Pro Val Ala  Lys Glu Glu
    1220                1225                1230

Cys Ser  Val Thr Pro Cys Gly  Gln Trp Lys Ala Leu  Asp Trp Ser
    1235                1240                1245

Ser Cys  Ser Val Thr Cys Gly  Gln Gly Arg Ala Thr  Arg Gln Val
    1250                1255                1260

Met Cys  Val Asn Tyr Ser Asp  His Val Ile Asp Arg  Ser Glu Cys
    1265                1270                1275

Asp Gln  Asp Tyr Ile Pro Glu  Thr Asp Gln Asp Cys  Ser Met Ser
    1280                1285                1290

Pro Cys  Pro Gln Arg Thr Pro  Asp Ser Gly Leu Ala  Gln His Pro
    1295                1300                1305

Phe Gln  Asn Glu Asp Tyr Arg  Pro Arg Ser Ala Ser  Pro Ser Arg
    1310                1315                1320
```

```
Thr His  Val Leu Gly Gly Asn  Gln Trp Arg Thr Gly  Pro Trp Gly
    1325                1330                1335

Ala Cys  Ser Ser Thr Cys Ala  Gly Gly Ser Gln Arg  Arg Val Val
    1340                1345                1350

Val Cys  Gln Asp Glu Asn Gly  Tyr Thr Ala Asn Asp  Cys Val Glu
    1355                1360                1365

Arg Ile  Lys Pro Asp Glu Gln  Arg Ala Cys Glu Ser  Gly Pro Cys
    1370                1375                1380

Pro Gln  Trp Ala Tyr Gly Asn  Trp Gly Glu Cys Thr  Lys Leu Cys
    1385                1390                1395

Gly Gly  Gly Ile Arg Thr Arg  Leu Val Val Cys Gln  Arg Ser Asn
    1400                1405                1410

Gly Glu  Arg Phe Pro Asp Leu  Ser Cys Glu Ile Leu  Asp Lys Pro
    1415                1420                1425

Pro Asp  Arg Glu Gln Cys Asn  Thr His Ala Cys Pro  His Asp Ala
    1430                1435                1440

Ala Trp  Ser Thr Gly Pro Trp  Ser Ser Cys Ser Val  Ser Cys Gly
    1445                1450                1455

Arg Gly  His Lys Gln Arg Asn  Val Tyr Cys Met Ala  Lys Asp Gly
    1460                1465                1470

Ser His  Leu Glu Ser Asp Tyr  Cys Lys His Leu Ala  Lys Pro His
    1475                1480                1485

Gly His  Arg Lys Cys Arg Gly  Gly Arg Cys Pro Lys  Trp Lys Ala
    1490                1495                1500

Gly Ala  Trp Ser Gln Cys Ser  Val Ser Cys Gly Arg  Gly Val Gln
    1505                1510                1515

Gln Arg  His Val Gly Cys Gln  Ile Gly Thr His Lys  Ile Ala Arg
    1520                1525                1530
```

```
Glu Thr  Glu Cys Asn Pro Tyr  Thr Arg Pro Glu Ser  Glu Arg Asp
    1535                1540                1545

Cys Gln  Gly Pro Arg Cys Pro  Leu Tyr Thr Trp Arg  Ala Glu Glu
    1550                1555                1560

Trp Gln  Glu Cys Thr Lys Thr  Cys Gly Glu Gly Ser  Arg Tyr Arg
    1565                1570                1575

Lys Val  Val Cys Val Asp Asp  Asn Lys Asn Glu Val  His Gly Ala
    1580                1585                1590

Arg Cys  Asp Val Ser Lys Arg  Pro Val Asp Arg Glu  Ser Cys Ser
    1595                1600                1605

Leu Gln  Pro Cys Glu Tyr Val  Trp Ile Thr Gly Glu  Trp Ser Glu
    1610                1615                1620

Cys Ser  Val Thr Cys Gly Lys  Gly Tyr Lys Gln Arg  Leu Val Ser
    1625                1630                1635

Cys Ser  Glu Ile Tyr Thr Gly  Lys Glu Asn Tyr Glu  Tyr Ser Tyr
    1640                1645                1650

Gln Thr  Thr Ile Asn Cys Pro  Gly Thr Gln Pro Pro  Ser Val His
    1655                1660                1665

Pro Cys  Tyr Leu Arg Asp Cys  Pro Val Ser Ala Thr  Trp Arg Val
    1670                1675                1680

Gly Asn  Trp Gly Ser Cys Ser  Val Ser Cys Gly Val  Gly Val Met
    1685                1690                1695

Gln Arg  Ser Val Gln Cys Leu  Thr Asn Glu Asp Gln  Pro Ser His
    1700                1705                1710

Leu Cys  His Thr Asp Leu Lys  Pro Glu Glu Arg Lys  Thr Cys Arg
    1715                1720                1725

Asn Val  Tyr Asn Cys Glu Leu  Pro Gln Asn Cys Lys  Glu Val Lys
    1730                1735                1740

Arg Leu  Lys Gly Ala Ser Glu  Asp Gly Glu Tyr Phe  Leu Met Ile
```

```
    1745                1750                1755

Arg Gly  Lys Leu Leu Lys Ile  Phe Cys Ala Gly Met  His Ser Asp
    1760                1765                1770

His Pro  Lys Glu Tyr Val Thr  Leu Val His Gly Asp  Ser Glu Asn
    1775                1780                1785

Phe Ser  Glu Val Tyr Gly His  Arg Leu His Asn Pro  Thr Glu Cys
    1790                1795                1800

Pro Tyr  Asn Gly Ser Arg Arg  Asp Asp Cys Gln Cys  Arg Lys Asp
    1805                1810                1815

Tyr Thr  Ala Ala Gly Phe Ser  Ser Phe Gln Lys Ile  Arg Ile Asp
    1820                1825                1830

Leu Thr  Ser Met Gln Ile Ile  Thr Thr Asp Leu Gln  Phe Ala Arg
    1835                1840                1845

Thr Ser  Glu Gly His Pro Val  Pro Phe Ala Thr Ala  Gly Asp Cys
    1850                1855                1860

Tyr Ser  Ala Ala Lys Cys Pro  Gln Gly Arg Phe Ser  Ile Asn Leu
    1865                1870                1875

Tyr Gly  Thr Gly Leu Ser Leu  Thr Glu Ser Ala Arg  Trp Ile Ser
    1880                1885                1890

Gln Gly  Asn Tyr Ala Val Ser  Asp Ile Lys Lys Ser  Pro Asp Gly
    1895                1900                1905

Thr Arg  Val Val Gly Lys Cys  Gly Gly Tyr Cys Gly  Lys Cys Thr
    1910                1915                1920

Pro Ser  Ser Gly Thr Gly Leu  Glu Val Arg Val Leu
    1925                1930                1935
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<210> 2314
<211> 488
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<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 575; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTS9; "

<220>
<221> source
<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000419217"

<400> 2314

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Met Gln Phe Val Ser Trp Ala Thr Leu Leu Thr Leu Leu Val Arg Asp
1               5                  10                  15

Leu Ala Glu Met Gly Ser Pro Asp Ala Ala Ala Ala Val Arg Lys Asp
            20                  25                  30

Arg Leu His Pro Arg Gln Val Lys Leu Leu Glu Thr Leu Ser Glu Tyr
        35                  40                  45

Glu Ile Val Ser Pro Ile Arg Val Asn Ala Leu Gly Glu Pro Phe Pro
    50                  55                  60

Thr Asn Val His Phe Lys Arg Thr Arg Arg Ser Ile Asn Ser Ala Thr
65                  70                  75                  80

Asp Pro Trp Pro Ala Phe Ala Ser Ser Ser Ser Ser Ser Thr Ser Ser
                85                  90                  95

Gln Ala His Tyr Arg Leu Ser Ala Phe Gly Gln Gln Phe Leu Phe Asn
            100                 105                 110

Leu Thr Ala Asn Ala Gly Phe Ile Ala Pro Leu Phe Thr Val Thr Leu
        115                 120                 125

Leu Gly Thr Pro Gly Val Asn Gln Thr Lys Phe Tyr Ser Glu Glu Glu
    130                 135                 140

Ala Glu Leu Lys His Cys Phe Tyr Lys Gly Tyr Val Asn Thr Asn Ser
145                 150                 155                 160
```

```
Glu His Thr Ala Val Ile Ser Leu Cys Ser Gly Met Leu Gly Thr Phe
                165                 170                 175

Arg Ser His Asp Gly Asp Tyr Phe Ile Glu Pro Leu Gln Ser Met Asp
            180                 185                 190

Glu Gln Glu Asp Glu Glu Glu Gln Asn Lys Pro His Ile Ile Tyr Arg
        195                 200                 205

Arg Ser Ala Pro Gln Arg Glu Pro Ser Thr Gly Arg His Ala Cys Asp
    210                 215                 220

Thr Ser Glu His Lys Asn Arg His Ser Lys Asp Lys Lys Lys Thr Arg
225                 230                 235                 240

Ala Arg Lys Trp Gly Glu Arg Ile Asn Leu Ala Gly Asp Val Ala Ala
                245                 250                 255

Leu Asn Ser Gly Leu Ala Thr Glu Ala Phe Ser Ala Tyr Gly Asn Lys
            260                 265                 270

Thr Asp Asn Thr Arg Glu Lys Arg Thr His Arg Arg Thr Lys Arg Phe
        275                 280                 285

Leu Ser Tyr Pro Arg Phe Val Glu Val Leu Val Val Ala Asp Asn Arg
    290                 295                 300

Met Val Ser Tyr His Gly Glu Asn Leu Gln His Tyr Ile Leu Thr Leu
305                 310                 315                 320

Met Ser Ile Val Ala Ser Ile Tyr Lys Asp Pro Ser Ile Gly Asn Leu
                325                 330                 335

Ile Asn Ile Val Ile Val Asn Leu Ile Val Ile His Asn Glu Gln Asp
            340                 345                 350

Gly Pro Ser Ile Ser Phe Asn Ala Gln Thr Thr Leu Lys Asn Phe Cys
        355                 360                 365

Gln Trp Gln His Ser Lys Asn Ser Pro Gly Gly Ile His His Asp Thr
    370                 375                 380
```

```
Ala Val Leu Leu Thr Arg Gln Asp Ile Cys Arg Ala His Asp Lys Cys
385                 390                 395                 400

Asp Thr Leu Gly Leu Ala Glu Leu Gly Thr Ile Cys Asp Pro Tyr Arg
                405                 410                 415

Ser Cys Ser Ile Ser Glu Asp Ser Gly Leu Ser Thr Ala Phe Thr Ile
            420                 425                 430

Ala His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Asn Asn
        435                 440                 445

Lys Cys Lys Glu Glu Gly Val Lys Ser Pro Gln His Val Met Ala Pro
    450                 455                 460

Thr Leu Asn Phe Tyr Thr Asn Pro Trp Met Trp Ser Lys Cys Ser Arg
465                 470                 475                 480

Lys Tyr Ile Thr Glu Phe Leu Glu
                485
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<210> 2315
<211> 69
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ADAMTS9; "

<220>
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<223> /note="Gene Name:
ADAM metallopeptidase with thrombospondin type 1
motif, 9; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478086"

<400> 2315

```
Ala Lys Cys Pro Gln Gly Arg Phe Ser Ile Asn Leu Tyr Gly Thr Gly
1               5                   10                  15

Leu Ser Leu Thr Glu Ser Ala Arg Trp Ile Ser Gln Gly Asn Tyr Ala
```

20 25 30

Val Ser Asp Ile Lys Lys Ser Pro Asp Gly Thr Arg Val Val Gly Lys
35 40 45

Cys Gly Gly Tyr Cys Gly Lys Cys Thr Pro Ser Ser Gly Thr Gly Leu
50 55 60

Glu Val Arg Val Leu
65

<210> 2316
<211> 470
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 576; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMDEC1; "

<220>
<221> source
<223> /note="Gene Name:
ADAM-like, decysin 1; "

<220>
<221> source
<223> /note="Uniprot ID: O15204; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000256412"

<400> 2316
Met Leu Arg Gly Ile Ser Gln Leu Pro Ala Val Ala Thr Met Ser Trp
1 5 10 15

Val Leu Leu Pro Val Leu Trp Leu Ile Val Gln Thr Gln Ala Ile Ala
20 25 30

Ile Lys Gln Thr Pro Glu Leu Thr Leu His Glu Ile Val Cys Pro Lys
35 40 45

Lys Leu His Ile Leu His Lys Arg Glu Ile Lys Asn Asn Gln Thr Glu
50 55 60

```
Lys His Gly Lys Glu Glu Arg Tyr Glu Pro Glu Val Gln Tyr Gln Met
65                  70                  75                  80

Ile Leu Asn Gly Glu Glu Ile Ile Leu Ser Leu Gln Lys Thr Lys His
                85                  90                  95

Leu Leu Gly Pro Asp Tyr Thr Glu Thr Leu Tyr Ser Pro Arg Gly Glu
            100                 105                 110

Glu Ile Thr Thr Lys Pro Glu Asn Met Glu His Cys Tyr Tyr Lys Gly
        115                 120                 125

Asn Ile Leu Asn Glu Lys Asn Ser Val Ala Ser Ile Ser Thr Cys Asp
    130                 135                 140

Gly Leu Arg Gly Tyr Phe Thr His His His Gln Arg Tyr Gln Ile Lys
145                 150                 155                 160

Pro Leu Lys Ser Thr Asp Glu Lys Glu His Ala Val Phe Thr Ser Asn
                165                 170                 175

Gln Glu Glu Gln Asp Pro Ala Asn His Thr Cys Gly Val Lys Ser Thr
            180                 185                 190

Asp Gly Lys Gln Gly Pro Ile Arg Ile Ser Arg Ser Leu Lys Ser Pro
        195                 200                 205

Glu Lys Glu Asp Phe Leu Arg Ala Gln Lys Tyr Ile Asp Leu Tyr Leu
    210                 215                 220

Val Leu Asp Asn Ala Phe Tyr Lys Asn Tyr Asn Glu Asn Leu Thr Leu
225                 230                 235                 240

Ile Arg Ser Phe Val Phe Asp Val Met Asn Leu Leu Asn Val Ile Tyr
                245                 250                 255

Asn Thr Ile Asp Val Gln Val Ala Leu Val Gly Met Glu Ile Trp Ser
            260                 265                 270

Asp Gly Asp Lys Ile Lys Val Val Pro Ser Ala Ser Thr Thr Phe Asp
        275                 280                 285
```

```
Asn Phe Leu Arg Trp His Ser Ser Asn Leu Gly Lys Lys Ile His Asp
    290                 295                 300

His Ala Gln Leu Leu Ser Gly Ile Ser Phe Asn Asn Arg Arg Val Gly
305                 310                 315                 320

Leu Ala Ala Ser Asn Ser Leu Cys Ser Pro Ser Ser Val Ala Val Ile
                325                 330                 335

Glu Ala Lys Lys Lys Asn Asn Val Ala Leu Val Gly Val Met Ser His
            340                 345                 350

Glu Leu Gly His Val Leu Gly Met Pro Asp Val Pro Phe Asn Thr Lys
        355                 360                 365

Cys Pro Ser Gly Ser Cys Val Met Asn Gln Tyr Leu Ser Ser Lys Phe
    370                 375                 380

Pro Lys Asp Phe Ser Thr Ser Cys Arg Ala His Phe Glu Arg Tyr Leu
385                 390                 395                 400

Leu Ser Gln Lys Pro Lys Cys Leu Leu Gln Ala Pro Ile Pro Thr Asn
                405                 410                 415

Ile Met Thr Thr Pro Val Cys Gly Asn His Leu Leu Glu Val Gly Glu
            420                 425                 430

Asp Cys Asp Cys Gly Ser Pro Lys Glu Cys Thr Asn Leu Cys Cys Glu
        435                 440                 445

Ala Leu Thr Cys Lys Leu Lys Pro Gly Thr Asp Cys Gly Gly Asp Ala
    450                 455                 460

Pro Asn His Thr Thr Glu
465                 470


<210> 2317
<211> 391
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 576; "
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<220>
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<223> /note="Gene Symbol: ADAMDEC1; "

<220>
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<223> /note="Gene Name:
ADAM-like, decysin 1; "

<220>
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<223> /note="Uniprot ID: O15204; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000428993"

<400> 2317
Met Ile Leu Asn Gly Glu Glu Ile Ile Leu Ser Leu Gln Lys Thr Lys
1 5 10 15

His Leu Leu Gly Pro Asp Tyr Thr Glu Thr Leu Tyr Ser Pro Arg Gly
20 25 30

Glu Glu Ile Thr Thr Lys Pro Glu Asn Met Glu His Cys Tyr Tyr Lys
35 40 45

Gly Asn Ile Leu Asn Glu Lys Asn Ser Val Ala Ser Ile Ser Thr Cys
50 55 60

Asp Gly Leu Arg Gly Tyr Phe Thr His His His Gln Arg Tyr Gln Ile
65 70 75 80

Lys Pro Leu Lys Ser Thr Asp Glu Lys Glu His Ala Val Phe Thr Ser
85 90 95

Asn Gln Glu Glu Gln Asp Pro Ala Asn His Thr Cys Gly Val Lys Ser
100 105 110

Thr Asp Gly Lys Gln Gly Pro Ile Arg Ile Ser Arg Ser Leu Lys Ser
115 120 125

Pro Glu Lys Glu Asp Phe Leu Arg Ala Gln Lys Tyr Ile Asp Leu Tyr
130 135 140

Leu Val Leu Asp Asn Ala Phe Tyr Lys Asn Tyr Asn Glu Asn Leu Thr
145 150 155 160

```
Leu Ile Arg Ser Phe Val Phe Asp Val Met Asn Leu Leu Asn Val Ile
                165                 170                 175

Tyr Asn Thr Ile Asp Val Gln Val Ala Leu Val Gly Met Glu Ile Trp
            180                 185                 190

Ser Asp Gly Asp Lys Ile Lys Val Val Pro Ser Ala Ser Thr Thr Phe
        195                 200                 205

Asp Asn Phe Leu Arg Trp His Ser Ser Asn Leu Gly Lys Lys Ile His
    210                 215                 220

Asp His Ala Gln Leu Leu Ser Gly Ile Ser Phe Asn Asn Arg Arg Val
225                 230                 235                 240

Gly Leu Ala Ala Ser Asn Ser Leu Cys Ser Pro Ser Ser Val Ala Val
                245                 250                 255

Ile Glu Ala Lys Lys Lys Asn Asn Val Ala Leu Val Gly Val Met Ser
            260                 265                 270

His Glu Leu Gly His Val Leu Gly Met Pro Asp Val Pro Phe Asn Thr
        275                 280                 285

Lys Cys Pro Ser Gly Ser Cys Val Met Asn Gln Tyr Leu Ser Ser Lys
    290                 295                 300

Phe Pro Lys Asp Phe Ser Thr Ser Cys Arg Ala His Phe Glu Arg Tyr
305                 310                 315                 320

Leu Leu Ser Gln Lys Pro Lys Cys Leu Leu Gln Ala Pro Ile Pro Thr
                325                 330                 335

Asn Ile Met Thr Thr Pro Val Cys Gly Asn His Leu Leu Glu Val Gly
            340                 345                 350

Glu Asp Cys Asp Cys Gly Ser Pro Lys Glu Cys Thr Asn Leu Cys Cys
        355                 360                 365

Glu Ala Leu Thr Cys Lys Leu Lys Pro Gly Thr Asp Cys Gly Gly Asp
    370                 375                 380
```

```
Ala Pro Asn His Thr Thr Glu
385                 390


<210> 2318
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 576; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMDEC1; "

<220>
<221> source
<223> /note="Gene Name:
      ADAM-like, decysin 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000431008"

<400> 2318
Met Leu Arg Gly Ile Ser Gln Leu Pro Ala Val Ala Thr Met Ser Trp
1               5                   10                  15


Val Leu Leu Pro Val Leu Trp Leu Ile Val Gln Thr Gln Ala Ser Asn
            20                  25                  30


Cys Ala Trp Pro Lys Val Ser Ile Gln
        35                  40


<210> 2319
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 577; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL1; "

<220>
<221> source
<223> /note="Gene Name:
      ADAMTS-like
      1; "
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<220>
<221> source
<223> /note="Uniprot ID: Q8N6G6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000276935"

<400> 2319
Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1   5   10   15

Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
            20   25   30

Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
        35   40   45

Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
    50   55   60

Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65   70   75   80

Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
                85   90   95

Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
            100   105   110

Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
        115   120   125

Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
    130   135   140

Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val
145   150   155   160

Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
                165   170   175

Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
            180   185   190

```
Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile
        195                 200                 205

Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His
    210                 215                 220

Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser
225                 230                 235                 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe
                245                 250                 255

Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu Thr
            260                 265                 270

Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr
        275                 280                 285

Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu Thr
    290                 295                 300

Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr
305                 310                 315                 320

Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln
                325                 330                 335

Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln
            340                 345                 350

Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly Tyr Lys Gln Ile
        355                 360                 365

Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp Glu Ala Thr Pro
    370                 375                 380

Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala
385                 390                 395                 400

Val Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu
                405                 410                 415
```

```
Glu Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys
            420                 425                 430

Asn Ile Phe Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys
        435                 440                 445

Thr Val Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile
    450                 455                 460

Asp His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro
465                 470                 475                 480

His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro Lys
                485                 490                 495

Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln Ala Gln
            500                 505                 510

Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser Phe Ile Pro
        515                 520                 525

Glu Ala Trp Ser Ala Cys Thr Val Thr Cys Gly Val Gly Thr Gln Val
    530                 535                 540

Arg Ile Val Arg Cys Gln Val Leu Leu Ser Phe Ser Gln Ser Val Ala
545                 550                 555                 560

Asp Leu Pro Ile Asp Glu Cys Glu Gly Pro Lys Pro Ala Ser Gln Arg
                565                 570                 575

Ala Cys Tyr Ala Gly Pro Cys Ser Gly Glu Ile Pro Glu Phe Asn Pro
            580                 585                 590

Asp Glu Thr Asp Gly Leu Phe Gly Gly Leu Gln Asp Phe Asp Glu Leu
        595                 600                 605

Tyr Asp Trp Glu Tyr Glu Gly Phe Thr Lys Cys Ser Glu Ser Cys Gly
    610                 615                 620

Gly Gly Val Gln Glu Ala Val Val Ser Cys Leu Asn Lys Gln Thr Arg
625                 630                 635                 640

Glu Pro Ala Glu Glu Asn Leu Cys Val Thr Ser Arg Arg Pro Pro Gln
```

645 650 655

Leu Leu Lys Ser Cys Asn Leu Asp Pro Cys Pro Ala Arg Ser Ser Ile
660 665 670

Asp Ser Ala Trp Asn Ala Cys Asn Val Leu Cys
675 680

<210> 2320
<211> 525
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: ADAMTSL1; "

<220>
<221> source
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ADAMTS-like
1; "

<220>
<221> source
<223> /note="Uniprot ID: Q8N6G6; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000327887"

<400> 2320
Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1 5 10 15

Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
20 25 30

Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
35 40 45

Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
50 55 60

Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65 70 75 80

```
Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
                85                  90                  95

Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
            100                 105                 110

Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
        115                 120                 125

Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
    130                 135                 140

Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val
145                 150                 155                 160

Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
                165                 170                 175

Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
            180                 185                 190

Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile
        195                 200                 205

Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His
    210                 215                 220

Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser
225                 230                 235                 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe
                245                 250                 255

Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu Thr
            260                 265                 270

Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr
        275                 280                 285

Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu Thr
    290                 295                 300
```

```
Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr
305                 310                 315                 320

Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln
                325                 330                 335

Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln
            340                 345                 350

Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly Tyr Lys Gln Ile
        355                 360                 365

Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp Glu Ala Thr Pro
    370                 375                 380

Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala
385                 390                 395                 400

Val Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu
                405                 410                 415

Glu Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys
            420                 425                 430

Asn Ile Phe Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys
        435                 440                 445

Thr Val Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile
    450                 455                 460

Asp His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro
465                 470                 475                 480

His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro Lys
                485                 490                 495

Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln Ala Gln
            500                 505                 510

Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser
        515                 520                 525
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<210> 2321
<211> 150
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
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<223> /note="Gene Name:
ADAMTS-like
1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000369911"

<400> 2321

```
Thr Ser Pro Leu Gly Thr Gln Leu Val Leu Asp Pro Gly Asn Ser Ala
1               5                  10                  15

Leu Leu Gly Cys Pro Ile Lys Gly His Pro Val Pro Asn Ile Thr Trp
            20                  25                  30

Phe His Gly Gly Gln Pro Ile Val Thr Ala Thr Gly Leu Thr His His
        35                  40                  45

Ile Leu Ala Ala Gly Gln Ile Leu Gln Val Ala Asn Leu Ser Gly Gly
    50                  55                  60

Ser Gln Gly Glu Phe Ser Cys Leu Ala Gln Asn Glu Ala Gly Val Leu
65                  70                  75                  80

Met Gln Lys Ala Ser Leu Val Ile Gln Asp Tyr Trp Trp Ser Val Asp
                85                  90                  95

Arg Leu Ala Thr Cys Ser Ala Ser Cys Gly Asn Arg Gly Val Gln Gln
            100                 105                 110

Pro Arg Leu Arg Cys Leu Leu Asn Ser Thr Glu Val Asn Pro Ala His
        115                 120                 125

Cys Ala Gly Lys Val Arg Pro Ala Val Gln Pro Ile Ala Cys Asn Arg
```

```
    130                 135                 140

Arg Asp Cys Pro Ser Arg
145                 150


<210> 2322
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      1; "

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<400> 2322
Met Ser Gly Val Phe Cys Phe Phe Phe Phe Phe Leu Gly Val Pro Glu
1               5                   10                  15


Ala Glu Val Thr Trp Phe Arg Asn Lys Ser Lys Leu Gly Ser Pro His
            20                  25                  30


His Leu His Glu Gly Ser Leu Leu Leu Thr Asn Val Ser Ser Ser Asp
        35                  40                  45


Gln Gly Leu Tyr Ser Cys Arg Ala Ala Asn Leu His Gly Glu Leu Thr
    50                  55                  60


Glu Ser Thr Gln Leu Leu Ile Leu Asp Pro Pro Gln Val Pro Thr Gln
65                  70                  75                  80


Leu Glu Asp Ile Arg Ala Leu Leu Ala Ala Thr Gly Pro Asn Leu Pro
                85                  90                  95
```

```
Ser Val Leu Thr Ser Pro Leu Gly Thr Gln Leu Val Leu Asp Pro Gly
            100                 105                 110

Asn Ser Ala Leu Leu Gly Cys Pro Ile Lys Gly His Pro Val Pro Asn
        115                 120                 125

Ile Thr Trp Phe His Gly Gly Gln Pro Ile Val Thr Ala Thr Gly Leu
    130                 135                 140

Thr His His Ile Leu Ala Ala Gly Gln Ile Leu Gln Val Ala Asn Leu
145                 150                 155                 160

Ser Gly Gly Ser Gln Gly Glu Phe Ser Cys Leu Ala Gln Asn Glu Ala
                165                 170                 175

Gly Val Leu Met Gln Lys Ala Ser Leu Val Ile Gln Asp Tyr Trp Trp
            180                 185                 190

Ser Val Asp Arg Leu Ala Thr Cys Ser Ala Ser Cys Gly Asn Arg Gly
        195                 200                 205

Val Gln Gln Pro Arg Leu Arg Cys Leu Leu Asn Ser Thr Glu Val Asn
    210                 215                 220

Pro Ala His Cys Ala Gly Lys Val Arg Pro Ala Val Gln Pro Ile Ala
225                 230                 235                 240

Cys Asn Arg Arg Asp Cys Pro Ser Arg Trp Met Val Thr Ser Trp Ser
                245                 250                 255

Ala Cys Thr Arg Ser Cys Gly Gly Gly Val Gln Thr Arg Arg Val Thr
            260                 265                 270

Cys Gln Lys Leu Lys Ala Ser Gly Ile Ser Thr Pro Val Ser Asn Asp
        275                 280                 285

Met Cys Thr Gln Val Ala Lys Arg Pro Val Asp Thr Gln Ala Cys Asn
    290                 295                 300

Gln Gln Leu Cys Val Glu Trp Ala Phe Ser Ser Trp Gly Gln Cys Asn
305                 310                 315                 320
```

```
Gly Pro Cys Ile Gly Pro His Leu Ala Val Gln His Arg Gln Val Phe
                325                 330                 335

Cys Gln Thr Arg Asp Gly Ile Thr Leu Pro Ser Glu Gln Cys Ser Ala
            340                 345                 350

Leu Pro Arg Pro Val Ser Thr Gln Asn Cys Trp Ser Glu Ala Cys Ser
        355                 360                 365

Val His Trp Arg Val Ser Leu Trp Thr Leu Cys Thr Ala Thr Cys Gly
    370                 375                 380

Asn Tyr Gly Phe Gln Ser Arg Arg Val Glu Cys Val His Ala Arg Thr
385                 390                 395                 400

Asn Lys Ala Val Pro Glu His Leu Cys Ser Trp Gly Pro Arg Pro Ala
                405                 410                 415

Asn Trp Gln Arg Cys Asn Ile Thr Pro Cys Glu Asn Met Glu Cys Arg
            420                 425                 430

Asp Thr Thr Arg Tyr Cys Glu Lys Val Lys Gln Leu Lys Leu Cys Gln
        435                 440                 445

Leu Ser Gln Phe Lys Ser Arg Cys Cys Gly Thr Cys Gly Lys Ala
    450                 455                 460


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<400> 2323

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Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1               5                  10                  15

Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
            20                  25                  30

Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
        35                  40                  45

Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
    50                  55                  60

Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65                  70                  75                  80

Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
                85                  90                  95

Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
            100                 105                 110

Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
        115                 120                 125

Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
    130                 135                 140

Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val
145                 150                 155                 160

Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
                165                 170                 175

Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
            180                 185                 190

Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile
```

```
        195                 200                 205

Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His
    210                 215                 220

Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser
225                 230                 235                 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe
                245                 250                 255

Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu Thr
            260                 265                 270

Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr
        275                 280                 285

Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu Thr
    290                 295                 300

Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr
305                 310                 315                 320

Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln
                325                 330                 335

Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln
            340                 345                 350

Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly Tyr Lys Gln Ile
        355                 360                 365

Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp Glu Ala Thr Pro
    370                 375                 380

Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala
385                 390                 395                 400

Val Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu
                405                 410                 415

Glu Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys
            420                 425                 430
```

```
Asn Ile Phe Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys
        435                 440                 445

Thr Val Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile
    450                 455                 460

Asp His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro
465                 470                 475                 480

His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro Lys
                485                 490                 495

Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln Ala Gln
            500                 505                 510

Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser Phe Ile Pro
        515                 520                 525

Glu Ala Trp Ser Ala Cys Thr Val Thr Cys Gly Val Gly Thr Gln Val
    530                 535                 540

Arg Ile Val Arg Cys Gln Val Leu Leu Ser Phe Ser Gln Ser Val Ala
545                 550                 555                 560

Asp Leu Pro Ile Asp Glu Cys Glu Gly Pro Lys Pro Ala Ser Gln Arg
                565                 570                 575

Ala Cys Tyr Ala Gly Pro Cys Ser Gly Glu Ile Pro Glu Phe Asn Pro
            580                 585                 590

Asp Glu Thr Asp Gly Leu Phe Gly Gly Leu Gln Asp Phe Asp Glu Leu
        595                 600                 605

Tyr Asp Trp Glu Tyr Glu Gly Phe Thr Lys Cys Ser Glu Ser Cys Gly
    610                 615                 620

Gly Gly Val Gln Glu Ala Val Val Ser Cys Leu Asn Lys Gln Thr Arg
625                 630                 635                 640

Glu Pro Ala Glu Glu Asn Leu Cys Val Thr Ser Arg Arg Pro Pro Gln
                645                 650                 655
```

```
Leu Leu Lys Ser Cys Asn Leu Asp Pro Cys Pro Ala Arg Trp Glu Ile
            660                 665                 670

Gly Lys Trp Ser Pro Cys Ser Leu Thr Cys Gly Val Gly Leu Gln Thr
        675                 680                 685

Arg Asp Val Phe Cys Ser His Leu Leu Ser Arg Glu Met Asn Glu Thr
    690                 695                 700

Val Ile Leu Ala Asp Glu Leu Cys Arg Gln Pro Lys Pro Ser Thr Val
705                 710                 715                 720

Gln Ala Cys Asn Arg Phe Asn Cys Pro Pro Ala Trp Tyr Pro Ala Gln
                725                 730                 735

Trp Gln Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Gln Lys Arg Glu
            740                 745                 750

Val Leu Cys Lys Gln Arg Met Ala Asp Gly Ser Phe Leu Glu Leu Pro
        755                 760                 765

Glu Thr Phe Cys Ser Ala Ser Lys Pro Ala Cys Gln Gln Ala Cys Lys
    770                 775                 780

Lys Asp Asp Cys Pro Ser Glu Trp Leu Leu Ser Asp Trp Thr Glu Cys
785                 790                 795                 800

Ser Thr Ser Cys Gly Glu Gly Thr Gln Thr Arg Ser Ala Ile Cys Arg
                805                 810                 815

Lys Met Leu Lys Thr Gly Leu Ser Thr Val Val Asn Ser Thr Leu Cys
            820                 825                 830

Pro Pro Leu Pro Phe Ser Ser Ser Ile Arg Pro Cys Met Leu Ala Thr
        835                 840                 845

Cys Ala Arg Pro Gly Arg Pro Ser Thr Lys His Ser Pro His Ile Ala
    850                 855                 860

Ala Ala Arg Lys Val Tyr Ile Gln Thr Arg Arg Gln Arg Lys Leu His
865                 870                 875                 880
```

```
Phe Val Val Gly Gly Phe Ala Tyr Leu Leu Pro Lys Thr Ala Val Val
                885                 890                 895

Leu Arg Cys Pro Ala Arg Arg Val Arg Lys Pro Leu Ile Thr Trp Glu
            900                 905                 910

Lys Asp Gly Gln His Leu Ile Ser Ser Thr His Val Thr Val Ala Pro
        915                 920                 925

Phe Gly Tyr Leu Lys Ile His Arg Leu Lys Pro Ser Asp Ala Gly Val
    930                 935                 940

Tyr Thr Cys Ser Ala Gly Pro Ala Arg Glu His Phe Val Ile Lys Leu
945                 950                 955                 960

Ile Gly Gly Asn Arg Lys Leu Val Ala Arg Pro Leu Ser Pro Arg Ser
                965                 970                 975

Glu Glu Glu Val Leu Ala Gly Arg Lys Gly Gly Pro Lys Glu Ala Leu
            980                 985                 990

Gln Thr His Lys His Gln Asn Gly  Ile Phe Ser Asn Gly  Ser Lys
Ala
        995                 1000                1005

Glu Lys  Arg Gly Leu Ala Ala  Asn Pro Gly Ser Arg  Tyr Asp Asp
    1010                1015                1020

Leu Val  Ser Arg Leu Leu Glu  Gln Gly Gly Trp Pro  Gly Glu Leu
    1025                1030                1035

Leu Ala  Ser Trp Glu Ala Gln  Asp Ser Ala Glu Arg  Asn Thr Thr
    1040                1045                1050

Ser Glu  Glu Asp Pro Gly Ala  Glu Gln Val Leu Leu  His Leu Pro
    1055                1060                1065

Phe Thr  Met Val Thr Glu Gln  Arg Arg Leu Asp Asp  Ile Leu Gly
    1070                1075                1080

Asn Leu  Ser Gln Gln Pro Glu  Glu Leu Arg Asp Leu  Tyr Ser Lys
    1085                1090                1095
```

```
His Leu  Val Ala Gln Leu Ala  Gln Glu Ile Phe Arg  Ser His Leu
    1100                1105                1110

Glu His  Gln Asp Thr Leu Leu  Lys Pro Ser Glu Arg  Arg Thr Ser
    1115                1120                1125

Pro Val  Thr Leu Ser Pro His  Lys His Val Ser Gly  Phe Ser Ser
    1130                1135                1140

Ser Leu  Arg Thr Ser Ser Thr  Gly Asp Ala Gly Gly  Gly Ser Arg
    1145                1150                1155

Arg Pro  His Arg Lys Pro Thr  Ile Leu Arg Lys Ile  Ser Ala Ala
    1160                1165                1170

Gln Gln  Leu Ser Ala Ser Glu  Val Val Thr His Leu  Gly Gln Thr
    1175                1180                1185

Val Ala  Leu Ala Ser Gly Thr  Leu Ser Val Leu Leu  His Cys Glu
    1190                1195                1200

Ala Ile  Gly His Pro Arg Pro  Thr Ile Ser Trp Ala  Arg Asn Gly
    1205                1210                1215

Glu Glu  Val Gln Phe Ser Asp  Arg Ile Leu Leu Gln  Pro Asp Asp
    1220                1225                1230

Ser Leu  Gln Ile Leu Ala Pro  Val Glu Ala Asp Val  Gly Phe Tyr
    1235                1240                1245

Thr Cys  Asn Ala Thr Asn Ala  Leu Gly Tyr Asp Ser  Val Ser Ile
    1250                1255                1260

Ala Val  Thr Leu Ala Gly Lys  Pro Leu Val Lys Thr  Ser Arg Met
    1265                1270                1275

Thr Val  Ile Asn Thr Glu Lys  Pro Ala Val Thr Val  Asp Ile Gly
    1280                1285                1290

Ser Thr  Ile Lys Thr Val Gln  Gly Val Asn Val Thr  Ile Asn Cys
    1295                1300                1305

Gln Val  Ala Gly Val Pro Glu  Ala Glu Val Thr Trp  Phe Arg Asn
```

1310 1315 1320

Lys Ser Lys Leu Gly Ser Pro His His Leu His Glu Gly Ser Leu
1325 1330 1335

Leu Leu Thr Asn Val Ser Ser Ser Asp Gln Gly Leu Tyr Ser Cys
1340 1345 1350

Arg Ala Ala Asn Leu His Gly Glu Leu Thr Glu Ser Thr Gln Leu
1355 1360 1365

Leu Ile Leu Asp Pro Pro Gln Val Pro Thr Gln Leu Glu Asp Ile
1370 1375 1380

Arg Ala Leu Leu Ala Ala Thr Gly Pro Asn Leu Pro Ser Val Leu
1385 1390 1395

Thr Ser Pro Leu Gly Thr Gln Leu Val Leu Asp Pro Gly Asn Ser
1400 1405 1410

Ala Leu Leu Gly Cys Pro Ile Lys Gly His Pro Val Pro Asn Ile
1415 1420 1425

Thr Trp Phe His Gly Gly Gln Pro Ile Val Thr Ala Thr Gly Leu
1430 1435 1440

Thr His His Ile Leu Ala Ala Gly Gln Ile Leu Gln Val Ala Asn
1445 1450 1455

Leu Ser Gly Gly Ser Gln Gly Glu Phe Ser Cys Leu Ala Gln Asn
1460 1465 1470

Glu Ala Gly Val Leu Met Gln Lys Ala Ser Leu Val Ile Gln Asp
1475 1480 1485

Tyr Trp Trp Ser Val Asp Arg Leu Ala Thr Cys Ser Ala Ser Cys
1490 1495 1500

Gly Asn Arg Gly Val Gln Gln Pro Arg Leu Arg Cys Leu Leu Asn
1505 1510 1515

Ser Thr Glu Val Asn Pro Ala His Cys Ala Gly Lys Val Arg Pro
1520 1525 1530

```
Ala Val  Gln Pro Ile Ala Cys  Asn Arg Arg Asp Cys  Pro Ser Arg
    1535                1540                1545

Trp Met  Val Thr Ser Trp Ser  Ala Cys Thr Arg Ser  Cys Gly Gly
    1550                1555                1560

Gly Val  Gln Thr Arg Arg Val  Thr Cys Gln Lys Leu  Lys Ala Ser
    1565                1570                1575

Gly Ile  Ser Thr Pro Val Ser  Asn Asp Met Cys Thr  Gln Val Ala
    1580                1585                1590

Lys Arg  Pro Val Asp Thr Gln  Ala Cys Asn Gln Gln  Leu Cys Val
    1595                1600                1605

Glu Trp  Ala Phe Ser Ser Trp  Gly Gln Cys Asn Gly  Pro Cys Ile
    1610                1615                1620

Gly Pro  His Leu Ala Val Gln  His Arg Gln Val Phe  Cys Gln Thr
    1625                1630                1635

Arg Asp  Gly Ile Thr Leu Pro  Ser Glu Gln Cys Ser  Ala Leu Pro
    1640                1645                1650

Arg Pro  Val Ser Thr Gln Asn  Cys Trp Ser Glu Ala  Cys Ser Val
    1655                1660                1665

His Trp  Arg Val Ser Leu Trp  Thr Leu Cys Thr Ala  Thr Cys Gly
    1670                1675                1680

Asn Tyr  Gly Phe Gln Ser Arg  Arg Val Glu Cys Val  His Ala Arg
    1685                1690                1695

Thr Asn  Lys Ala Val Pro Glu  His Leu Cys Ser Trp  Gly Pro Arg
    1700                1705                1710

Pro Ala  Asn Trp Gln Arg Cys  Asn Ile Thr Pro Cys  Glu Asn Met
    1715                1720                1725

Glu Cys  Arg Asp Thr Thr Arg  Tyr Cys Glu Lys Val  Lys Gln Leu
    1730                1735                1740
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```
Lys Leu  Cys Gln Leu Ser Gln  Phe Lys Ser Arg Cys  Cys Gly Thr
    1745                1750                1755


Cys Gly  Lys Ala
    1760


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Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1               5                   10                  15


Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
            20                  25                  30


Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
        35                  40                  45


Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
    50                  55                  60


Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65                  70                  75                  80
```

```
Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
                85                  90                  95

Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
            100                 105                 110

Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
        115                 120                 125

Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
    130                 135                 140

Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val
145                 150                 155                 160

Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
                165                 170                 175

Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
            180                 185                 190

Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile
        195                 200                 205

Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His
    210                 215                 220

Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser
225                 230                 235                 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe
                245                 250                 255

Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu Thr
            260                 265                 270

Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr
        275                 280                 285

Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu Thr
    290                 295                 300

Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr
```

```
305                 310                 315                 320

Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln
                325                 330                 335

Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln
            340                 345                 350

Glu Cys Asn Leu Asp Pro Cys Pro Ala Arg Trp Glu Ala Thr Pro Trp
        355                 360                 365

Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val
    370                 375                 380

Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu
385                 390                 395                 400

Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn
                405                 410                 415

Ile Phe Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Val Thr
            420                 425                 430

Val Pro Ser Phe Phe Val His
        435


<210> 2325
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Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1 5 10 15

Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
20 25 30

Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
35 40 45

Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
50 55 60

Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65 70 75 80

Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
85 90 95

Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
100 105 110

Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
115 120 125

Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
130 135 140

Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val
145 150 155 160

Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
165 170 175

Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
180 185 190

Lys Ser Gln Leu Ser Ala Thr Lys Cys Lys Thr His Arg Asp Gly Arg
195 200 205

Pro Leu Asp Leu Leu Thr Tyr Pro Leu Leu Ala
210 215

<210> 2326
<211> 275
<212> PRT
<213> Homo sapiens

<220>
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<400> 2326
Met Ser Gly Val Phe Cys Phe Phe Phe Phe Phe Leu Gly Val Pro Glu
1 5 10 15

Ala Glu Val Thr Trp Phe Arg Asn Lys Ser Lys Leu Gly Ser Pro His
20 25 30

His Leu His Glu Gly Ser Leu Leu Leu Thr Asn Val Ser Ser Ser Asp
35 40 45

Gln Gly Leu Tyr Ser Cys Arg Ala Ala Asn Leu His Gly Glu Leu Thr
50 55 60

Glu Ser Thr Gln Leu Leu Ile Leu Asp Pro Pro Gln Val Pro Thr Gln
65 70 75 80

Leu Glu Asp Ile Arg Ala Leu Leu Ala Ala Thr Gly Pro Asn Leu Pro
85 90 95

Ser Val Leu Thr Ser Pro Leu Gly Thr Gln Leu Val Leu Asp Pro Gly
100 105 110

Asn Ser Ala Leu Leu Gly Cys Pro Ile Lys Gly His Pro Val Pro Asn
115 120 125

```
Ile Thr Trp Phe His Gly Gly Gln Pro Ile Val Thr Ala Thr Gly Leu
    130                 135                 140

Thr His His Ile Leu Ala Ala Gly Gln Ile Leu Gln Val Ala Asn Leu
145                 150                 155                 160

Ser Gly Gly Ser Gln Gly Glu Phe Ser Cys Leu Ala Gln Asn Glu Ala
                165                 170                 175

Gly Val Leu Met Gln Lys Ala Ser Leu Val Ile Gln Val Gln Trp Ala
            180                 185                 190

Leu His Arg Ala Ser Pro Ser Cys Ala Thr Gln Thr Ser Leu Leu Pro
        195                 200                 205

Asp Thr Gly Trp His His Leu Thr Ile Arg Ala Val Gln Cys Ser Ser
    210                 215                 220

Glu Ala Cys Glu His Pro Glu Leu Leu Val Arg Gly Leu Gln Cys Thr
225                 230                 235                 240

Leu Glu Ser Gln Pro Val Asp Pro Val His Ser Tyr Leu Trp Gln Leu
                245                 250                 255

Arg Leu Pro Val Pro Ala Cys Gly Val Cys Ala Cys Pro His Gln Gln
            260                 265                 270

Gly Ser Ala
        275


<210> 2327
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<212> PRT
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<220>
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<223> /note="ENSP ID: ENSP00000401157"

<400> 2327
Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1 5 10 15

Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
20 25 30

Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
35 40 45

Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
50 55 60

Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65 70 75 80

Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
85 90 95

Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
100 105 110

Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
115 120 125

Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
130 135 140

Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Val Ser
145 150 155 160

Ala Asp Leu Phe Ser Phe Asn Leu Ser Arg Gly Phe Gln Cys Leu Cys
165 170 175

Val Asn Gly Leu His Ser Leu Thr Leu
180 185

<210> 2328
<211> 258

<212> PRT
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<400> 2328
Met Ser Gly Val Phe Cys Phe Phe Phe Phe Phe Leu Gly Val Pro Glu
1   5   10   15

Ala Glu Val Thr Trp Phe Arg Asn Lys Ser Lys Leu Gly Ser Pro His
            20   25   30

His Leu His Glu Gly Ser Leu Leu Leu Thr Asn Val Ser Ser Ser Asp
        35   40   45

Gln Gly Leu Tyr Ser Cys Arg Ala Ala Asn Leu His Gly Glu Leu Thr
    50   55   60

Glu Ser Thr Gln Leu Leu Ile Leu Asp Pro Pro Gln Val Pro Thr Gln
65   70   75   80

Leu Glu Asp Ile Arg Ala Leu Leu Ala Ala Thr Gly Pro Asn Leu Pro
                85   90   95

Ser Val Leu Thr Ser Pro Leu Gly Thr Gln Leu Val Leu Asp Pro Gly
            100   105   110

Asn Ser Ala Leu Leu Gly Cys Pro Ile Lys Gly His Pro Val Pro Asn
        115   120   125

```
Ile Thr Trp Phe His Gly Gly Gln Pro Ile Val Thr Ala Thr Gly Leu
    130                 135                 140

Thr His His Ile Leu Ala Ala Gly Gln Ile Leu Gln Val Ala Asn Leu
145                 150                 155                 160

Ser Gly Gly Ser Gln Gly Glu Phe Ser Cys Leu Ala Gln Asn Glu Ala
                165                 170                 175

Gly Val Leu Met Gln Lys Ala Ser Leu Val Ile Gln Asp Tyr Trp Trp
            180                 185                 190

Ser Val Asp Arg Leu Ala Thr Cys Ser Ala Ser Cys Gly Asn Arg Gly
        195                 200                 205

Val Gln Gln Pro Arg Leu Arg Cys Leu Leu Asn Ser Thr Glu Val Asn
    210                 215                 220

Pro Ala His Cys Ala Gly Lys Val Arg Pro Ala Val Gln Pro Ile Ala
225                 230                 235                 240

Cys Asn Arg Arg Asp Cys Pro Ser Arg Ala Met Gly Leu Ala Ser Gly
                245                 250                 255

Leu Thr
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<210> 2329
<211> 951
<212> PRT
<213> Homo sapiens

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<223> /note="Payload ID: 578; "

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<223> /note="Gene Symbol: ADAMTSL2; "

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<223> /note="Gene Name:
ADAMTS-like 2; "

<220>
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<223> /note="Uniprot ID: Q86TH1; "

<220>
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<223> /note="ENSP ID: ENSP00000346478"

<400> 2329

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Met Asp Gly Arg Trp Gln Cys Ser Cys Trp Ala Trp Phe Leu Leu Val
1               5                  10                  15

Leu Ala Val Val Ala Gly Asp Thr Val Ser Thr Gly Ser Thr Asp Asn
            20                  25                  30

Ser Pro Thr Ser Asn Ser Leu Glu Gly Gly Thr Asp Ala Thr Ala Phe
        35                  40                  45

Trp Trp Gly Glu Trp Thr Lys Trp Thr Ala Cys Ser Arg Ser Cys Gly
    50                  55                  60

Gly Gly Val Thr Ser Gln Glu Arg His Cys Leu Gln Gln Arg Arg Lys
65                  70                  75                  80

Ser Val Pro Gly Pro Gly Asn Arg Thr Cys Thr Gly Thr Ser Lys Arg
                85                  90                  95

Tyr Gln Leu Cys Arg Val Gln Glu Cys Pro Pro Asp Gly Arg Ser Phe
            100                 105                 110

Arg Glu Glu Gln Cys Val Ser Phe Asn Ser His Val Tyr Asn Gly Arg
        115                 120                 125

Thr His Gln Trp Lys Pro Leu Tyr Pro Asp Asp Tyr Val His Ile Ser
    130                 135                 140

Ser Lys Pro Cys Asp Leu His Cys Thr Thr Val Asp Gly Gln Arg Gln
145                 150                 155                 160

Leu Met Val Pro Ala Arg Asp Gly Thr Ser Cys Lys Leu Thr Asp Leu
                165                 170                 175

Arg Gly Val Cys Val Ser Gly Lys Cys Glu Pro Ile Gly Cys Asp Gly
            180                 185                 190

Val Leu Phe Ser Thr His Thr Leu Asp Lys Cys Gly Ile Cys Gln Gly
        195                 200                 205
```

```
Asp Gly Ser Ser Cys Thr His Val Thr Gly Asn Tyr Arg Lys Gly Asn
    210                 215                 220

Ala His Leu Gly Tyr Ser Leu Val Thr His Ile Pro Ala Gly Ala Arg
225                 230                 235                 240

Asp Ile Gln Ile Val Glu Arg Lys Lys Ser Ala Asp Val Leu Ala Leu
                245                 250                 255

Ala Asp Glu Ala Gly Tyr Tyr Phe Phe Asn Gly Asn Tyr Lys Val Asp
            260                 265                 270

Ser Pro Lys Asn Phe Asn Ile Ala Gly Thr Val Val Lys Tyr Arg Arg
        275                 280                 285

Pro Met Asp Val Tyr Glu Thr Gly Ile Glu Tyr Ile Val Ala Gln Gly
    290                 295                 300

Pro Thr Asn Gln Gly Leu Asn Val Met Val Trp Asn Gln Asn Gly Lys
305                 310                 315                 320

Ser Pro Ser Ile Thr Phe Glu Tyr Thr Leu Leu Gln Pro Pro His Glu
                325                 330                 335

Ser Arg Pro Gln Pro Ile Tyr Tyr Gly Phe Ser Glu Ser Ala Glu Ser
            340                 345                 350

Gln Gly Leu Asp Gly Ala Gly Leu Met Gly Phe Val Pro His Asn Gly
        355                 360                 365

Ser Leu Tyr Gly Gln Ala Ser Ser Glu Arg Leu Gly Leu Asp Asn Arg
    370                 375                 380

Leu Phe Gly His Pro Gly Leu Asp Met Glu Leu Gly Pro Ser Gln Gly
385                 390                 395                 400

Gln Glu Thr Asn Glu Val Cys Glu Gln Ala Gly Gly Gly Ala Cys Glu
                405                 410                 415

Gly Pro Pro Arg Gly Lys Gly Phe Arg Asp Arg Asn Val Thr Gly Thr
            420                 425                 430
```

```
Pro Leu Thr Gly Asp Lys Asp Asp Glu Glu Val Asp Thr His Phe Ala
        435                 440                 445

Ser Gln Glu Phe Phe Ser Ala Asn Ala Ile Ser Asp Gln Leu Leu Gly
    450                 455                 460

Ala Gly Ser Asp Leu Lys Asp Phe Thr Leu Asn Glu Thr Val Asn Ser
465                 470                 475                 480

Ile Phe Ala Gln Gly Ala Pro Arg Ser Ser Leu Ala Glu Ser Phe Phe
                485                 490                 495

Val Asp Tyr Glu Glu Asn Glu Gly Ala Gly Pro Tyr Leu Leu Asn Gly
            500                 505                 510

Ser Tyr Leu Glu Leu Ser Ser Asp Arg Val Ala Asn Ser Ser Ser Glu
        515                 520                 525

Ala Pro Phe Pro Asn Val Ser Thr Ser Leu Leu Thr Ser Ala Gly Asn
    530                 535                 540

Arg Thr His Lys Ala Arg Thr Arg Pro Lys Ala Arg Lys Gln Gly Val
545                 550                 555                 560

Ser Pro Ala Asp Met Tyr Arg Trp Lys Leu Ser Ser His Glu Pro Cys
                565                 570                 575

Ser Ala Thr Cys Thr Thr Gly Val Met Ser Ala Tyr Ala Met Cys Val
            580                 585                 590

Arg Tyr Asp Gly Val Glu Val Asp Asp Ser Tyr Cys Asp Ala Leu Thr
        595                 600                 605

Arg Pro Glu Pro Val His Glu Phe Cys Ala Gly Arg Glu Cys Gln Pro
    610                 615                 620

Arg Trp Glu Thr Ser Ser Trp Ser Glu Cys Ser Arg Thr Cys Gly Glu
625                 630                 635                 640

Gly Tyr Gln Phe Arg Val Val Arg Cys Trp Lys Met Leu Ser Pro Gly
                645                 650                 655
```

```
Phe Asp Ser Ser Val Tyr Ser Asp Leu Cys Glu Ala Ala Glu Ala Val
            660                 665                 670

Arg Pro Glu Glu Arg Lys Thr Cys Arg Asn Pro Ala Cys Gly Pro Gln
        675                 680                 685

Trp Glu Met Ser Glu Trp Ser Glu Cys Thr Ala Lys Cys Gly Glu Arg
    690                 695                 700

Ser Val Val Thr Arg Asp Ile Arg Cys Ser Glu Asp Glu Lys Leu Cys
705                 710                 715                 720

Asp Pro Asn Thr Arg Pro Val Gly Glu Lys Asn Cys Thr Gly Pro Pro
                725                 730                 735

Cys Asp Arg Gln Trp Thr Val Ser Asp Trp Gly Pro Cys Ser Gly Ser
            740                 745                 750

Cys Gly Gln Gly Arg Thr Ile Arg His Val Tyr Cys Lys Thr Ser Asp
        755                 760                 765

Gly Arg Val Val Pro Glu Ser Gln Cys Gln Met Glu Thr Lys Pro Leu
    770                 775                 780

Ala Ile His Pro Cys Gly Asp Lys Asn Cys Pro Ala His Trp Leu Ala
785                 790                 795                 800

Gln Asp Trp Glu Arg Cys Asn Thr Thr Cys Gly Arg Gly Val Lys Lys
                805                 810                 815

Arg Leu Val Leu Cys Met Glu Leu Ala Asn Gly Lys Pro Gln Thr Arg
            820                 825                 830

Ser Gly Pro Glu Cys Gly Leu Ala Lys Lys Pro Pro Glu Glu Ser Thr
        835                 840                 845

Cys Phe Glu Arg Pro Cys Phe Lys Trp Tyr Thr Ser Pro Trp Ser Glu
    850                 855                 860

Cys Thr Lys Thr Cys Gly Val Gly Val Arg Met Arg Asp Val Lys Cys
865                 870                 875                 880

Tyr Gln Gly Thr Asp Ile Val Arg Gly Cys Asp Pro Leu Val Lys Pro
```

885 890 895

Val Gly Arg Gln Ala Cys Asp Leu Gln Pro Cys Pro Thr Glu Pro Pro
900 905 910

Asp Asp Ser Cys Gln Asp Gln Pro Gly Thr Asn Cys Ala Leu Ala Ile
915 920 925

Lys Val Asn Leu Cys Gly His Trp Tyr Tyr Ser Lys Ala Cys Cys Arg
930 935 940

Ser Cys Arg Pro Pro His Ser
945 950

<210> 2330
<211> 951
<212> PRT
<213> Homo sapiens

<220>
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<221> source
<223> /note="Gene Symbol: ADAMTSL2; "

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ADAMTS-like 2; "

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<223> /note="Uniprot ID: Q86TH1; "

<220>
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<400> 2330
Met Asp Gly Arg Trp Gln Cys Ser Cys Trp Ala Trp Phe Leu Leu Val
1 5 10 15

Leu Ala Val Val Ala Gly Asp Thr Val Ser Thr Gly Ser Thr Asp Asn
20 25 30

Ser Pro Thr Ser Asn Ser Leu Glu Gly Gly Thr Asp Ala Thr Ala Phe
35 40 45

```
Trp Trp Gly Glu Trp Thr Lys Trp Thr Ala Cys Ser Arg Ser Cys Gly
    50                  55                  60

Gly Gly Val Thr Ser Gln Glu Arg His Cys Leu Gln Gln Arg Arg Lys
65                  70                  75                  80

Ser Val Pro Gly Pro Gly Asn Arg Thr Cys Thr Gly Thr Ser Lys Arg
                85                  90                  95

Tyr Gln Leu Cys Arg Val Gln Glu Cys Pro Pro Asp Gly Arg Ser Phe
            100                 105                 110

Arg Glu Glu Gln Cys Val Ser Phe Asn Ser His Val Tyr Asn Gly Arg
        115                 120                 125

Thr His Gln Trp Lys Pro Leu Tyr Pro Asp Asp Tyr Val His Ile Ser
    130                 135                 140

Ser Lys Pro Cys Asp Leu His Cys Thr Thr Val Asp Gly Gln Arg Gln
145                 150                 155                 160

Leu Met Val Pro Ala Arg Asp Gly Thr Ser Cys Lys Leu Thr Asp Leu
                165                 170                 175

Arg Gly Val Cys Val Ser Gly Lys Cys Glu Pro Ile Gly Cys Asp Gly
            180                 185                 190

Val Leu Phe Ser Thr His Thr Leu Asp Lys Cys Gly Ile Cys Gln Gly
        195                 200                 205

Asp Gly Ser Ser Cys Thr His Val Thr Gly Asn Tyr Arg Lys Gly Asn
    210                 215                 220

Ala His Leu Gly Tyr Ser Leu Val Thr His Ile Pro Ala Gly Ala Arg
225                 230                 235                 240

Asp Ile Gln Ile Val Glu Arg Lys Lys Ser Ala Asp Val Leu Ala Leu
                245                 250                 255

Ala Asp Glu Ala Gly Tyr Tyr Phe Phe Asn Gly Asn Tyr Lys Val Asp
            260                 265                 270
```

```
Ser Pro Lys Asn Phe Asn Ile Ala Gly Thr Val Val Lys Tyr Arg Arg
        275                 280                 285

Pro Met Asp Val Tyr Glu Thr Gly Ile Glu Tyr Ile Val Ala Gln Gly
    290                 295                 300

Pro Thr Asn Gln Gly Leu Asn Val Met Val Trp Asn Gln Asn Gly Lys
305                 310                 315                 320

Ser Pro Ser Ile Thr Phe Glu Tyr Thr Leu Leu Gln Pro Pro His Glu
                325                 330                 335

Ser Arg Pro Gln Pro Ile Tyr Tyr Gly Phe Ser Glu Ser Ala Glu Ser
            340                 345                 350

Gln Gly Leu Asp Gly Ala Gly Leu Met Gly Phe Val Pro His Asn Gly
        355                 360                 365

Ser Leu Tyr Gly Gln Ala Ser Ser Glu Arg Leu Gly Leu Asp Asn Arg
    370                 375                 380

Leu Phe Gly His Pro Gly Leu Asp Met Glu Leu Gly Pro Ser Gln Gly
385                 390                 395                 400

Gln Glu Thr Asn Glu Val Cys Glu Gln Ala Gly Gly Gly Ala Cys Glu
                405                 410                 415

Gly Pro Pro Arg Gly Lys Gly Phe Arg Asp Arg Asn Val Thr Gly Thr
            420                 425                 430

Pro Leu Thr Gly Asp Lys Asp Asp Glu Glu Val Asp Thr His Phe Ala
        435                 440                 445

Ser Gln Glu Phe Phe Ser Ala Asn Ala Ile Ser Asp Gln Leu Leu Gly
    450                 455                 460

Ala Gly Ser Asp Leu Lys Asp Phe Thr Leu Asn Glu Thr Val Asn Ser
465                 470                 475                 480

Ile Phe Ala Gln Gly Ala Pro Arg Ser Ser Leu Ala Glu Ser Phe Phe
                485                 490                 495

Val Asp Tyr Glu Glu Asn Glu Gly Ala Gly Pro Tyr Leu Leu Asn Gly
```

```
            500                 505                 510

Ser Tyr Leu Glu Leu Ser Ser Asp Arg Val Ala Asn Ser Ser Ser Glu
        515                 520                 525

Ala Pro Phe Pro Asn Val Ser Thr Ser Leu Leu Thr Ser Ala Gly Asn
    530                 535                 540

Arg Thr His Lys Ala Arg Thr Arg Pro Lys Ala Arg Lys Gln Gly Val
545                 550                 555                 560

Ser Pro Ala Asp Met Tyr Arg Trp Lys Leu Ser Ser His Glu Pro Cys
                565                 570                 575

Ser Ala Thr Cys Thr Thr Gly Val Met Ser Ala Tyr Ala Met Cys Val
            580                 585                 590

Arg Tyr Asp Gly Val Glu Val Asp Asp Ser Tyr Cys Asp Ala Leu Thr
        595                 600                 605

Arg Pro Glu Pro Val His Glu Phe Cys Ala Gly Arg Glu Cys Gln Pro
    610                 615                 620

Arg Trp Glu Thr Ser Ser Trp Ser Glu Cys Ser Arg Thr Cys Gly Glu
625                 630                 635                 640

Gly Tyr Gln Phe Arg Val Val Arg Cys Trp Lys Met Leu Ser Pro Gly
                645                 650                 655

Phe Asp Ser Ser Val Tyr Ser Asp Leu Cys Glu Ala Ala Glu Ala Val
            660                 665                 670

Arg Pro Glu Glu Arg Lys Thr Cys Arg Asn Pro Ala Cys Gly Pro Gln
        675                 680                 685

Trp Glu Met Ser Glu Trp Ser Glu Cys Thr Ala Lys Cys Gly Glu Arg
    690                 695                 700

Ser Val Val Thr Arg Asp Ile Arg Cys Ser Glu Asp Glu Lys Leu Cys
705                 710                 715                 720

Asp Pro Asn Thr Arg Pro Val Gly Glu Lys Asn Cys Thr Gly Pro Pro
                725                 730                 735
```

```
Cys Asp Arg Gln Trp Thr Val Ser Asp Trp Gly Pro Cys Ser Gly Ser
            740                 745                 750

Cys Gly Gln Gly Arg Thr Ile Arg His Val Tyr Cys Lys Thr Ser Asp
        755                 760                 765

Gly Arg Val Val Pro Glu Ser Gln Cys Gln Met Glu Thr Lys Pro Leu
    770                 775                 780

Ala Ile His Pro Cys Gly Asp Lys Asn Cys Pro Ala His Trp Leu Ala
785                 790                 795                 800

Gln Asp Trp Glu Arg Cys Asn Thr Thr Cys Gly Arg Gly Val Lys Lys
                805                 810                 815

Arg Leu Val Leu Cys Met Glu Leu Ala Asn Gly Lys Pro Gln Thr Arg
            820                 825                 830

Ser Gly Pro Glu Cys Gly Leu Ala Lys Lys Pro Pro Glu Glu Ser Thr
        835                 840                 845

Cys Phe Glu Arg Pro Cys Phe Lys Trp Tyr Thr Ser Pro Trp Ser Glu
    850                 855                 860

Cys Thr Lys Thr Cys Gly Val Gly Val Arg Met Arg Asp Val Lys Cys
865                 870                 875                 880

Tyr Gln Gly Thr Asp Ile Val Arg Gly Cys Asp Pro Leu Val Lys Pro
                885                 890                 895

Val Gly Arg Gln Ala Cys Asp Leu Gln Pro Cys Pro Thr Glu Pro Pro
            900                 905                 910

Asp Asp Ser Cys Gln Asp Gln Pro Gly Thr Asn Cys Ala Leu Ala Ile
        915                 920                 925

Lys Val Asn Leu Cys Gly His Trp Tyr Tyr Ser Lys Ala Cys Cys Arg
    930                 935                 940

Ser Cys Arg Pro Pro His Ser
945                 950
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<210> 2331
<211> 1060
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 578; "

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<221> source
<223> /note="Gene Symbol: ADAMTSL2; "

<220>
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ADAMTS-like 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000376781"

<400> 2331

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Met Leu Phe Glu Val Gly Glu Gly Gly Gly Ala Gly Glu Glu Gly Lys
1               5                  10                  15

Gly Arg Gly Arg Pro Gly Arg Ser Leu Cys Thr His Ala Ala Pro Ala
            20                  25                  30

Arg Thr Ala His Leu Ala Pro Ser Ala Leu Arg Ser Ala Arg Pro Phe
        35                  40                  45

Leu Trp Glu Asp Asn Leu Leu Thr Arg Ser Gln Gly Leu Pro Asp Asn
    50                  55                  60

His Asp Gln Leu Val Pro Asp Asn Leu Glu Ala Trp Ala Leu Ala Gly
65                  70                  75                  80

Pro Arg Gly Leu Phe Pro Lys Arg Thr Leu Val Ile Trp Lys Arg Ile
                85                  90                  95

Gly Ala Gly Leu Val Val Thr Val Ala Leu Leu Pro Arg Met Asp Gly
            100                 105                 110

Arg Trp Gln Cys Ser Cys Trp Ala Trp Phe Leu Leu Val Leu Ala Val
        115                 120                 125

Val Ala Gly Asp Thr Val Ser Thr Gly Ser Thr Asp Asn Ser Pro Thr
```

```
    130                 135                 140

Ser Asn Ser Leu Glu Gly Gly Thr Asp Ala Thr Ala Phe Trp Trp Gly
145                 150                 155                 160

Glu Trp Thr Lys Trp Thr Ala Cys Ser Arg Ser Cys Gly Gly Gly Val
                165                 170                 175

Thr Ser Gln Glu Arg His Cys Leu Gln Gln Arg Arg Lys Ser Val Pro
            180                 185                 190

Gly Pro Gly Asn Arg Thr Cys Thr Gly Thr Ser Lys Arg Tyr Gln Leu
        195                 200                 205

Cys Arg Val Gln Glu Cys Pro Pro Asp Gly Arg Ser Phe Arg Glu Glu
    210                 215                 220

Gln Cys Val Ser Phe Asn Ser His Val Tyr Asn Gly Arg Thr His Gln
225                 230                 235                 240

Trp Lys Pro Leu Tyr Pro Asp Asp Tyr Val His Ile Ser Ser Lys Pro
                245                 250                 255

Cys Asp Leu His Cys Thr Thr Val Asp Gly Gln Arg Gln Leu Met Val
            260                 265                 270

Pro Ala Arg Asp Gly Thr Ser Cys Lys Leu Thr Asp Leu Arg Gly Val
        275                 280                 285

Cys Val Ser Gly Lys Cys Glu Pro Ile Gly Cys Asp Gly Val Leu Phe
    290                 295                 300

Ser Thr His Thr Leu Asp Lys Cys Gly Ile Cys Gln Gly Asp Gly Ser
305                 310                 315                 320

Ser Cys Thr His Val Thr Gly Asn Tyr Arg Lys Gly Asn Ala His Leu
                325                 330                 335

Gly Tyr Ser Leu Val Thr His Ile Pro Ala Gly Ala Arg Asp Ile Gln
            340                 345                 350

Ile Val Glu Arg Lys Lys Ser Ala Asp Val Leu Ala Leu Ala Asp Glu
        355                 360                 365
```

```
Ala Gly Tyr Tyr Phe Phe Asn Gly Asn Tyr Lys Val Asp Ser Pro Lys
    370                 375                 380

Asn Phe Asn Ile Ala Gly Thr Val Val Lys Tyr Arg Arg Pro Met Asp
385                 390                 395                 400

Val Tyr Glu Thr Gly Ile Glu Tyr Ile Val Ala Gln Gly Pro Thr Asn
                405                 410                 415

Gln Gly Leu Asn Val Met Val Trp Asn Gln Asn Gly Lys Ser Pro Ser
            420                 425                 430

Ile Thr Phe Glu Tyr Thr Leu Leu Gln Pro Pro His Glu Ser Arg Pro
        435                 440                 445

Gln Pro Ile Tyr Tyr Gly Phe Ser Glu Ser Ala Glu Ser Gln Gly Leu
    450                 455                 460

Asp Gly Ala Gly Leu Met Gly Phe Val Pro His Asn Gly Ser Leu Tyr
465                 470                 475                 480

Gly Gln Ala Ser Ser Glu Arg Leu Gly Leu Asp Asn Arg Leu Phe Gly
                485                 490                 495

His Pro Gly Leu Asp Met Glu Leu Gly Pro Ser Gln Gly Gln Glu Thr
            500                 505                 510

Asn Glu Val Cys Glu Gln Ala Gly Gly Gly Ala Cys Glu Gly Pro Pro
        515                 520                 525

Arg Gly Lys Gly Phe Arg Asp Arg Asn Val Thr Gly Thr Pro Leu Thr
    530                 535                 540

Gly Asp Lys Asp Asp Glu Glu Val Asp Thr His Phe Ala Ser Gln Glu
545                 550                 555                 560

Phe Phe Ser Ala Asn Ala Ile Ser Asp Gln Leu Leu Gly Ala Gly Ser
                565                 570                 575

Asp Leu Lys Asp Phe Thr Leu Asn Glu Thr Val Asn Ser Ile Phe Ala
            580                 585                 590
```

```
Gln Gly Ala Pro Arg Ser Ser Leu Ala Glu Ser Phe Phe Val Asp Tyr
        595                 600                 605

Glu Glu Asn Glu Gly Ala Gly Pro Tyr Leu Leu Asn Gly Ser Tyr Leu
    610                 615                 620

Glu Leu Ser Ser Asp Arg Val Ala Asn Ser Ser Ser Glu Ala Pro Phe
625                 630                 635                 640

Pro Asn Val Ser Thr Ser Leu Leu Thr Ser Ala Gly Asn Arg Thr His
                645                 650                 655

Lys Ala Arg Thr Arg Pro Lys Ala Arg Lys Gln Gly Val Ser Pro Ala
            660                 665                 670

Asp Met Tyr Arg Trp Lys Leu Ser Ser His Glu Pro Cys Ser Ala Thr
        675                 680                 685

Cys Thr Thr Gly Val Met Ser Ala Tyr Ala Met Cys Val Arg Tyr Asp
    690                 695                 700

Gly Val Glu Val Asp Asp Ser Tyr Cys Asp Ala Leu Thr Arg Pro Glu
705                 710                 715                 720

Pro Val His Glu Phe Cys Ala Gly Arg Glu Cys Gln Pro Arg Trp Glu
                725                 730                 735

Thr Ser Ser Trp Ser Glu Cys Ser Arg Thr Cys Gly Glu Gly Tyr Gln
            740                 745                 750

Phe Arg Val Val Arg Cys Trp Lys Met Leu Ser Pro Gly Phe Asp Ser
        755                 760                 765

Ser Val Tyr Ser Asp Leu Cys Glu Ala Ala Glu Ala Val Arg Pro Glu
    770                 775                 780

Glu Arg Lys Thr Cys Arg Asn Pro Ala Cys Gly Pro Gln Trp Glu Met
785                 790                 795                 800

Ser Glu Trp Ser Glu Cys Thr Ala Lys Cys Gly Glu Arg Ser Val Val
                805                 810                 815
```

```
Thr Arg Asp Ile Arg Cys Ser Glu Asp Glu Lys Leu Cys Asp Pro Asn
            820                 825                 830

Thr Arg Pro Val Gly Glu Lys Asn Cys Thr Gly Pro Pro Cys Asp Arg
        835                 840                 845

Gln Trp Thr Val Ser Asp Trp Gly Pro Cys Ser Gly Ser Cys Gly Gln
    850                 855                 860

Gly Arg Thr Ile Arg His Val Tyr Cys Lys Thr Ser Asp Gly Arg Val
865                 870                 875                 880

Val Pro Glu Ser Gln Cys Gln Met Glu Thr Lys Pro Leu Ala Ile His
                885                 890                 895

Pro Cys Gly Asp Lys Asn Cys Pro Ala His Trp Leu Ala Gln Asp Trp
            900                 905                 910

Glu Arg Cys Asn Thr Thr Cys Gly Arg Gly Val Lys Lys Arg Leu Val
        915                 920                 925

Leu Cys Met Glu Leu Ala Asn Gly Lys Pro Gln Thr Arg Ser Gly Pro
    930                 935                 940

Glu Cys Gly Leu Ala Lys Lys Pro Pro Glu Glu Ser Thr Cys Phe Glu
945                 950                 955                 960

Arg Pro Cys Phe Lys Trp Tyr Thr Ser Pro Trp Ser Glu Cys Thr Lys
                965                 970                 975

Thr Cys Gly Val Gly Val Arg Met Arg Asp Val Lys Cys Tyr Gln Gly
            980                 985                 990

Thr Asp Ile Val Arg Gly Cys Asp  Pro Leu Val Lys Pro  Val Gly
Arg
        995                 1000                1005

Gln Ala  Cys Asp Leu Gln Pro  Cys Pro Thr Glu Pro  Pro Asp Asp
    1010                1015                1020

Ser Cys  Gln Asp Gln Pro Gly  Thr Asn Cys Ala Leu  Ala Ile Lys
    1025                1030                1035
```

Val Asn Leu Cys Gly His Trp Tyr Tyr Ser Lys Ala Cys Cys Arg
1040 1045 1050

Ser Cys Arg Pro Pro His Ser
1055 1060

<210> 2332
<211> 1691
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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ADAMTS-like 3; "

<220>
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<223> /note="Uniprot ID: P82987; "

<220>
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<223> /note="ENSP ID: ENSP00000286744"

<400> 2332
Met Ala Ser Trp Thr Ser Pro Trp Trp Val Leu Ile Gly Met Val Phe
1 5 10 15

Met His Ser Pro Leu Pro Gln Thr Thr Ala Glu Lys Ser Pro Gly Ala
20 25 30

Tyr Phe Leu Pro Glu Phe Ala Leu Ser Pro Gln Gly Ser Phe Leu Glu
35 40 45

Asp Thr Thr Gly Glu Gln Phe Leu Thr Tyr Arg Tyr Asp Asp Gln Thr
50 55 60

Ser Arg Asn Thr Arg Ser Asp Glu Asp Lys Asp Gly Asn Trp Asp Ala
65 70 75 80

Trp Gly Asp Trp Ser Asp Cys Ser Arg Thr Cys Gly Gly Gly Ala Ser
85 90 95

```
Tyr Ser Leu Arg Arg Cys Leu Thr Gly Arg Asn Cys Glu Gly Gln Asn
            100                 105                 110

Ile Arg Tyr Lys Thr Cys Ser Asn His Asp Cys Pro Pro Asp Ala Glu
        115                 120                 125

Asp Phe Arg Ala Gln Gln Cys Ser Ala Tyr Asn Asp Val Gln Tyr Gln
    130                 135                 140

Gly His Tyr Tyr Glu Trp Leu Pro Arg Tyr Asn Asp Pro Ala Ala Pro
145                 150                 155                 160

Cys Ala Leu Lys Cys His Ala Gln Gly Gln Asn Leu Val Val Glu Leu
                165                 170                 175

Ala Pro Lys Val Leu Asp Gly Thr Arg Cys Asn Thr Asp Ser Leu Asp
            180                 185                 190

Met Cys Ile Ser Gly Ile Cys Gln Ala Val Gly Cys Asp Arg Gln Leu
        195                 200                 205

Gly Ser Asn Ala Lys Glu Asp Asn Cys Gly Val Cys Ala Gly Asp Gly
    210                 215                 220

Ser Thr Cys Arg Leu Val Arg Gly Gln Ser Lys Ser His Val Ser Pro
225                 230                 235                 240

Glu Lys Arg Glu Glu Asn Val Ile Ala Val Pro Leu Gly Ser Arg Ser
                245                 250                 255

Val Arg Ile Thr Val Lys Gly Pro Ala His Leu Phe Ile Glu Ser Lys
            260                 265                 270

Thr Leu Gln Gly Ser Lys Gly Glu His Ser Phe Asn Ser Pro Gly Val
        275                 280                 285

Phe Leu Val Glu Asn Thr Thr Val Glu Phe Gln Arg Gly Ser Glu Arg
    290                 295                 300

Gln Thr Phe Lys Ile Pro Gly Pro Leu Met Ala Asp Phe Ile Phe Lys
305                 310                 315                 320
```

```
Thr Arg Tyr Thr Ala Ala Lys Asp Ser Val Val Gln Phe Phe Phe Tyr
                325                 330                 335

Gln Pro Ile Ser His Gln Trp Arg Gln Thr Asp Phe Phe Pro Cys Thr
            340                 345                 350

Val Thr Cys Gly Gly Gly Tyr Gln Leu Asn Ser Ala Glu Cys Val Asp
        355                 360                 365

Ile Arg Leu Lys Arg Val Val Pro Asp His Tyr Cys His Tyr Tyr Pro
    370                 375                 380

Glu Asn Val Lys Pro Lys Pro Lys Leu Lys Glu Cys Ser Met Asp Pro
385                 390                 395                 400

Cys Pro Ser Ser Asp Gly Phe Lys Glu Ile Met Pro Tyr Asp His Phe
                405                 410                 415

Gln Pro Leu Pro Arg Trp Glu His Asn Pro Trp Thr Ala Cys Ser Val
            420                 425                 430

Ser Cys Gly Gly Gly Ile Gln Arg Arg Ser Phe Val Cys Val Glu Glu
        435                 440                 445

Ser Met His Gly Glu Ile Leu Gln Val Glu Glu Trp Lys Cys Met Tyr
    450                 455                 460

Ala Pro Lys Pro Lys Val Met Gln Thr Cys Asn Leu Phe Asp Cys Pro
465                 470                 475                 480

Lys Trp Ile Ala Met Glu Trp Ser Gln Cys Thr Val Thr Cys Gly Arg
                485                 490                 495

Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asn His Arg Gly Glu His
            500                 505                 510

Val Gly Gly Cys Asn Pro Gln Leu Lys Leu His Ile Lys Glu Glu Cys
        515                 520                 525

Val Ile Pro Ile Pro Cys Tyr Lys Pro Lys Glu Lys Ser Pro Val Glu
    530                 535                 540
```

```
Ala Lys Leu Pro Trp Leu Lys Gln Ala Gln Glu Leu Glu Glu Thr Arg
545                 550                 555                 560

Ile Ala Thr Glu Glu Pro Thr Phe Ile Pro Glu Pro Trp Ser Ala Cys
                565                 570                 575

Ser Thr Thr Cys Gly Pro Gly Val Gln Val Arg Glu Val Lys Cys Arg
            580                 585                 590

Val Leu Leu Thr Phe Thr Gln Thr Glu Thr Glu Leu Pro Glu Glu Glu
        595                 600                 605

Cys Glu Gly Pro Lys Leu Pro Thr Glu Arg Pro Cys Leu Leu Glu Ala
    610                 615                 620

Cys Asp Glu Ser Pro Ala Ser Arg Glu Leu Asp Ile Pro Leu Pro Glu
625                 630                 635                 640

Asp Ser Glu Thr Thr Tyr Asp Trp Glu Tyr Ala Gly Phe Thr Pro Cys
                645                 650                 655

Thr Ala Thr Cys Val Gly Gly His Gln Glu Ala Ile Ala Val Cys Leu
            660                 665                 670

His Ile Gln Thr Gln Gln Thr Val Asn Asp Ser Leu Cys Asp Met Val
        675                 680                 685

His Arg Pro Pro Ala Met Ser Gln Ala Cys Asn Thr Glu Pro Cys Pro
    690                 695                 700

Pro Arg Trp His Val Gly Ser Trp Gly Pro Cys Ser Ala Thr Cys Gly
705                 710                 715                 720

Val Gly Ile Gln Thr Arg Asp Val Tyr Cys Leu His Pro Gly Glu Thr
                725                 730                 735

Pro Ala Pro Pro Glu Glu Cys Arg Asp Glu Lys Pro His Ala Leu Gln
            740                 745                 750

Ala Cys Asn Gln Phe Asp Cys Pro Pro Gly Trp His Ile Glu Glu Trp
        755                 760                 765

Gln Gln Cys Ser Arg Thr Cys Gly Gly Gly Thr Gln Asn Arg Arg Val
```

770 775 780

Thr Cys Arg Gln Leu Leu Thr Asp Gly Ser Phe Leu Asn Leu Ser Asp
785 790 795 800

Glu Leu Cys Gln Gly Pro Lys Ala Ser Ser His Lys Ser Cys Ala Arg
805 810 815

Thr Asp Cys Pro Pro His Leu Ala Val Gly Asp Trp Ser Lys Cys Ser
820 825 830

Val Ser Cys Gly Val Gly Ile Gln Arg Arg Lys Gln Val Cys Gln Arg
835 840 845

Leu Ala Ala Lys Gly Arg Arg Ile Pro Leu Ser Glu Met Met Cys Arg
850 855 860

Asp Leu Pro Gly Leu Pro Leu Val Arg Ser Cys Gln Met Pro Glu Cys
865 870 875 880

Ser Lys Ile Lys Ser Glu Met Lys Thr Lys Leu Gly Glu Gln Gly Pro
885 890 895

Gln Ile Leu Ser Val Gln Arg Val Tyr Ile Gln Thr Arg Glu Glu Lys
900 905 910

Arg Ile Asn Leu Thr Ile Gly Ser Arg Ala Tyr Leu Leu Pro Asn Thr
915 920 925

Ser Val Ile Ile Lys Cys Pro Val Arg Arg Phe Gln Lys Ser Leu Ile
930 935 940

Gln Trp Glu Lys Asp Gly Arg Cys Leu Gln Asn Ser Lys Arg Leu Gly
945 950 955 960

Ile Thr Lys Ser Gly Ser Leu Lys Ile His Gly Leu Ala Ala Pro Asp
965 970 975

Ile Gly Val Tyr Arg Cys Ile Ala Gly Ser Ala Gln Glu Thr Val Val
980 985 990

Leu Lys Leu Ile Gly Thr Asp Asn Arg Leu Ile Ala Arg Pro Ala
Leu

995 1000 1005

Arg Glu Pro Met Arg Glu Tyr Pro Gly Met Asp His Ser Glu Ala
1010 1015 1020

Asn Ser Leu Gly Val Thr Trp His Lys Met Arg Gln Met Trp Asn
1025 1030 1035

Asn Lys Asn Asp Leu Tyr Leu Asp Asp Asp His Ile Ser Asn Gln
1040 1045 1050

Pro Phe Leu Arg Ala Leu Leu Gly His Cys Ser Asn Ser Ala Gly
1055 1060 1065

Ser Thr Asn Ser Trp Glu Leu Lys Asn Lys Gln Phe Glu Ala Ala
1070 1075 1080

Val Lys Gln Gly Ala Tyr Ser Met Asp Thr Ala Gln Phe Asp Glu
1085 1090 1095

Leu Ile Arg Asn Met Ser Gln Leu Met Glu Thr Gly Glu Val Ser
1100 1105 1110

Asp Asp Leu Ala Ser Gln Leu Ile Tyr Gln Leu Val Ala Glu Leu
1115 1120 1125

Ala Lys Ala Gln Pro Thr His Met Gln Trp Arg Gly Ile Gln Glu
1130 1135 1140

Glu Thr Pro Pro Ala Ala Gln Leu Arg Gly Glu Thr Gly Ser Val
1145 1150 1155

Ser Gln Ser Ser His Ala Lys Asn Ser Gly Lys Leu Thr Phe Lys
1160 1165 1170

Pro Lys Gly Pro Val Leu Met Arg Gln Ser Gln Pro Pro Ser Ile
1175 1180 1185

Ser Phe Asn Lys Thr Ile Asn Ser Arg Ile Gly Asn Thr Val Tyr
1190 1195 1200

Ile Thr Lys Arg Thr Glu Val Ile Asn Ile Leu Cys Asp Leu Ile
1205 1210 1215

```
Thr Pro  Ser Glu Ala Thr Tyr  Thr Trp Thr Lys Asp  Gly Thr Leu
    1220                 1225                 1230

Leu Gln  Pro Ser Val Lys Ile  Ile Leu Asp Gly Thr  Gly Lys Ile
    1235                 1240                 1245

Gln Ile  Gln Asn Pro Thr Arg  Lys Glu Gln Gly Ile  Tyr Glu Cys
    1250                 1255                 1260

Ser Val  Ala Asn His Leu Gly  Ser Asp Val Glu Ser  Ser Ser Val
    1265                 1270                 1275

Leu Tyr  Ala Glu Ala Pro Val  Ile Leu Ser Val Glu  Arg Asn Ile
    1280                 1285                 1290

Thr Lys  Pro Glu His Asn His  Leu Ser Val Val Val  Gly Gly Ile
    1295                 1300                 1305

Val Glu  Ala Ala Leu Gly Ala  Asn Val Thr Ile Arg  Cys Pro Val
    1310                 1315                 1320

Lys Gly  Val Pro Gln Pro Asn  Ile Thr Trp Leu Lys  Arg Gly Gly
    1325                 1330                 1335

Ser Leu  Ser Gly Asn Val Ser  Leu Leu Phe Asn Gly  Ser Leu Leu
    1340                 1345                 1350

Leu Gln  Asn Val Ser Leu Glu  Asn Glu Gly Thr Tyr  Val Cys Ile
    1355                 1360                 1365

Ala Thr  Asn Ala Leu Gly Lys  Ala Val Ala Thr Ser  Val Leu His
    1370                 1375                 1380

Leu Leu  Glu Arg Arg Trp Pro  Glu Ser Arg Ile Val  Phe Leu Gln
    1385                 1390                 1395

Gly His  Lys Lys Tyr Ile Leu  Gln Ala Thr Asn Thr  Arg Thr Asn
    1400                 1405                 1410

Ser Asn  Asp Pro Thr Gly Glu  Pro Pro Pro Gln Glu  Pro Phe Trp
    1415                 1420                 1425
```

```
Glu Pro  Gly Asn Trp Ser His  Cys Ser Ala Thr Cys  Gly His Leu
    1430                 1435                 1440

Gly Ala  Arg Ile Gln Arg Pro  Gln Cys Val Met Ala  Asn Gly Gln
    1445                 1450                 1455

Glu Val  Ser Glu Ala Leu Cys  Asp His Leu Gln Lys  Pro Leu Ala
    1460                 1465                 1470

Gly Phe  Glu Pro Cys Asn Ile  Arg Asp Cys Pro Ala  Arg Trp Phe
    1475                 1480                 1485

Thr Ser  Val Trp Ser Gln Cys  Ser Val Ser Cys Gly  Glu Gly Tyr
    1490                 1495                 1500

His Ser  Arg Gln Val Thr Cys  Lys Arg Thr Lys Ala  Asn Gly Thr
    1505                 1510                 1515

Val Gln  Val Val Ser Pro Arg  Ala Cys Ala Pro Lys  Asp Arg Pro
    1520                 1525                 1530

Leu Gly  Arg Lys Pro Cys Phe  Gly His Pro Cys Val  Gln Trp Glu
    1535                 1540                 1545

Pro Gly  Asn Arg Cys Pro Gly  Arg Cys Met Gly Arg  Ala Val Arg
    1550                 1555                 1560

Met Gln  Gln Arg His Thr Ala  Cys Gln His Asn Ser  Ser Asp Ser
    1565                 1570                 1575

Asn Cys  Asp Asp Arg Lys Arg  Pro Thr Leu Arg Arg  Asn Cys Thr
    1580                 1585                 1590

Ser Gly  Ala Cys Asp Val Cys  Trp His Thr Gly Pro  Trp Lys Pro
    1595                 1600                 1605

Cys Thr  Ala Ala Cys Gly Arg  Gly Phe Gln Ser Arg  Lys Val Asp
    1610                 1615                 1620

Cys Ile  His Thr Arg Ser Cys  Lys Pro Val Ala Lys  Arg His Cys
    1625                 1630                 1635
```

```
Val Gln  Lys Lys Lys Pro Ile  Ser Trp Arg His Cys  Leu Gly Pro
    1640                1645                1650


Ser Cys  Asp Arg Asp Cys Thr  Asp Thr Thr His Tyr  Cys Met Phe
    1655                1660                1665


Val Lys  His Leu Asn Leu Cys  Ser Leu Asp Arg Tyr  Lys Gln Arg
    1670                1675                1680


Cys Cys  Gln Ser Cys Gln Glu  Gly
    1685                1690


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Met Ala Ser Trp Thr Ser Pro Trp Trp Val Leu Ile Gly Met Val Phe
1               5                  10                  15


Met His Ser Pro Leu Pro Gln Thr Thr Ala Glu Lys Ser Pro Gly Ala
            20                  25                  30


Tyr Phe Leu Pro Glu Phe Ala Leu Ser Pro Gln Gly Ser Phe Leu Glu
        35                  40                  45


Asp Thr Thr Gly Glu Gln Phe Leu Thr Tyr Arg Tyr Asp Asp Gln Thr
    50                  55                  60
```

Ser Arg Asn Thr Arg Ser Asp Glu Asp Lys Asp Gly Asn Trp Asp Ala
65 70 75 80

Trp Gly Asp Trp Ser Asp Cys Ser Arg Thr Cys Gly Gly Gly Ala Ser
85 90 95

Tyr Ser Leu Arg Arg Cys Leu Thr Gly Arg Asn Cys Glu Gly Gln Asn
100 105 110

Ile Arg Tyr Lys Thr Cys Ser Asn His Asp Cys Pro Pro Asp Ala Glu
115 120 125

Asp Phe Arg Ala Gln Gln Cys Ser Ala Tyr Asn Asp Val Gln Tyr Gln
130 135 140

Gly His Tyr Tyr Glu Trp Leu Pro Arg Tyr Asn Asp Pro Ala Ala Pro
145 150 155 160

Cys Ala Leu Lys Cys His Ala Gln Gly Gln Asn Leu Val Val Glu Leu
165 170 175

Ala Pro Lys Val Leu Asp Gly Thr Arg Cys Asn Thr Asp Ser Leu Asp
180 185 190

Met Cys Ile Ser Gly Ile Cys Gln Ala Val Gly Cys Asp Arg Gln Leu
195 200 205

Gly Ser Asn Ala Lys Glu Asp Asn Cys Gly Val Cys Ala Gly Asp Gly
210 215 220

Ser Thr Cys Arg Leu Val Arg Gly Gln Ser Lys Ser His Val Ser Pro
225 230 235 240

Glu Lys Arg Glu Glu Asn Val Ile Ala Val Pro Leu Gly Ser Arg Ser
245 250 255

Val Arg Ile Thr Val Lys Gly Pro Ala His Leu Phe Ile Glu Ser Lys
260 265 270

Thr Leu Gln Gly Ser Lys Gly Glu His Ser Phe Asn Ser Pro Gly Val
275 280 285

```
Phe Leu Val Glu Asn Thr Thr Val Glu Phe Gln Arg Gly Ser Glu Arg
    290                 295                 300

Gln Thr Phe Lys Ile Pro Gly Pro Leu Met Ala Asp Phe Ile Phe Lys
305                 310                 315                 320

Thr Arg Tyr Thr Ala Ala Lys Asp Ser Val Val Gln Phe Phe Phe Tyr
                325                 330                 335

Gln Pro Ile Ser His Gln Trp Arg Gln Thr Asp Phe Phe Pro Cys Thr
            340                 345                 350

Val Thr Cys Gly Gly Gly Tyr Gln Leu Asn Ser Ala Glu Cys Val Asp
        355                 360                 365

Ile Arg Leu Lys Arg Val Val Pro Asp His Tyr Cys His Tyr Tyr Pro
    370                 375                 380

Glu Asn Val Lys Pro Lys Pro Lys Leu Lys Glu Cys Ser Met Asp Pro
385                 390                 395                 400

Cys Pro Ser Ser Asp Gly Phe Lys Glu Ile Met Pro Tyr Asp His Phe
                405                 410                 415

Gln Pro Leu Pro Arg Trp Glu His Asn Pro Trp Thr Ala Cys Ser Val
            420                 425                 430

Ser Cys Gly Gly Gly Ile Gln Arg Arg Ser Phe Val Cys Val Glu Glu
        435                 440                 445

Ser Met His Gly Glu Ile Leu Gln Val Glu Glu Trp Lys Cys Met Tyr
    450                 455                 460

Ala Pro Lys Pro Lys Val Met Gln Thr Cys Asn Leu Phe Asp Cys Pro
465                 470                 475                 480

Lys Trp Ile Ala Met Glu Trp Ser Gln Cys Thr Val Thr Cys Gly Arg
                485                 490                 495

Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asn His Arg Gly Glu His
            500                 505                 510
```

```
Val Gly Gly Cys Asn Pro Gln Leu Lys Leu His Ile Lys Glu Glu Cys
        515                 520                 525

Val Ile Pro Ile Pro Cys Tyr Lys Pro Lys Glu Lys Ser Pro Val Glu
    530                 535                 540

Ala Lys Leu Pro Trp Leu Lys Gln Ala Gln Glu Leu Glu Glu Thr Arg
545                 550                 555                 560

Ile Ala Thr Glu Glu Pro Thr Phe Ile Pro Glu Pro Trp Ser Ala Cys
                565                 570                 575

Ser Thr Thr Cys Gly Pro Gly Val Gln Val Arg Glu Val Lys Cys Arg
            580                 585                 590

Val Leu Leu Thr Phe Thr Gln Thr Glu Thr Glu Leu Pro Glu Glu Glu
        595                 600                 605

Cys Glu Gly Pro Lys Leu Pro Thr Glu Arg Pro Cys Leu Leu Glu Ala
    610                 615                 620

Cys Asp Glu Ser Pro Ala Ser Arg Glu Leu Asp Ile Pro Leu Pro Glu
625                 630                 635                 640

Asp Ser Glu Thr Thr Tyr Asp Trp Glu Tyr Ala Gly Phe Thr Pro Cys
                645                 650                 655

Thr Ala Thr Cys Val Gly Gly His Gln Glu Ala Ile Ala Val Cys Leu
            660                 665                 670

His Ile Gln Thr Gln Gln Thr Val Asn Asp Ser Leu Cys Asp Met Val
        675                 680                 685

His Arg Pro Pro Ala Met Ser Gln Ala Cys Asn Thr Glu Pro Cys Pro
    690                 695                 700

Pro Arg Trp His Val Gly Ser Trp Gly Pro Cys Ser Ala Thr Cys Gly
705                 710                 715                 720

Val Gly Ile Gln Thr Arg Asp Val Tyr Cys Leu His Pro Gly Glu Thr
                725                 730                 735

Pro Ala Pro Pro Glu Glu Cys Arg Asp Glu Lys Pro His Ala Leu Gln
```

740 745 750

Ala Cys Asn Gln Phe Asp Cys Pro Pro Gly Trp His Ile Glu Glu Trp
755 760 765

Gln Gln Cys Ser Arg Thr Cys Gly Gly Gly Thr Gln Asn Arg Arg Val
770 775 780

Thr Cys Arg Gln Leu Leu Thr Asp Gly Ser Phe Leu Asn Leu Ser Asp
785 790 795 800

Glu Leu Cys Gln Gly Pro Lys Ala Ser Ser His Lys Ser Cys Ala Arg
805 810 815

Thr Asp Cys Pro Pro His Leu Ala Val Gly Asp Trp Ser Lys Cys Ser
820 825 830

Val Ser Cys Gly Val Gly Ile Gln Arg Arg Lys Gln Val Cys Gln Arg
835 840 845

Leu Ala Ala Lys Gly Arg Arg Ile Pro Leu Ser Glu Met Met Cys Arg
850 855 860

Asp Leu Pro Gly Leu Pro Leu Val Arg Ser Cys Gln Met Pro Glu Cys
865 870 875 880

Ser Lys Ile Lys Ser Glu Met Lys Thr Lys Leu Gly Glu Gln Gly Pro
885 890 895

Gln Ile Leu Ser Val Gln Arg Val Tyr Ile Gln Thr Arg Glu Glu Lys
900 905 910

Arg Ile Asn Leu Thr Ile Gly Ser Arg Ala Tyr Leu Leu Pro Asn Thr
915 920 925

Ser Val Ile Ile Lys Cys Pro Val Arg Arg Phe Gln Lys Ser Leu Ile
930 935 940

Gln Trp Glu Lys Asp Gly Arg Cys Leu Gln Asn Ser Lys Arg Leu Gly
945 950 955 960

Ile Thr Lys Ser Gly Ser Leu Lys Ile His Gly Leu Ala Ala Pro Asp
965 970 975

```
Ile Gly Val Tyr Arg Cys Ile Ala Gly Ser Ala Gln Glu Thr Val Val
            980                 985                 990

Leu Lys Leu Ile Gly Thr Asp Asn  Arg Leu Ile Ala Arg  Pro Ala
Leu
        995                 1000                1005

Arg Glu  Pro Met Arg Glu Tyr  Pro Gly Met Asp His  Ser Glu Ala
    1010                1015                1020

Asn Ser  Leu Gly Val Thr Trp  His Lys Met Arg Gln  Met Trp Asn
    1025                1030                1035

Asn Lys  Asn Asp Leu Tyr Leu  Asp Asp Asp His Ile  Ser Asn Gln
    1040                1045                1050

Pro Phe  Leu Arg Ala Leu Leu  Gly His Cys Ser Asn  Ser Ala Gly
    1055                1060                1065

Ser Thr  Asn Ser Trp Glu Leu  Lys Asn Lys Gln Phe  Glu Ala Ala
    1070                1075                1080

Val Lys  Gln Gly Ala Tyr Ser  Met Asp Thr Ala Gln  Phe Asp Glu
    1085                1090                1095

Leu Ile  Arg Asn Met Ser Gln  Leu Met Glu Thr Gly  Glu Val Ser
    1100                1105                1110

Asp Asp  Leu Ala Ser Gln Leu  Ile Tyr Gln Leu Val  Ala Glu Leu
    1115                1120                1125

Ala Lys  Ala Gln Pro Thr His  Met Gln Trp Arg Gly  Ile Gln Glu
    1130                1135                1140

Glu Thr  Pro Pro Ala Ala Gln  Leu Arg Gly Glu Thr  Gly Ser Val
    1145                1150                1155

Ser Gln  Ser Ser His Ala Lys  Asn Ser Gly Lys Leu  Thr Phe Lys
    1160                1165                1170

Pro Lys  Gly Pro Val Leu Met  Arg Gln Ser Gln Pro  Pro Ser Ile
    1175                1180                1185
```

```
Ser Phe  Asn Lys Thr Ile Asn  Ser Arg Ile Gly Asn  Thr Val Tyr
    1190                1195                1200

Ile Thr  Lys Arg Thr Glu Val  Ile Asn Ile Leu Cys  Asp Leu Ile
    1205                1210                1215

Thr Pro  Ser Glu Ala Thr Tyr  Thr Trp Thr Lys Asp  Gly Thr Leu
    1220                1225                1230

Leu Gln  Pro Ser Val Lys Ile  Ile Leu Asp Gly Thr  Gly Lys Ile
    1235                1240                1245

Gln Ile  Gln Asn Pro Thr Arg  Lys Glu Gln Gly Ile  Tyr Glu Cys
    1250                1255                1260

Ser Val  Ala Asn His Leu Gly  Ser Asp Val Glu Ser  Ser Ser Val
    1265                1270                1275

Leu Tyr  Ala Glu Ala Pro Val  Ile Leu Ser Val Glu  Arg Asn Ile
    1280                1285                1290

Thr Lys  Pro Glu His Asn His  Leu Ser Val Val Val  Gly Gly Ile
    1295                1300                1305

Val Glu  Ala Ala Leu Gly Ala  Asn Val Thr Ile Arg  Cys Pro Val
    1310                1315                1320

Lys Gly  Val Pro Gln Pro Asn  Ile Thr Trp Leu Lys  Arg Gly Gly
    1325                1330                1335

Ser Leu  Ser Gly Asn Val Ser  Leu Leu Phe Asn Gly  Ser Leu Leu
    1340                1345                1350

Leu Gln  Asn Val Ser Leu Glu  Asn Glu Gly Thr Tyr  Val Cys Ile
    1355                1360                1365

Ala Thr  Asn Ala Leu Gly Lys  Ala Val Ala Thr Ser  Val Leu His
    1370                1375                1380

Leu Leu  Glu Arg Arg Trp Pro  Glu Ser Arg Ile Val  Phe Leu Gln
    1385                1390                1395
```

```
Gly His  Lys Lys Tyr Ile Leu  Gln Ala Thr Asn Thr  Arg Thr Asn
    1400                1405                1410

Ser Asn  Asp Pro Thr Gly Glu  Pro Pro Pro Gln Glu  Pro Phe Trp
    1415                1420                1425

Glu Pro  Gly Asn Trp Ser His  Cys Ser Ala Thr Cys  Gly His Leu
    1430                1435                1440

Gly Ala  Arg Ile Gln Arg Pro  Gln Cys Val Met Ala  Asn Gly Gln
    1445                1450                1455

Glu Val  Ser Glu Ala Leu Cys  Asp His Leu Gln Lys  Pro Leu Ala
    1460                1465                1470

Gly Phe  Glu Pro Cys Asn Ile  Arg Asp Cys Pro Ala  Arg Trp Phe
    1475                1480                1485

Thr Ser  Val Trp Ser Gln Cys  Ser Val Ser Cys Gly  Glu Gly Tyr
    1490                1495                1500

His Ser  Arg Gln Val Thr Cys  Lys Arg Thr Lys Ala  Asn Gly Thr
    1505                1510                1515

Val Gln  Val Val Ser Pro Arg  Ala Cys Ala Pro Lys  Asp Arg Pro
    1520                1525                1530

Leu Gly  Arg Lys Pro Cys Phe  Gly His Pro Cys Val  Gln Trp Glu
    1535                1540                1545

Pro Gly  Asn Arg Cys Pro Gly  Arg Cys Met Gly Arg  Ala Val Arg
    1550                1555                1560

Met Gln  Gln Arg His Thr Ala  Cys Gln His Asn Ser  Ser Asp Ser
    1565                1570                1575

Asn Cys  Asp Asp Arg Lys Arg  Pro Thr Leu Arg Arg  Asn Cys Thr
    1580                1585                1590

Ser Gly  Ala Cys Asp Val Cys  Trp His Thr Gly Pro  Trp Lys Pro
    1595                1600                1605
```

```
Cys Thr  Ala Ala Cys Gly Arg  Gly Phe Gln Ser Arg  Lys Val Asp
    1610                1615                1620

Cys Ile  His Thr Arg Ser Cys  Lys Pro Val Ala Lys  Arg His Cys
    1625                1630                1635

Val Gln  Lys Lys Lys Pro Ile  Ser Trp Arg His Cys  Leu Gly Pro
    1640                1645                1650

Ser Cys  Asp Ser Thr Tyr Thr  Ser Gln Thr Ala Thr  Asn Lys Gly
    1655                1660                1665

Ala Ala  Ser His Val Lys Arg  Asp Lys Pro Leu Glu  Gly Ser
    1670                1675                1680


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Met Glu Asn Trp Thr Gly Arg Pro Trp Leu Tyr Leu Leu Leu Leu Leu
1               5                  10                  15

Ser Leu Pro Gln Leu Cys Leu Asp Gln Glu Val Leu Ser Gly His Ser
            20                  25                  30

Leu Gln Thr Pro Thr Glu Glu Gly Gln Gly Pro Glu Gly Val Trp Gly
        35                  40                  45
```

```
Pro Trp Val Gln Trp Ala Ser Cys Ser Gln Pro Cys Gly Val Gly Val
    50                  55                  60

Gln Arg Arg Ser Arg Thr Cys Gln Leu Pro Thr Val Gln Leu His Pro
65                  70                  75                  80

Ser Leu Pro Leu Pro Pro Arg Pro Pro Arg His Pro Glu Ala Leu Leu
                85                  90                  95

Pro Arg Gly Gln Gly Pro Arg Pro Gln Thr Ser Pro Glu Thr Leu Pro
            100                 105                 110

Leu Tyr Arg Thr Gln Ser Arg Gly Arg Gly Gly Pro Leu Arg Gly Pro
        115                 120                 125

Ala Ser His Leu Gly Arg Glu Glu Thr Gln Glu Ile Arg Ala Ala Arg
    130                 135                 140

Arg Ser Arg Leu Arg Asp Pro Ile Lys Pro Gly Met Phe Gly Tyr Gly
145                 150                 155                 160

Arg Val Pro Phe Ala Leu Pro Leu His Arg Asn Arg Arg His Pro Arg
                165                 170                 175

Ser Pro Pro Arg Ser Glu Leu Ser Leu Ile Ser Ser Arg Gly Glu Glu
            180                 185                 190

Ala Ile Pro Ser Pro Thr Pro Arg Ala Glu Pro Phe Ser Ala Asn Gly
        195                 200                 205

Ser Pro Gln Thr Glu Leu Pro Pro Thr Glu Leu Ser Val His Thr Pro
    210                 215                 220

Ser Pro Gln Ala Glu Pro Leu Ser Pro Glu Thr Ala Gln Thr Glu Val
225                 230                 235                 240

Ala Pro Arg Thr Arg Pro Ala Pro Leu Arg His His Pro Arg Ala Gln
                245                 250                 255

Ala Ser Gly Thr Glu Pro Pro Ser Pro Thr His Ser Leu Gly Glu Gly
            260                 265                 270
```

```
Gly Phe Phe Arg Ala Ser Pro Gln Pro Arg Arg Pro Ser Ser Gln Gly
        275                 280                 285

Trp Ala Ser Pro Gln Val Ala Gly Arg Arg Pro Asp Pro Phe Pro Ser
    290                 295                 300

Val Pro Arg Gly Arg Gly Gln Gln Gly Gln Gly Pro Trp Gly Thr Gly
305                 310                 315                 320

Gly Thr Pro His Gly Pro Arg Leu Glu Pro Asp Pro Gln His Pro Gly
                325                 330                 335

Ala Trp Leu Pro Leu Leu Ser Asn Gly Pro His Ala Ser Ser Leu Trp
            340                 345                 350

Ser Leu Phe Ala Pro Ser Ser Pro Ile Pro Arg Cys Ser Gly Glu Ser
        355                 360                 365

Glu Gln Leu Arg Ala Cys Ser Gln Ala Pro Cys Pro Pro Glu Gln Pro
    370                 375                 380

Asp Pro Arg Ala Leu Gln Cys Ala Ala Phe Asn Ser Gln Glu Phe Met
385                 390                 395                 400

Gly Gln Leu Tyr Gln Trp Glu Pro Phe Thr Glu Val Gln Gly Ser Gln
                405                 410                 415

Arg Cys Glu Leu Asn Cys Arg Pro Arg Gly Phe Arg Phe Tyr Val Arg
            420                 425                 430

His Thr Glu Lys Val Gln Asp Gly Thr Leu Cys Gln Pro Gly Ala Pro
        435                 440                 445

Asp Ile Cys Val Ala Gly Arg Cys Leu Ser Pro Gly Cys Asp Gly Ile
    450                 455                 460

Leu Gly Ser Gly Arg Arg Pro Asp Gly Cys Gly Val Cys Gly Gly Asp
465                 470                 475                 480

Asp Ser Thr Cys Arg Leu Val Ser Gly Asn Leu Thr Asp Arg Gly Gly
                485                 490                 495
```

```
Pro Leu Gly Tyr Gln Lys Ile Leu Trp Ile Pro Ala Gly Ala Leu Arg
            500                 505                 510

Leu Gln Ile Ala Gln Leu Arg Pro Ser Ser Asn Tyr Leu Ala Leu Arg
        515                 520                 525

Gly Pro Gly Gly Arg Ser Ile Ile Asn Gly Asn Trp Ala Val Asp Pro
    530                 535                 540

Pro Gly Ser Tyr Arg Ala Gly Gly Thr Val Phe Arg Tyr Asn Arg Pro
545                 550                 555                 560

Pro Arg Glu Glu Gly Lys Gly Glu Ser Leu Ser Ala Glu Gly Pro Thr
                565                 570                 575

Thr Gln Pro Val Asp Val Tyr Met Ile Phe Gln Glu Glu Asn Pro Gly
            580                 585                 590

Val Phe Tyr Gln Tyr Val Ile Ser Ser Pro Pro Pro Ile Leu Glu Asn
        595                 600                 605

Pro Thr Pro Glu Pro Pro Val Pro Gln Leu Gln Pro Glu Ile Leu Arg
    610                 615                 620

Val Glu Pro Pro Leu Ala Pro Ala Pro Arg Pro Ala Arg Thr Pro Gly
625                 630                 635                 640

Thr Leu Gln Arg Gln Val Arg Ile Pro Gln Met Pro Ala Pro Pro His
                645                 650                 655

Pro Arg Thr Pro Leu Gly Ser Pro Ala Ala Tyr Trp Lys Arg Val Gly
            660                 665                 670

His Ser Ala Cys Ser Ala Ser Cys Gly Lys Gly Val Trp Arg Pro Ile
        675                 680                 685

Phe Leu Cys Ile Ser Arg Glu Ser Gly Glu Glu Leu Asp Glu Arg Ser
    690                 695                 700

Cys Ala Ala Gly Ala Arg Pro Pro Ala Ser Pro Glu Pro Cys His Gly
705                 710                 715                 720

Thr Pro Cys Pro Pro Tyr Trp Glu Ala Gly Glu Trp Thr Ser Cys Ser
```

```
                725                 730                 735

Arg Ser Cys Gly Pro Gly Thr Gln His Arg Gln Leu Gln Cys Arg Gln
            740                 745                 750

Glu Phe Gly Gly Gly Gly Ser Ser Val Pro Pro Glu Arg Cys Gly His
        755                 760                 765

Leu Pro Arg Pro Asn Ile Thr Gln Ser Cys Gln Leu Arg Leu Cys Gly
    770                 775                 780

His Trp Glu Val Gly Ser Pro Trp Ser Gln Cys Ser Val Arg Cys Gly
785                 790                 795                 800

Arg Gly Gln Arg Ser Arg Gln Val Arg Cys Val Gly Asn Asn Gly Asp
                805                 810                 815

Glu Val Ser Glu Gln Glu Cys Ala Ser Gly Pro Pro Gln Pro Pro Ser
            820                 825                 830

Arg Glu Ala Cys Asp Met Gly Pro Cys Thr Thr Ala Trp Phe His Ser
        835                 840                 845

Asp Trp Ser Ser Lys Cys Ser Ala Glu Cys Gly Thr Gly Ile Gln Arg
    850                 855                 860

Arg Ser Val Val Cys Leu Gly Ser Gly Ala Ala Leu Gly Pro Gly Gln
865                 870                 875                 880

Gly Glu Ala Gly Ala Gly Thr Gly Gln Ser Cys Pro Thr Gly Ser Arg
                885                 890                 895

Pro Pro Asp Met Arg Ala Cys Ser Leu Gly Pro Cys Glu Arg Thr Trp
            900                 905                 910

Arg Trp Tyr Thr Gly Pro Trp Gly Glu Cys Ser Ser Glu Cys Gly Ser
        915                 920                 925

Gly Thr Gln Arg Arg Asp Ile Ile Cys Val Ser Lys Leu Gly Thr Glu
    930                 935                 940

Phe Asn Val Thr Ser Pro Ser Asn Cys Ser His Leu Pro Arg Pro Pro
945                 950                 955                 960
```

```
Ala Leu Gln Pro Cys Gln Gly Gln Ala Cys Gln Asp Arg Trp Phe Ser
                965                 970                 975

Thr Pro Trp Ser Pro Cys Ser Arg Ser Cys Gln Gly Gly Thr Gln Thr
            980                 985                 990

Arg Glu Val Gln Cys Leu Ser Thr  Asn Gln Thr Leu Ser  Thr Arg
Cys
        995                 1000                1005

Pro Pro  Gln Leu Arg Pro Ser  Arg Lys Arg Pro Cys  Asn Ser Gln
    1010                1015                1020

Pro Cys  Ser Gln Arg Pro Asp  Asp Gln Cys Lys Asp  Ser Ser Pro
    1025                1030                1035

His Cys  Pro Leu Val Val Gln  Ala Arg Leu Cys Val  Tyr Pro Tyr
    1040                1045                1050

Tyr Thr  Ala Thr Cys Cys Arg  Ser Cys Ala His Val  Leu Glu Arg
    1055                1060                1065

Ser Pro  Gln Asp Pro Ser
    1070


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<223> /note="Gene Name:
      ADAMTS-like 4; "

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<223> /note="Uniprot ID:  Q6UY14; "
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<220>
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<400> 2335
Met Glu Asn Trp Thr Gly Arg Pro Trp Leu Tyr Leu Leu Leu Leu Leu
1   5   10   15

Ser Leu Pro Gln Leu Cys Leu Asp Gln Glu Val Leu Ser Gly His Ser
            20   25   30

Leu Gln Thr Pro Thr Glu Glu Gly Gln Gly Pro Glu Gly Val Trp Gly
        35   40   45

Pro Trp Val Gln Trp Ala Ser Cys Ser Gln Pro Cys Gly Val Gly Val
    50   55   60

Gln Arg Arg Ser Arg Thr Cys Gln Leu Pro Thr Val Gln Leu His Pro
65   70   75   80

Ser Leu Pro Leu Pro Pro Arg Pro Pro Arg His Pro Glu Ala Leu Leu
                85   90   95

Pro Arg Gly Gln Gly Pro Arg Pro Gln Thr Ser Pro Glu Thr Leu Pro
            100   105   110

Leu Tyr Arg Thr Gln Ser Arg Gly Arg Gly Gly Pro Leu Arg Gly Pro
        115   120   125

Ala Ser His Leu Gly Arg Glu Glu Thr Gln Glu Ile Arg Ala Ala Arg
    130   135   140

Arg Ser Arg Leu Arg Asp Pro Ile Lys Pro Gly Met Phe Gly Tyr Gly
145   150   155   160

Arg Val Pro Phe Ala Leu Pro Leu His Arg Asn Arg Arg His Pro Arg
                165   170   175

Ser Pro Pro Arg Ser Glu Leu Ser Leu Ile Ser Ser Arg Gly Glu Glu
            180   185   190

Ala Ile Pro Ser Pro Thr Pro Arg Ala Glu Pro Phe Ser Ala Asn Gly
        195   200   205

```
Ser Pro Gln Thr Glu Leu Pro Pro Thr Glu Leu Ser Val His Thr Pro
    210                 215                 220

Ser Pro Gln Ala Glu Pro Leu Ser Pro Glu Thr Ala Gln Thr Glu Val
225                 230                 235                 240

Ala Pro Arg Thr Arg Pro Ala Pro Leu Arg His His Pro Arg Ala Gln
                245                 250                 255

Ala Ser Gly Thr Glu Pro Pro Ser Pro Thr His Ser Leu Gly Glu Gly
            260                 265                 270

Gly Phe Phe Arg Ala Ser Pro Gln Pro Arg Arg Pro Ser Ser Gln Gly
        275                 280                 285

Trp Ala Ser Pro Gln Val Ala Gly Arg Arg Pro Asp Pro Phe Pro Ser
    290                 295                 300

Val Pro Arg Gly Arg Gly Gln Gln Gly Gln Gly Pro Trp Gly Thr Gly
305                 310                 315                 320

Gly Thr Pro His Gly Pro Arg Leu Glu Pro Asp Pro Gln His Pro Gly
                325                 330                 335

Ala Trp Leu Pro Leu Leu Ser Asn Gly Pro His Ala Ser Ser Leu Trp
            340                 345                 350

Ser Leu Phe Ala Pro Ser Ser Pro Ile Pro Arg Cys Ser Gly Glu Ser
        355                 360                 365

Glu Gln Leu Arg Ala Cys Ser Gln Ala Pro Cys Pro Pro Glu Gln Pro
    370                 375                 380

Asp Pro Arg Ala Leu Gln Cys Ala Ala Phe Asn Ser Gln Glu Phe Met
385                 390                 395                 400

Gly Gln Leu Tyr Gln Trp Glu Pro Phe Thr Glu Val Gln Gly Ser Gln
                405                 410                 415

Arg Cys Glu Leu Asn Cys Arg Pro Arg Gly Phe Arg Phe Tyr Val Arg
            420                 425                 430

His Thr Glu Lys Val Gln Asp Gly Thr Leu Cys Gln Pro Gly Ala Pro
```

```
        435                 440                 445

Asp Ile Cys Val Ala Gly Arg Cys Leu Ser Pro Gly Cys Asp Gly Ile
    450                 455                 460

Leu Gly Ser Gly Arg Arg Pro Asp Gly Cys Gly Val Cys Gly Gly Asp
465                 470                 475                 480

Asp Ser Thr Cys Arg Leu Val Ser Gly Asn Leu Thr Asp Arg Gly Gly
                485                 490                 495

Pro Leu Gly Tyr Gln Lys Ile Leu Trp Ile Pro Ala Gly Ala Leu Arg
            500                 505                 510

Leu Gln Ile Ala Gln Leu Arg Pro Ser Ser Asn Tyr Leu Ala Leu Arg
        515                 520                 525

Gly Pro Gly Gly Arg Ser Ile Ile Asn Gly Asn Trp Ala Val Asp Pro
    530                 535                 540

Pro Gly Ser Tyr Arg Ala Gly Gly Thr Val Phe Arg Tyr Asn Arg Pro
545                 550                 555                 560

Pro Arg Glu Glu Gly Lys Gly Glu Ser Leu Ser Ala Glu Gly Pro Thr
                565                 570                 575

Thr Gln Pro Val Asp Val Tyr Met Ile Phe Gln Glu Glu Asn Pro Gly
            580                 585                 590

Val Phe Tyr Gln Tyr Val Ile Ser Ser Pro Pro Pro Ile Leu Glu Asn
        595                 600                 605

Pro Thr Pro Glu Pro Pro Val Pro Gln Leu Gln Pro Glu Ile Leu Arg
    610                 615                 620

Val Glu Pro Pro Leu Ala Pro Ala Pro Arg Pro Ala Arg Thr Pro Gly
625                 630                 635                 640

Thr Leu Gln Arg Gln Val Arg Ile Pro Gln Met Pro Ala Pro Pro His
                645                 650                 655

Pro Arg Thr Pro Leu Gly Ser Pro Ala Ala Tyr Trp Lys Arg Val Gly
            660                 665                 670
```

```
His Ser Ala Cys Ser Ala Ser Cys Gly Lys Gly Val Trp Arg Pro Ile
        675                 680                 685

Phe Leu Cys Ile Ser Arg Glu Ser Gly Glu Glu Leu Asp Glu Arg Ser
    690                 695                 700

Cys Ala Ala Gly Ala Arg Pro Pro Ala Ser Pro Glu Pro Cys His Gly
705                 710                 715                 720

Thr Pro Cys Pro Pro Tyr Trp Glu Ala Gly Glu Trp Thr Ser Cys Ser
                725                 730                 735

Arg Ser Cys Gly Pro Gly Thr Gln His Arg Gln Leu Gln Cys Arg Gln
            740                 745                 750

Glu Phe Gly Gly Gly Gly Ser Ser Val Pro Pro Glu Arg Cys Gly His
        755                 760                 765

Leu Pro Arg Pro Asn Ile Thr Gln Ser Cys Gln Leu Arg Leu Cys Gly
    770                 775                 780

His Trp Glu Val Gly Ser Pro Trp Ser Gln Cys Ser Val Arg Cys Gly
785                 790                 795                 800

Arg Gly Gln Arg Ser Arg Gln Val Arg Cys Val Gly Asn Asn Gly Asp
                805                 810                 815

Glu Val Ser Glu Gln Glu Cys Ala Ser Gly Pro Pro Gln Pro Pro Ser
            820                 825                 830

Arg Glu Ala Cys Asp Met Gly Pro Cys Thr Thr Ala Trp Phe His Ser
        835                 840                 845

Asp Trp Ser Ser Lys Cys Ser Ala Glu Cys Gly Thr Gly Ile Gln Arg
    850                 855                 860

Arg Ser Val Val Cys Leu Gly Ser Gly Ala Ala Leu Gly Pro Gly Gln
865                 870                 875                 880

Gly Glu Ala Gly Ala Gly Thr Gly Gln Ser Cys Pro Thr Gly Ser Arg
                885                 890                 895
```

```
Pro Pro Asp Met Arg Ala Cys Ser Leu Gly Pro Cys Glu Arg Thr Trp
            900                 905                 910

Arg Trp Tyr Thr Gly Pro Trp Gly Glu Cys Ser Ser Glu Cys Gly Ser
        915                 920                 925

Gly Thr Gln Arg Arg Asp Ile Ile Cys Val Ser Lys Leu Gly Thr Glu
    930                 935                 940

Phe Asn Val Thr Ser Pro Ser Asn Cys Ser His Leu Pro Arg Pro Pro
945                 950                 955                 960

Ala Leu Gln Pro Cys Gln Gly Gln Ala Cys Gln Asp Arg Trp Phe Ser
                965                 970                 975

Thr Pro Trp Ser Pro Cys Ser Arg Ser Cys Gln Gly Gly Thr Gln Thr
            980                 985                 990

Arg Glu Val Gln Cys Leu Ser Thr  Asn Gln Thr Leu Ser  Thr Arg
Cys
        995                 1000                1005

Pro Pro  Gln Leu Arg Pro Ser  Arg Lys Arg Pro Cys  Asn Ser Gln
    1010                1015                1020

Pro Cys  Ser Gln Arg Pro Asp  Asp Gln Cys Lys Asp  Ser Ser Pro
    1025                1030                1035

His Cys  Pro Leu Val Val Gln  Ala Arg Leu Cys Val  Tyr Pro Tyr
    1040                1045                1050

Tyr Thr  Ala Thr Cys Cys Arg  Ser Cys Ala His Val  Leu Glu Arg
    1055                1060                1065

Ser Pro  Gln Asp Pro Ser
    1070
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<210> 2336
<211> 1097
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 580; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL4; "

<220>
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<223> /note="Gene Name:
ADAMTS-like 4; "

<220>
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<223> /note="Uniprot ID: Q6UY14; "

<220>
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<223> /note="ENSP ID: ENSP00000358035"

<400> 2336

```
Met Glu Asn Trp Thr Gly Arg Pro Trp Leu Tyr Leu Leu Leu Leu Leu
1               5                  10                  15

Ser Leu Pro Gln Leu Cys Leu Asp Gln Glu Val Leu Ser Gly His Ser
            20                  25                  30

Leu Gln Thr Pro Thr Glu Glu Gly Gln Gly Pro Glu Gly Val Trp Gly
        35                  40                  45

Pro Trp Val Gln Trp Ala Ser Cys Ser Gln Pro Cys Gly Val Gly Val
    50                  55                  60

Gln Arg Arg Ser Arg Thr Cys Gln Leu Pro Thr Val Gln Leu His Pro
65                  70                  75                  80

Ser Leu Pro Leu Pro Pro Arg Pro Pro Arg His Pro Glu Ala Leu Leu
                85                  90                  95

Pro Arg Gly Gln Gly Pro Arg Pro Gln Thr Ser Pro Glu Thr Leu Pro
            100                 105                 110

Leu Tyr Arg Thr Gln Ser Arg Gly Arg Gly Gly Pro Leu Arg Gly Pro
        115                 120                 125

Ala Ser His Leu Gly Arg Glu Glu Thr Gln Glu Ile Arg Ala Ala Arg
    130                 135                 140

Arg Ser Arg Leu Arg Asp Pro Ile Lys Pro Gly Met Phe Gly Tyr Gly
```

145 150 155 160

Arg Val Pro Phe Ala Leu Pro Leu His Arg Asn Arg Arg His Pro Arg
165 170 175

Ser Pro Pro Arg Ser Glu Leu Ser Leu Ile Ser Ser Arg Gly Glu Glu
180 185 190

Ala Ile Pro Ser Pro Thr Pro Arg Ala Glu Pro Phe Ser Ala Asn Gly
195 200 205

Ser Pro Gln Thr Glu Leu Pro Pro Thr Glu Leu Ser Val His Thr Pro
210 215 220

Ser Pro Gln Ala Glu Pro Leu Ser Pro Glu Thr Ala Gln Thr Glu Val
225 230 235 240

Ala Pro Arg Thr Arg Pro Ala Pro Leu Arg His His Pro Arg Ala Gln
245 250 255

Ala Ser Gly Thr Glu Pro Pro Ser Pro Thr His Ser Leu Gly Glu Gly
260 265 270

Gly Phe Phe Arg Ala Ser Pro Gln Pro Arg Arg Pro Ser Ser Gln Gly
275 280 285

Trp Ala Ser Pro Gln Val Ala Gly Arg Arg Pro Asp Pro Phe Pro Ser
290 295 300

Val Pro Arg Gly Arg Gly Gln Gln Gly Gln Gly Pro Trp Gly Thr Gly
305 310 315 320

Gly Thr Pro His Gly Pro Arg Leu Glu Pro Asp Pro Gln His Pro Gly
325 330 335

Ala Trp Leu Pro Leu Leu Ser Asn Gly Pro His Ala Ser Ser Leu Trp
340 345 350

Ser Leu Phe Ala Pro Ser Ser Pro Ile Pro Arg Cys Ser Gly Glu Ser
355 360 365

Glu Gln Leu Arg Ala Cys Ser Gln Ala Pro Cys Pro Pro Glu Gln Pro
370 375 380

```
Asp Pro Arg Ala Leu Gln Cys Ala Ala Phe Asn Ser Gln Glu Phe Met
385                 390                 395                 400

Gly Gln Leu Tyr Gln Trp Glu Pro Phe Thr Glu Ala Pro Leu Leu Pro
                405                 410                 415

Leu Arg His Ala Phe Phe Leu Leu Pro Gly Ala Gly Ser Gly Asp Ser
            420                 425                 430

Thr Gly Val Gln Gly Ser Gln Arg Cys Glu Leu Asn Cys Arg Pro Arg
        435                 440                 445

Gly Phe Arg Phe Tyr Val Arg His Thr Glu Lys Val Gln Asp Gly Thr
    450                 455                 460

Leu Cys Gln Pro Gly Ala Pro Asp Ile Cys Val Ala Gly Arg Cys Leu
465                 470                 475                 480

Ser Pro Gly Cys Asp Gly Ile Leu Gly Ser Gly Arg Arg Pro Asp Gly
                485                 490                 495

Cys Gly Val Cys Gly Gly Asp Asp Ser Thr Cys Arg Leu Val Ser Gly
            500                 505                 510

Asn Leu Thr Asp Arg Gly Gly Pro Leu Gly Tyr Gln Lys Ile Leu Trp
        515                 520                 525

Ile Pro Ala Gly Ala Leu Arg Leu Gln Ile Ala Gln Leu Arg Pro Ser
    530                 535                 540

Ser Asn Tyr Leu Ala Leu Arg Gly Pro Gly Gly Arg Ser Ile Ile Asn
545                 550                 555                 560

Gly Asn Trp Ala Val Asp Pro Pro Gly Ser Tyr Arg Ala Gly Gly Thr
                565                 570                 575

Val Phe Arg Tyr Asn Arg Pro Pro Arg Glu Glu Gly Lys Gly Glu Ser
            580                 585                 590

Leu Ser Ala Glu Gly Pro Thr Thr Gln Pro Val Asp Val Tyr Met Ile
        595                 600                 605
```

```
Phe Gln Glu Glu Asn Pro Gly Val Phe Tyr Gln Tyr Val Ile Ser Ser
    610                 615                 620

Pro Pro Pro Ile Leu Glu Asn Pro Thr Pro Glu Pro Pro Val Pro Gln
625                 630                 635                 640

Leu Gln Pro Glu Ile Leu Arg Val Glu Pro Pro Leu Ala Pro Ala Pro
                645                 650                 655

Arg Pro Ala Arg Thr Pro Gly Thr Leu Gln Arg Gln Val Arg Ile Pro
            660                 665                 670

Gln Met Pro Ala Pro Pro His Pro Arg Thr Pro Leu Gly Ser Pro Ala
        675                 680                 685

Ala Tyr Trp Lys Arg Val Gly His Ser Ala Cys Ser Ala Ser Cys Gly
    690                 695                 700

Lys Gly Val Trp Arg Pro Ile Phe Leu Cys Ile Ser Arg Glu Ser Gly
705                 710                 715                 720

Glu Glu Leu Asp Glu Arg Ser Cys Ala Ala Gly Ala Arg Pro Pro Ala
                725                 730                 735

Ser Pro Glu Pro Cys His Gly Thr Pro Cys Pro Pro Tyr Trp Glu Ala
            740                 745                 750

Gly Glu Trp Thr Ser Cys Ser Arg Ser Cys Gly Pro Gly Thr Gln His
        755                 760                 765

Arg Gln Leu Gln Cys Arg Gln Glu Phe Gly Gly Gly Gly Ser Ser Val
    770                 775                 780

Pro Pro Glu Arg Cys Gly His Leu Pro Arg Pro Asn Ile Thr Gln Ser
785                 790                 795                 800

Cys Gln Leu Arg Leu Cys Gly His Trp Glu Val Gly Ser Pro Trp Ser
                805                 810                 815

Gln Cys Ser Val Arg Cys Gly Arg Gly Gln Arg Ser Arg Gln Val Arg
            820                 825                 830
```

```
Cys Val Gly Asn Asn Gly Asp Glu Val Ser Glu Gln Glu Cys Ala Ser
        835                 840                 845

Gly Pro Pro Gln Pro Pro Ser Arg Glu Ala Cys Asp Met Gly Pro Cys
    850                 855                 860

Thr Thr Ala Trp Phe His Ser Asp Trp Ser Ser Lys Cys Ser Ala Glu
865                 870                 875                 880

Cys Gly Thr Gly Ile Gln Arg Arg Ser Val Val Cys Leu Gly Ser Gly
                885                 890                 895

Ala Ala Leu Gly Pro Gly Gln Gly Glu Ala Gly Ala Gly Thr Gly Gln
            900                 905                 910

Ser Cys Pro Thr Gly Ser Arg Pro Pro Asp Met Arg Ala Cys Ser Leu
        915                 920                 925

Gly Pro Cys Glu Arg Thr Trp Arg Trp Tyr Thr Gly Pro Trp Gly Glu
    930                 935                 940

Cys Ser Ser Glu Cys Gly Ser Gly Thr Gln Arg Arg Asp Ile Ile Cys
945                 950                 955                 960

Val Ser Lys Leu Gly Thr Glu Phe Asn Val Thr Ser Pro Ser Asn Cys
                965                 970                 975

Ser His Leu Pro Arg Pro Pro Ala Leu Gln Pro Cys Gln Gly Gln Ala
            980                 985                 990

Cys Gln Asp Arg Trp Phe Ser Thr  Pro Trp Ser Pro Cys  Ser Arg
Ser
        995                 1000                1005

Cys Gln  Gly Gly Thr Gln Thr  Arg Glu Val Gln Cys  Leu Ser Thr
    1010                1015                1020

Asn Gln  Thr Leu Ser Thr Arg  Cys Pro Pro Gln Leu  Arg Pro Ser
    1025                1030                1035

Arg Lys  Arg Pro Cys Asn Ser  Gln Pro Cys Ser Gln  Arg Pro Asp
    1040                1045                1050
```

```
Asp Gln  Cys Lys Asp Ser Ser  Pro His Cys Pro Leu  Val Val Gln
    1055                1060                1065

Ala Arg  Leu Cys Val Tyr Pro  Tyr Tyr Thr Ala Thr  Cys Cys Arg
    1070                1075                1080

Ser Cys  Ala His Val Leu Glu  Arg Ser Pro Gln Asp  Pro Ser
    1085                1090                1095
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<210> 2337
<211> 877
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 580; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL4; "

<220>
<221> source
<223> /note="Gene Name:
ADAMTS-like 4; "

<220>
<221> source
<223> /note="Uniprot ID: Q6UY14; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000358037"

<400> 2337

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Met Glu Asn Trp Thr Gly Arg Pro Trp Leu Tyr Leu Leu Leu Leu Leu
1               5                  10                  15

Ser Leu Pro Gln Leu Cys Leu Asp Gln Glu Val Leu Ser Gly His Ser
            20                  25                  30

Leu Gln Thr Pro Thr Glu Glu Gly Gln Gly Pro Glu Gly Val Trp Gly
        35                  40                  45

Pro Trp Val Gln Trp Ala Ser Cys Ser Gln Pro Cys Gly Val Gly Val
    50                  55                  60

Gln Arg Arg Ser Arg Thr Cys Gln Leu Pro Thr Val Gln Leu His Pro
65                  70                  75                  80
```

Ser Leu Pro Leu Pro Pro Arg Pro Pro Arg His Pro Glu Ala Leu Leu
85 90 95

Pro Arg Gly Gln Gly Pro Arg Pro Gln Thr Ser Pro Glu Thr Leu Pro
100 105 110

Leu Tyr Arg Thr Gln Ser Arg Gly Arg Gly Gly Pro Leu Arg Gly Pro
115 120 125

Ala Ser His Leu Gly Arg Glu Glu Thr Gln Glu Ile Arg Ala Ala Arg
130 135 140

Arg Ser Arg Leu Arg Asp Pro Ile Lys Pro Gly Met Phe Gly Tyr Gly
145 150 155 160

Arg Val Pro Phe Ala Leu Pro Leu His Arg Asn Arg Arg His Pro Arg
165 170 175

Ser Pro Pro Arg Ser Glu Leu Ser Leu Ile Ser Ser Arg Gly Glu Glu
180 185 190

Ala Ile Pro Ser Pro Thr Pro Arg Ala Glu Pro Phe Ser Ala Asn Gly
195 200 205

Ser Pro Gln Thr Glu Leu Pro Pro Thr Glu Leu Ser Val His Thr Pro
210 215 220

Ser Pro Gln Ala Glu Pro Leu Ser Pro Glu Thr Ala Gln Thr Glu Val
225 230 235 240

Ala Pro Arg Thr Arg Pro Ala Pro Leu Arg His His Pro Arg Ala Gln
245 250 255

Ala Ser Gly Thr Glu Pro Pro Ser Pro Thr His Ser Leu Gly Glu Gly
260 265 270

Gly Phe Phe Arg Ala Ser Pro Gln Pro Arg Arg Pro Ser Ser Gln Gly
275 280 285

Trp Ala Ser Pro Gln Val Ala Gly Arg Arg Pro Asp Pro Phe Pro Ser
290 295 300

```
Val Pro Arg Gly Arg Gly Gln Gln Gly Gln Gly Pro Trp Gly Thr Gly
305                 310                 315                 320

Gly Thr Pro His Gly Pro Arg Leu Glu Pro Asp Pro Gln His Pro Gly
                325                 330                 335

Ala Trp Leu Pro Leu Leu Ser Asn Gly Pro His Ala Ser Ser Leu Trp
            340                 345                 350

Ser Leu Phe Ala Pro Ser Ser Pro Ile Pro Arg Cys Ser Gly Glu Ser
        355                 360                 365

Glu Gln Leu Arg Ala Cys Ser Gln Ala Pro Cys Pro Pro Glu Gln Pro
    370                 375                 380

Asp Pro Arg Ala Leu Gln Cys Ala Ala Phe Asn Ser Gln Glu Phe Met
385                 390                 395                 400

Gly Gln Leu Tyr Gln Trp Glu Pro Phe Thr Glu Val Gln Gly Ser Gln
                405                 410                 415

Arg Cys Glu Leu Asn Cys Arg Pro Arg Gly Phe Arg Phe Tyr Val Arg
            420                 425                 430

His Thr Glu Lys Val Gln Asp Gly Thr Leu Cys Gln Pro Gly Ala Pro
        435                 440                 445

Asp Ile Cys Val Ala Gly Arg Cys Leu Ser Pro Gly Cys Asp Gly Ile
    450                 455                 460

Leu Gly Ser Gly Arg Arg Pro Asp Gly Cys Gly Val Cys Gly Gly Asp
465                 470                 475                 480

Asp Ser Thr Cys Arg Leu Val Ser Gly Asn Leu Thr Asp Arg Gly Gly
                485                 490                 495

Pro Leu Gly Tyr Gln Lys Ile Leu Trp Ile Pro Ala Gly Ala Leu Arg
            500                 505                 510

Leu Gln Ile Ala Gln Leu Arg Pro Ser Ser Asn Tyr Leu Ala Leu Arg
        515                 520                 525
```

```
Gly Pro Gly Gly Arg Ser Ile Ile Asn Gly Asn Trp Ala Val Asp Pro
    530                 535                 540

Pro Gly Ser Tyr Arg Ala Gly Gly Thr Val Phe Arg Tyr Asn Arg Pro
545                 550                 555                 560

Pro Arg Glu Glu Gly Lys Gly Glu Ser Leu Ser Ala Glu Gly Pro Thr
                565                 570                 575

Thr Gln Pro Val Asp Val Tyr Met Ile Phe Gln Glu Glu Asn Pro Gly
            580                 585                 590

Val Phe Tyr Gln Tyr Val Ile Ser Ser Pro Pro Pro Ile Leu Glu Asn
        595                 600                 605

Pro Thr Pro Glu Pro Pro Val Pro Gln Leu Gln Pro Glu Ile Leu Arg
    610                 615                 620

Val Glu Pro Pro Leu Ala Pro Ala Pro Arg Pro Ala Arg Thr Pro Gly
625                 630                 635                 640

Thr Leu Gln Arg Gln Val Arg Ile Pro Gln Met Pro Ala Pro Pro His
                645                 650                 655

Pro Arg Thr Pro Leu Gly Ser Pro Ala Ala Tyr Trp Lys Arg Val Gly
            660                 665                 670

His Ser Ala Cys Ser Ala Ser Cys Gly Lys Gly Val Trp Arg Pro Ile
        675                 680                 685

Phe Leu Cys Ile Ser Arg Glu Ser Gly Glu Glu Leu Asp Glu Arg Ser
    690                 695                 700

Cys Ala Ala Gly Ala Arg Pro Pro Ala Ser Pro Glu Pro Cys His Gly
705                 710                 715                 720

Thr Pro Cys Pro Pro Tyr Trp Glu Ala Gly Glu Trp Thr Ser Cys Ser
                725                 730                 735

Arg Ser Cys Gly Pro Gly Thr Gln His Arg Gln Leu Gln Cys Arg Gln
            740                 745                 750

Glu Phe Gly Gly Gly Gly Ser Ser Val Pro Pro Glu Arg Cys Gly His
```

```
        755                 760                 765

Leu Pro Arg Pro Asn Ile Thr Gln Ser Cys Gln Leu Arg Leu Cys Gly
    770                 775                 780

His Trp Glu Val Gly Ser Pro Trp Ser Gln Cys Ser Val Arg Cys Gly
785                 790                 795                 800

Arg Gly Gln Arg Ser Arg Gln Val Arg Cys Val Gly Asn Asn Gly Asp
                805                 810                 815

Glu Val Ser Glu Gln Glu Cys Ala Ser Gly Pro Pro Gln Pro Pro Ser
            820                 825                 830

Arg Glu Ala Cys Asp Met Gly Pro Cys Thr Thr Ala Trp Phe His Ser
        835                 840                 845

Asp Trp Ser Ser Lys Val Ser Pro Glu Pro Pro Ala Ile Ser Cys Ile
    850                 855                 860

Leu Gly Asn His Ala Gln Asp Thr Ser Ala Phe Pro Ala
865                 870                 875


<210> 2338
<211> 435
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 580; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL4; "

<220>
<221> source
<223> /note="Gene Name:
      ADAMTS-like 4; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000477897"

<400> 2338
Met Gly Ser Leu Ala Leu Ala Gly Val Leu Met Ala Val Glu Ser Val
1               5                   10                  15
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```
Gly Val Met Ile Leu Pro Val Ala Leu Phe Arg Gly Thr Ser Leu Thr
            20                  25                  30

Glu Gly Ala Pro Trp Ala Ile Arg Arg Ser Cys Gly Phe Gln Arg Glu
        35                  40                  45

Pro Cys Gly Ser Arg Leu Pro Ser Ser Gly Leu Ala Pro Thr Thr Trp
    50                  55                  60

His Phe Val Ala Leu Gly Ala Gly Pro Ile Asn Gly Asn Trp Ala Val
65                  70                  75                  80

Asp Pro Pro Gly Ser Tyr Arg Ala Gly Gly Thr Val Phe Arg Tyr Asn
                85                  90                  95

Arg Pro Pro Arg Glu Glu Gly Lys Gly Glu Ser Leu Ser Ala Glu Gly
            100                 105                 110

Pro Thr Thr Gln Pro Val Asp Val Tyr Met Ile Phe Gln Glu Glu Asn
        115                 120                 125

Pro Gly Val Phe Tyr Gln Tyr Val Ile Ser Ser Pro Pro Pro Ile Leu
    130                 135                 140

Glu Asn Pro Thr Pro Glu Pro Pro Val Pro Gln Leu Gln Pro Glu Ile
145                 150                 155                 160

Leu Arg Val Glu Pro Pro Leu Ala Pro Ala Pro Arg Pro Ala Arg Thr
                165                 170                 175

Pro Gly Thr Leu Gln Arg Gln Val Arg Ile Pro Gln Met Pro Ala Pro
            180                 185                 190

Pro His Pro Arg Thr Pro Leu Gly Ser Pro Ala Ala Tyr Trp Lys Arg
        195                 200                 205

Val Gly His Ser Ala Cys Ser Ala Ser Cys Gly Lys Gly Val Trp Arg
    210                 215                 220

Pro Ile Phe Leu Cys Ile Ser Arg Glu Ser Gly Glu Glu Leu Asp Glu
225                 230                 235                 240
```

```
Arg Ser Cys Ala Ala Gly Ala Arg Pro Pro Ala Ser Pro Glu Pro Cys
                245                 250                 255

His Gly Thr Pro Cys Pro Pro Tyr Trp Glu Ala Gly Glu Trp Thr Ser
            260                 265                 270

Cys Ser Arg Ser Cys Gly Pro Gly Thr Gln His Arg Gln Leu Gln Cys
        275                 280                 285

Arg Gln Glu Phe Gly Gly Gly Gly Ser Ser Val Pro Pro Glu Arg Cys
    290                 295                 300

Gly His Leu Pro Arg Pro Asn Ile Thr Gln Ser Cys Gln Leu Arg Leu
305                 310                 315                 320

Cys Gly His Trp Glu Val Gly Ser Pro Trp Ser Gln Cys Ser Val Arg
                325                 330                 335

Cys Gly Arg Gly Gln Arg Ser Arg Gln Val Arg Cys Val Gly Asn Asn
            340                 345                 350

Gly Asp Glu Val Ser Glu Gln Glu Cys Ala Ser Gly Pro Pro Gln Pro
        355                 360                 365

Pro Ser Arg Glu Ala Cys Asp Met Gly Pro Cys Thr Thr Ala Trp Phe
    370                 375                 380

His Ser Asp Trp Ser Ser Lys Cys Ser Ala Glu Cys Gly Thr Gly Ile
385                 390                 395                 400

Gln Arg Arg Ser Val Val Cys Leu Gly Ser Gly Ala Ala Leu Gly Pro
                405                 410                 415

Gly Gln Gly Glu Ala Gly Ala Gly Thr Gly Gln Ser Cys Pro Thr Gly
            420                 425                 430

Ser Arg Pro
        435
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<210> 2339
<211> 471
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 581; "

<220>
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<223> /note="Gene Symbol: ADAMTSL5; "

<220>
<221> source
<223> /note="Gene Name:
ADAMTS-like 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000327608"

<400> 2339

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Met Asp Ser Ala Pro Leu Phe Pro Arg Pro His Leu Phe Gln Asn Leu
1               5                   10                  15

Leu Leu Phe Leu Trp Ala Leu Leu Asn Cys Gly Leu Gly Val Ser Ala
            20                  25                  30

Gln Gly Pro Gly Glu Trp Thr Pro Trp Val Ser Trp Thr Arg Cys Ser
        35                  40                  45

Ser Ser Cys Gly Arg Gly Val Ser Val Arg Ser Arg Arg Cys Leu Arg
    50                  55                  60

Leu Pro Gly Glu Glu Pro Cys Trp Gly Asp Ser His Glu Tyr Arg Leu
65                  70                  75                  80

Cys Gln Leu Pro Asp Cys Pro Pro Gly Ala Val Pro Phe Arg Asp Leu
                85                  90                  95

Gln Cys Ala Leu Tyr Asn Gly Arg Pro Val Leu Gly Thr Gln Lys Thr
            100                 105                 110

Tyr Gln Trp Val Pro Phe His Gly Ala Pro Asn Gln Cys Asp Leu Asn
        115                 120                 125

Cys Leu Ala Glu Gly His Ala Phe Tyr His Ser Phe Gly Arg Val Leu
    130                 135                 140

Asp Gly Thr Ala Cys Ser Pro Gly Ala Gln Gly Val Cys Val Ala Gly
145                 150                 155                 160
```

```
Arg Cys Leu Ser Ala Gly Cys Asp Gly Leu Leu Gly Ser Gly Ala Leu
                165                 170                 175

Glu Asp Arg Cys Gly Arg Cys Gly Gly Ala Asn Asp Ser Cys Leu Phe
            180                 185                 190

Val Gln Arg Val Phe Arg Asp Ala Gly Ala Phe Ala Gly Tyr Trp Asn
        195                 200                 205

Val Thr Leu Ile Pro Glu Gly Ala Arg His Ile Arg Val Glu His Arg
    210                 215                 220

Ser Arg Asn His Leu Ala Leu Met Gly Gly Asp Gly Arg Tyr Val Leu
225                 230                 235                 240

Asn Gly His Trp Val Val Ser Pro Pro Gly Thr Tyr Glu Ala Ala Gly
                245                 250                 255

Thr His Val Val Tyr Thr Arg Asp Thr Gly Pro Gln Glu Thr Leu Gln
            260                 265                 270

Ala Ala Gly Pro Thr Ser His Asp Leu Leu Leu Gln Val Leu Leu Gln
        275                 280                 285

Glu Pro Asn Pro Gly Ile Glu Phe Glu Phe Trp Leu Pro Arg Glu Arg
    290                 295                 300

Tyr Ser Pro Phe Gln Ala Arg Val Gln Ala Leu Gly Trp Pro Leu Arg
305                 310                 315                 320

Gln Pro Gln Pro Arg Gly Val Glu Pro Gln Pro Pro Ala Ala Pro Ala
                325                 330                 335

Val Thr Pro Ala Gln Thr Pro Thr Leu Ala Pro Asp Pro Cys Pro Pro
            340                 345                 350

Cys Pro Asp Thr Arg Gly Arg Ala His Arg Leu Leu His Tyr Cys Gly
        355                 360                 365

Ser Asp Phe Val Phe Gln Ala Arg Val Leu Gly His His His Gln Ala
    370                 375                 380
```

```
Gln Glu Thr Arg Tyr Glu Val Arg Ile Gln Leu Val Tyr Lys Asn Arg
385                 390                 395                 400

Ser Pro Leu Arg Ala Arg Glu Tyr Val Trp Ala Pro Gly His Cys Pro
                405                 410                 415

Cys Pro Met Leu Ala Pro His Arg Asp Tyr Leu Met Ala Val Gln Arg
            420                 425                 430

Leu Val Ser Pro Asp Gly Thr Gln Asp Gln Leu Leu Leu Pro His Ala
        435                 440                 445

Gly Tyr Ala Arg Pro Trp Ser Pro Ala Glu Asp Ser Arg Ile Arg Leu
    450                 455                 460

Thr Ala Arg Arg Cys Pro Gly
465                 470


<210> 2340
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 581; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL5; "

<220>
<221> source
<223> /note="Gene Name:
      ADAMTS-like 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000378850"

<400> 2340
Met Gly Gly Asp Gly Arg Tyr Val Leu Asn Gly His Trp Val Val Ser
1               5                   10                  15

Pro Pro Gly Thr Tyr Glu Ala Ala Gly Thr His Val Val Tyr Thr Arg
            20                  25                  30

Asp Thr Gly Pro Gln Glu Thr Leu Gln Ala Ala Gly Pro Thr Ser His
        35                  40                  45
```

```
Asp Leu Leu Leu Gln Val Leu Leu Gln Glu Pro Asn Pro Gly Ile Glu
    50                  55                  60

Phe Glu Phe Trp Leu Pro Arg Glu Arg Tyr Ser Pro Phe Gln Ala Arg
65                  70                  75                  80

Val Gln Ala Leu Gly Trp Pro Leu Arg Gln Pro Gln Pro Arg Gly Val
                85                  90                  95

Glu Pro Gln Pro Pro Ala Ala Pro Ala Val Thr Pro Ala Gln Thr Pro
            100                 105                 110

Thr Leu Ala Pro Gly Pro Ser Ala Gly Pro Pro Pro Pro Gly Pro Gly
        115                 120                 125

Asp Pro Leu
    130
```

<210> 2341
<211> 135
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 581; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL5; "

<220>
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<223> /note="Gene Name:
ADAMTS-like 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466231"

<400> 2341

```
Arg His Ile Arg Val Glu His Arg Ser Arg Asn His Leu Gly Ile Leu
1               5                   10                  15

Gly Ser Leu Met Gly Gly Asp Gly Arg Tyr Val Leu Asn Gly His Trp
            20                  25                  30
```

```
Val Val Ser Pro Pro Gly Thr Tyr Glu Ala Ala Gly Thr His Val Val
        35                  40                  45

Tyr Thr Arg Asp Thr Gly Pro Gln Glu Thr Leu Gln Ala Ala Gly Pro
    50                  55                  60

Thr Ser His Asp Leu Leu Leu Gln Val Leu Leu Gln Glu Pro Asn Pro
65                  70                  75                  80

Gly Ile Glu Phe Glu Phe Trp Leu Pro Arg Glu Arg Tyr Ser Pro Phe
                85                  90                  95

Gln Ala Arg Val Gln Ala Leu Gly Trp Pro Leu Arg Gln Pro Gln Pro
            100                 105                 110

Arg Gly Val Glu Pro Gln Pro Pro Ala Ala Pro Ala Val Thr Pro Ala
        115                 120                 125

Gln Thr Pro Thr Leu Ala Pro
    130                 135


<210> 2342
<211> 141
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL5; "

<220>
<221> source
<223> /note="Gene Name:
      ADAMTS-like 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479786"

<400> 2342
Met Gly Lys Leu Arg Pro Gly Arg Val Glu Trp Leu Ala Ser Gly His
1               5                   10                  15

Thr Glu Arg Pro His Leu Phe Gln Asn Leu Leu Leu Phe Leu Trp Ala
            20                  25                  30
```

```
Leu Leu Asn Cys Gly Leu Gly Val Ser Ala Gln Gly Pro Gly Glu Trp
        35                  40                  45

Thr Pro Trp Val Ser Trp Thr Arg Cys Ser Ser Ser Cys Gly Arg Gly
    50                  55                  60

Val Ser Val Arg Ser Arg Arg Cys Leu Arg Leu Pro Gly Glu Glu Pro
65                  70                  75                  80

Cys Trp Gly Asp Ser His Glu Tyr Arg Leu Cys Gln Leu Pro Asp Cys
                85                  90                  95

Pro Pro Gly Ala Val Pro Phe Arg Asp Leu Gln Cys Ala Leu Tyr Asn
            100                 105                 110

Gly Arg Pro Val Leu Gly Thr Gln Lys Thr Tyr Gln Trp Val Pro Phe
        115                 120                 125

His Gly Ala Pro Asn Gln Cys Asp Leu Asn Cys Leu Ala
    130                 135                 140


<210> 2343
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 581; "

<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL5; "

<220>
<221> source
<223> /note="Gene Name:
      ADAMTS-like 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000482683"

<400> 2343
Met Gly Lys Leu Arg Pro Gly Arg Val Glu Trp Leu Ala Ser Gly His
1               5                   10                  15
```

```
Thr Glu Arg Pro His Leu Phe Gln Asn Leu Leu Leu Phe Leu Trp Ala
            20                  25                  30

Leu Leu Asn Cys Gly Leu Gly Val Ser Ala Gln Gly Pro Gly Glu Trp
        35                  40                  45

Thr Pro Trp Val Ser Trp Thr Arg Cys Ser Ser Ser Cys Gly Arg Gly
    50                  55                  60

Val Ser Val Arg Ser Arg Arg Cys Leu Arg Leu Pro Gly Glu Glu Pro
65                  70                  75                  80

Cys Trp Gly Asp Ser His Glu Tyr Arg Leu Cys Gln Leu Pro Asp Cys
                85                  90                  95

Pro Pro Gly Ala Val Pro Phe Arg Asp Leu Gln Cys Ala Leu Tyr Asn
            100                 105                 110

Gly Arg Pro Val Leu Gly Thr Gln Lys Thr Tyr Gln Trp Val Pro Phe
        115                 120                 125

His Gly Ala Pro Asn Gln Cys Asp Leu Asn Cys Leu Ala Glu Gly His
    130                 135                 140

Ala Phe Tyr His Ser Phe Gly Arg Val Leu Asp Gly Thr Ala Cys Ser
145                 150                 155                 160

Pro Gly Ala Gln Gly Val Cys Val Ala Gly Arg Cys Leu Ser Ala Gly
                165                 170                 175

Cys Asp Gly Leu Leu Gly Ser Gly Ala Leu Glu Asp Arg Cys Gly Arg
            180                 185                 190

Cys Gly Gly Ala Asn Asp Ser Cys Leu Phe Val Gln Arg Val Phe Arg
        195                 200                 205

Asp Ala
    210
```

<210> 2344
<211> 130
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: ADAMTSL5; "

<220>
<221> source
<223> /note="Gene Name:
ADAMTS-like 5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484344"

<400> 2344
Met Gly Lys Leu Arg Pro Gly Arg Val Glu Trp Leu Ala Ser Gly His
1 5 10 15

Thr Glu Arg Pro His Leu Phe Gln Asn Leu Leu Leu Phe Leu Trp Ala
20 25 30

Leu Leu Asn Cys Gly Leu Gly Val Ser Ala Gln Gly Pro Gly Glu Trp
35 40 45

Thr Pro Trp Val Ser Trp Thr Arg Cys Ser Ser Ser Cys Gly Arg Gly
50 55 60

Val Ser Val Arg Ser Arg Arg Cys Leu Arg Leu Pro Gly Glu Glu Pro
65 70 75 80

Cys Trp Gly Asp Ser His Glu Tyr Arg Leu Cys Gln Leu Pro Asp Cys
85 90 95

Pro Pro Gly Ala Val Pro Phe Arg Asp Leu Gln Cys Ala Leu Tyr Asn
100 105 110

Gly Arg Pro Val Leu Gly Thr Gln Lys Thr Tyr Gln Trp Val Pro Phe
115 120 125

His Gly
130

<210> 2345
<211> 709
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 582; "

<220>
<221> source
<223> /note="Gene Symbol: APPL1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor prt, phosphotyr interaction, PH domain and leu
zipper containing 1; "

<220>
<221> source
<223> /note="Uniprot ID: Q9UKG1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000288266"

<400> 2345
Met Pro Gly Ile Asp Lys Leu Pro Ile Glu Glu Thr Leu Glu Asp Ser
1 5 10 15

Pro Gln Thr Arg Ser Leu Leu Gly Val Phe Glu Glu Asp Ala Thr Ala
20 25 30

Ile Ser Asn Tyr Met Asn Gln Leu Tyr Gln Ala Met His Arg Ile Tyr
35 40 45

Asp Ala Gln Asn Glu Leu Ser Ala Ala Thr His Leu Thr Ser Lys Leu
50 55 60

Leu Lys Glu Tyr Glu Lys Gln Arg Phe Pro Leu Gly Gly Asp Asp Glu
65 70 75 80

Val Met Ser Ser Thr Leu Gln Gln Phe Ser Lys Val Ile Asp Glu Leu
85 90 95

Ser Ser Cys His Ala Val Leu Ser Thr Gln Leu Ala Asp Ala Met Met
100 105 110

Phe Pro Ile Thr Gln Phe Lys Glu Arg Asp Leu Lys Glu Ile Leu Thr
115 120 125

```
Leu Lys Glu Val Phe Gln Ile Ala Ser Asn Asp His Asp Ala Ala Ile
    130                 135                 140

Asn Arg Tyr Ser Arg Leu Ser Lys Lys Arg Glu Asn Asp Lys Val Lys
145                 150                 155                 160

Tyr Glu Val Thr Glu Asp Val Tyr Thr Ser Arg Lys Lys Gln His Gln
                165                 170                 175

Thr Met Met His Tyr Phe Cys Ala Leu Asn Thr Leu Gln Tyr Lys Lys
            180                 185                 190

Lys Ile Ala Leu Leu Glu Pro Leu Leu Gly Tyr Met Gln Ala Gln Ile
        195                 200                 205

Ser Phe Phe Lys Met Gly Ser Glu Asn Leu Asn Glu Gln Leu Glu Glu
    210                 215                 220

Phe Leu Ala Asn Ile Gly Thr Ser Val Gln Asn Val Arg Arg Glu Met
225                 230                 235                 240

Asp Ser Asp Ile Glu Thr Met Gln Gln Thr Ile Glu Asp Leu Glu Val
                245                 250                 255

Ala Ser Asp Pro Leu Tyr Val Pro Asp Pro Asp Pro Thr Lys Phe Pro
            260                 265                 270

Val Asn Arg Asn Leu Thr Arg Lys Ala Gly Tyr Leu Asn Ala Arg Asn
        275                 280                 285

Lys Thr Gly Leu Val Ser Ser Thr Trp Asp Arg Gln Phe Tyr Phe Thr
    290                 295                 300

Gln Gly Gly Asn Leu Met Ser Gln Ala Arg Gly Asp Val Ala Gly Gly
305                 310                 315                 320

Leu Ala Met Asp Ile Asp Asn Cys Ser Val Met Ala Val Asp Cys Glu
                325                 330                 335

Asp Arg Arg Tyr Cys Phe Gln Ile Thr Ser Phe Asp Gly Lys Lys Ser
            340                 345                 350

Ser Ile Leu Gln Ala Glu Ser Lys Lys Asp His Glu Glu Trp Ile Cys
```

```
        355                 360                 365

Thr Ile Asn Asn Ile Ser Lys Gln Ile Tyr Leu Ser Glu Asn Pro Glu
    370                 375                 380

Glu Thr Ala Ala Arg Val Asn Gln Ser Ala Leu Glu Ala Val Thr Pro
385                 390                 395                 400

Ser Pro Ser Phe Gln Gln Arg His Glu Ser Leu Arg Pro Ala Ala Gly
                405                 410                 415

Gln Ser Arg Pro Pro Thr Ala Arg Thr Ser Ser Ser Gly Ser Leu Gly
            420                 425                 430

Ser Glu Ser Thr Asn Leu Ala Ala Leu Ser Leu Asp Ser Leu Val Ala
        435                 440                 445

Pro Asp Thr Pro Ile Gln Phe Asp Ile Ile Ser Pro Val Cys Glu Asp
    450                 455                 460

Gln Pro Gly Gln Ala Lys Ala Phe Gly Gln Gly Gly Arg Arg Thr Asn
465                 470                 475                 480

Pro Phe Gly Glu Ser Gly Gly Ser Thr Lys Ser Glu Thr Glu Asp Ser
                485                 490                 495

Ile Leu His Gln Leu Phe Ile Val Arg Phe Leu Gly Ser Met Glu Val
            500                 505                 510

Lys Ser Asp Asp His Pro Asp Val Val Tyr Glu Thr Met Arg Gln Ile
        515                 520                 525

Leu Ala Ala Arg Ala Ile His Asn Ile Phe Arg Met Thr Glu Ser His
    530                 535                 540

Leu Leu Val Thr Cys Asp Cys Leu Lys Leu Ile Asp Pro Gln Thr Gln
545                 550                 555                 560

Val Thr Arg Leu Thr Phe Pro Leu Pro Cys Val Val Leu Tyr Ala Thr
                565                 570                 575

His Gln Glu Asn Lys Arg Leu Phe Gly Phe Val Leu Arg Thr Ser Ser
            580                 585                 590
```

```
Gly Arg Ser Glu Ser Asn Leu Ser Ser Val Cys Tyr Ile Phe Glu Ser
        595                 600                 605

Asn Asn Glu Gly Glu Lys Ile Cys Asp Ser Val Gly Leu Ala Lys Gln
    610                 615                 620

Ile Ala Leu His Ala Glu Leu Asp Arg Arg Ala Ser Glu Lys Gln Lys
625                 630                 635                 640

Glu Ile Glu Arg Val Lys Glu Lys Gln Gln Lys Glu Leu Asn Lys Gln
                645                 650                 655

Lys Gln Ile Glu Lys Asp Leu Glu Glu Gln Ser Arg Leu Ile Ala Ala
            660                 665                 670

Ser Ser Arg Pro Asn Gln Ala Ser Ser Glu Gly Gln Phe Val Val Leu
        675                 680                 685

Ser Ser Ser Gln Ser Glu Glu Ser Asp Leu Gly Glu Gly Gly Lys Lys
    690                 695                 700

Arg Glu Ser Glu Ala
705


<210> 2346
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 582; "

<220>
<221> source
<223> /note="Gene Symbol: APPL1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor prt, phosphotyr interaction, PH domain and leu
      zipper containing 1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000406095"
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<400> 2346
Met Thr Arg Ser Leu Leu Gly Val Phe Glu Glu Asp Ala Thr Ala Ile
1   5   10   15

Ser Asn Tyr Met Asn Gln Leu Tyr Gln Ala Met His Arg Ile Tyr Asp
            20   25   30

Ala Gln Asn Glu Leu Ser Ala Ala Thr His Leu Thr Ser Lys Leu Leu
        35   40   45

Lys Glu Tyr Glu Lys Gln Arg Phe Pro Leu Gly Gly Asp Asp Glu Val
    50   55   60

Met Ser Ser Thr Leu Gln Gln Phe Ser Lys Val Ile Asp Glu Leu Ser
65   70   75   80

Ser Cys His Ala Val Leu Ser Thr Gln Leu Ala Asp Ala Met Met Phe
                85   90   95

Pro Ile Thr Gln Phe Lys Glu Arg Asp Leu Lys Glu Ile Leu Thr Leu
            100   105   110

Lys Glu Val Phe Gln Ile Ala Ser Asn Asp His Asp Ala Ala Ile Asn
        115   120   125

Arg Tyr Ser Arg Leu
    130

<210> 2347
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 582; "

<220>
<221> source
<223> /note="Gene Symbol: APPL1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor prt, phosphotyr interaction, PH domain and
      leu zipper containing 1; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000419644"

<400> 2347
Met Pro Gly Ile Asp Lys Leu Pro Ile Glu Glu Thr Leu Glu Asp Ser
1   5   10   15

Pro Gln Thr Arg Ser Leu Leu Gly Val Phe Glu Glu Asp Ala Thr Ala
            20   25   30

Ile Ser Asn Tyr Met Asn Gln Leu Tyr Gln Ala Met His Arg Ile Tyr
        35   40   45

Asp Ala Gln Asn Glu Leu Ser Ala Ala Thr His Leu Thr Ser Lys Leu
    50   55   60

Leu Lys Glu Tyr Glu Lys Gln Leu Ser Ser Cys His Ala Val Leu Ser
65   70   75   80

Thr Gln Leu Ala Asp Ala Met Met Phe Pro Ile Thr Gln Phe Lys Glu
                85   90   95

Arg Asp Leu Lys Glu Ile Leu Thr Leu Lys Glu Val Phe Gln Ile Ala
            100   105   110

Ser Asn

<210> 2348
<211> 664
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 583; "

<220>
<221> source
<223> /note="Gene Symbol: APPL2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor prt, phosphotyr interaction, PH domain and
      leu
      zipper containing 2; "

<220>

<221> source
<223> /note="Uniprot ID: Q8NEU8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000258530"

<400> 2348
Met Pro Ala Val Asp Lys Leu Leu Leu Glu Glu Ala Leu Gln Asp Ser
1   5   10   15

Pro Gln Thr Arg Ser Leu Leu Ser Val Phe Glu Glu Asp Ala Gly Thr
            20   25   30

Leu Thr Asp Tyr Thr Asn Gln Leu Leu Gln Ala Met Gln Arg Val Tyr
        35   40   45

Gly Ala Gln Asn Glu Met Cys Leu Ala Thr Gln Gln Leu Ser Lys Gln
    50   55   60

Leu Leu Ala Tyr Glu Lys Gln Asn Phe Ala Leu Gly Lys Gly Asp Glu
65   70   75   80

Glu Val Ile Ser Thr Leu His Tyr Phe Ser Lys Val Val Asp Glu Leu
                85   90   95

Asn Leu Leu His Thr Glu Leu Ala Lys Gln Leu Ala Asp Thr Met Val
            100   105   110

Leu Pro Ile Ile Gln Phe Arg Glu Lys Asp Leu Thr Glu Val Ser Thr
        115   120   125

Leu Lys Asp Leu Phe Gly Leu Ala Ser Asn Glu His Asp Leu Ser Met
    130   135   140

Ala Lys Tyr Ser Arg Leu Pro Lys Lys Lys Glu Asn Glu Lys Val Lys
145   150   155   160

Thr Glu Val Gly Lys Glu Val Ala Ala Ala Arg Arg Lys Gln His Leu
                165   170   175

Ser Ser Leu Gln Tyr Tyr Cys Ala Leu Asn Ala Leu Gln Tyr Arg Lys
            180   185   190

Gln Met Ala Met Met Glu Pro Met Ile Gly Phe Ala His Gly Gln Ile

```
        195                 200                 205

Asn Phe Phe Lys Lys Gly Ala Glu Met Phe Ser Lys Arg Met Asp Ser
    210                 215                 220

Phe Leu Ser Ser Val Ala Asp Met Val Gln Ser Ile Gln Val Glu Leu
225                 230                 235                 240

Glu Ala Glu Ala Glu Lys Met Arg Val Ser Gln Gln Glu Leu Leu Ser
                245                 250                 255

Val Asp Glu Ser Val Tyr Thr Pro Asp Ser Asp Val Ala Ala Pro Gln
            260                 265                 270

Ile Asn Arg Asn Leu Ile Gln Lys Ala Gly Tyr Leu Asn Leu Arg Asn
        275                 280                 285

Lys Thr Gly Leu Val Thr Thr Thr Trp Glu Arg Leu Tyr Phe Phe Thr
    290                 295                 300

Gln Gly Gly Asn Leu Met Cys Gln Pro Arg Gly Ala Val Ala Gly Gly
305                 310                 315                 320

Leu Ile Gln Asp Leu Asp Asn Cys Ser Val Met Ala Val Asp Cys Glu
                325                 330                 335

Asp Arg Arg Tyr Cys Phe Gln Ile Thr Thr Pro Asn Gly Lys Ser Gly
            340                 345                 350

Ile Ile Leu Gln Ala Glu Ser Arg Lys Glu Asn Glu Glu Trp Ile Cys
        355                 360                 365

Ala Ile Asn Asn Ile Ser Arg Gln Ile Tyr Leu Thr Asp Asn Pro Glu
    370                 375                 380

Ala Val Ala Ile Lys Leu Asn Gln Thr Ala Leu Gln Ala Val Thr Pro
385                 390                 395                 400

Ile Thr Ser Phe Gly Lys Lys Gln Glu Ser Ser Cys Pro Ser Gln Asn
                405                 410                 415

Leu Lys Asn Ser Glu Met Glu Asn Glu Asn Asp Lys Ile Val Pro Lys
            420                 425                 430
```

```
Ala Thr Ala Ser Leu Pro Glu Ala Glu Glu Leu Ile Ala Pro Gly Thr
        435                 440                 445

Pro Ile Gln Phe Asp Ile Val Leu Pro Ala Thr Glu Phe Leu Asp Gln
    450                 455                 460

Asn Arg Gly Ser Arg Arg Thr Asn Pro Phe Gly Glu Thr Glu Asp Glu
465                 470                 475                 480

Ser Phe Pro Glu Ala Glu Asp Ser Leu Leu Gln Gln Met Phe Ile Val
                485                 490                 495

Arg Phe Leu Gly Ser Met Ala Val Lys Thr Asp Ser Thr Thr Glu Val
            500                 505                 510

Ile Tyr Glu Ala Met Arg Gln Val Leu Ala Ala Arg Ala Ile His Asn
        515                 520                 525

Ile Phe Arg Met Thr Glu Ser His Leu Met Val Thr Ser Gln Ser Leu
    530                 535                 540

Arg Leu Ile Asp Pro Gln Thr Gln Val Ser Arg Ala Asn Phe Glu Leu
545                 550                 555                 560

Thr Ser Val Thr Gln Phe Ala Ala His Gln Glu Asn Lys Arg Leu Val
                565                 570                 575

Gly Phe Val Ile Arg Val Pro Glu Ser Thr Gly Glu Glu Ser Leu Ser
            580                 585                 590

Thr Tyr Ile Phe Glu Ser Asn Ser Glu Gly Glu Lys Ile Cys Tyr Ala
        595                 600                 605

Ile Asn Leu Gly Lys Glu Ile Ile Glu Val Gln Lys Asp Pro Glu Ala
    610                 615                 620

Leu Ala Gln Leu Met Leu Ser Ile Pro Leu Thr Asn Asp Gly Lys Tyr
625                 630                 635                 640

Val Leu Leu Asn Asp Gln Pro Asp Asp Asp Asp Gly Asn Pro Asn Glu
                645                 650                 655
```

His Arg Gly Ala Glu Ser Glu Ala
            660

<210> 2349
<211> 621
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 583; "

<220>
<221> source
<223> /note="Gene Symbol: APPL2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor prt, phosphotyr interaction, PH domain and
      leu
      zipper containing 2; "

<220>
<221> source
<223> /note="Uniprot ID: Q8NEU8; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000444472"

<400> 2349
Met Gln Arg Val Tyr Gly Ala Gln Asn Glu Met Cys Leu Ala Thr Gln
1   5   10   15

Gln Leu Ser Lys Gln Leu Leu Ala Tyr Glu Lys Gln Asn Phe Ala Leu
            20   25   30

Gly Lys Gly Asp Glu Glu Val Ile Ser Thr Leu His Tyr Phe Ser Lys
        35   40   45

Val Val Asp Glu Leu Asn Leu Leu His Thr Glu Leu Ala Lys Gln Leu
    50   55   60

Ala Asp Thr Met Val Leu Pro Ile Ile Gln Phe Arg Glu Lys Asp Leu
65   70   75   80

Thr Glu Val Ser Thr Leu Lys Asp Leu Phe Gly Leu Ala Ser Asn Glu
                85   90   95

```
His Asp Leu Ser Met Ala Lys Tyr Ser Arg Leu Pro Lys Lys Lys Glu
            100                 105                 110

Asn Glu Lys Val Lys Thr Glu Val Gly Lys Glu Val Ala Ala Ala Arg
        115                 120                 125

Arg Lys Gln His Leu Ser Ser Leu Gln Tyr Tyr Cys Ala Leu Asn Ala
    130                 135                 140

Leu Gln Tyr Arg Lys Gln Met Ala Met Met Glu Pro Met Ile Gly Phe
145                 150                 155                 160

Ala His Gly Gln Ile Asn Phe Phe Lys Lys Gly Ala Glu Met Phe Ser
                165                 170                 175

Lys Arg Met Asp Ser Phe Leu Ser Ser Val Ala Asp Met Val Gln Ser
            180                 185                 190

Ile Gln Val Glu Leu Glu Ala Glu Ala Glu Lys Met Arg Val Ser Gln
        195                 200                 205

Gln Glu Leu Leu Ser Val Asp Glu Ser Val Tyr Thr Pro Asp Ser Asp
    210                 215                 220

Val Ala Ala Pro Gln Ile Asn Arg Asn Leu Ile Gln Lys Ala Gly Tyr
225                 230                 235                 240

Leu Asn Leu Arg Asn Lys Thr Gly Leu Val Thr Thr Thr Trp Glu Arg
                245                 250                 255

Leu Tyr Phe Phe Thr Gln Gly Gly Asn Leu Met Cys Gln Pro Arg Gly
            260                 265                 270

Ala Val Ala Gly Gly Leu Ile Gln Asp Leu Asp Asn Cys Ser Val Met
        275                 280                 285

Ala Val Asp Cys Glu Asp Arg Arg Tyr Cys Phe Gln Ile Thr Thr Pro
    290                 295                 300

Asn Gly Lys Ser Gly Ile Ile Leu Gln Ala Glu Ser Arg Lys Glu Asn
305                 310                 315                 320
```

```
Glu Glu Trp Ile Cys Ala Ile Asn Asn Ile Ser Arg Gln Ile Tyr Leu
                325                 330                 335

Thr Asp Asn Pro Glu Ala Val Ala Ile Lys Leu Asn Gln Thr Ala Leu
            340                 345                 350

Gln Ala Val Thr Pro Ile Thr Ser Phe Gly Lys Lys Gln Glu Ser Ser
        355                 360                 365

Cys Pro Ser Gln Asn Leu Lys Asn Ser Glu Met Glu Asn Glu Asn Asp
    370                 375                 380

Lys Ile Val Pro Lys Ala Thr Ala Ser Leu Pro Glu Ala Glu Glu Leu
385                 390                 395                 400

Ile Ala Pro Gly Thr Pro Ile Gln Phe Asp Ile Val Leu Pro Ala Thr
                405                 410                 415

Glu Phe Leu Asp Gln Asn Arg Gly Ser Arg Arg Thr Asn Pro Phe Gly
            420                 425                 430

Glu Thr Glu Asp Glu Ser Phe Pro Glu Ala Glu Asp Ser Leu Leu Gln
        435                 440                 445

Gln Met Phe Ile Val Arg Phe Leu Gly Ser Met Ala Val Lys Thr Asp
    450                 455                 460

Ser Thr Thr Glu Val Ile Tyr Glu Ala Met Arg Gln Val Leu Ala Ala
465                 470                 475                 480

Arg Ala Ile His Asn Ile Phe Arg Met Thr Glu Ser His Leu Met Val
                485                 490                 495

Thr Ser Gln Ser Leu Arg Leu Ile Asp Pro Gln Thr Gln Val Ser Arg
            500                 505                 510

Ala Asn Phe Glu Leu Thr Ser Val Thr Gln Phe Ala Ala His Gln Glu
        515                 520                 525

Asn Lys Arg Leu Val Gly Phe Val Ile Arg Val Pro Glu Ser Thr Gly
    530                 535                 540

Glu Glu Ser Leu Ser Thr Tyr Ile Phe Glu Ser Asn Ser Glu Gly Glu
```

```
545                 550                 555                 560

Lys Ile Cys Tyr Ala Ile Asn Leu Gly Lys Glu Ile Ile Glu Val Gln
                565                 570                 575

Lys Asp Pro Glu Ala Leu Ala Gln Leu Met Leu Ser Ile Pro Leu Thr
            580                 585                 590

Asn Asp Gly Lys Tyr Val Leu Leu Asn Asp Gln Pro Asp Asp Asp Asp
        595                 600                 605

Gly Asn Pro Asn Glu His Arg Gly Ala Glu Ser Glu Ala
    610                 615                 620


<210> 2350
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 583; "

<220>
<221> source
<223> /note="Gene Symbol: APPL2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor prt, phosphotyr interaction, PH domain and
      leu
      zipper containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000446510"

<400> 2350
Asp Ile Val Leu Pro Ala Thr Glu Phe Leu Asp Gln Asn Arg Gly Ser
1               5                   10                  15

Arg Arg Thr Asn Pro Phe Gly Glu Thr Glu Asp Glu Ser Phe Pro Glu
            20                  25                  30

Ala Glu Val Lys Thr Asp Ser Thr Thr Glu Val Ile Tyr Glu Ala Met
        35                  40                  45

Arg Gln Val Leu Ala Ala Arg Ala Ile His Asn Ile Phe Arg Met Thr
```

```
    50                  55                  60

Glu Ser His Leu Met Val Thr Ser Gln Ser Leu Arg Leu Ile Asp Pro
65                  70                  75                  80

Gln Thr Gln Val Ser Arg Ala Asn Phe Glu Leu Thr Ser Val Thr Gln
                85                  90                  95

Phe Ala Ala His Gln Glu Asn Lys Arg Leu Val Gly Phe Val Ile Arg
            100                 105                 110

Val Pro Glu Ser Thr Gly Glu Glu Ser Leu Ser Thr Tyr Ile Phe Glu
        115                 120                 125

Ser Asn Ser Glu Gly Glu Lys Ile Cys Tyr Ala Ile Asn Leu Gly Lys
    130                 135                 140

Glu Ile Ile Glu Val Gln Lys Asp Pro Glu Ala Leu Ala Gln Leu Met
145                 150                 155                 160

Leu Ser Ile Pro Leu Thr Asn Asp Gly Lys Tyr Val Leu Leu Asn Asp
                165                 170                 175

Gln Pro Asp Asp Asp Asp Gly Asn Pro Asn Glu His
            180                 185


<210> 2351
<211> 670
<212> PRT
<213> Homo sapiens

<220>
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<220>
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      leu
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<220>
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<223> /note="Uniprot ID: Q8NEU8; "

<220>
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<400> 2351

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Met Pro Ala Val Asp Lys Leu Leu Leu Glu Glu Ala Leu Gln Asp Ser
1               5                  10                  15

Pro Gln Thr Arg Ser Leu Leu Ser Val Phe Glu Glu Asp Ala Gly Thr
            20                  25                  30

Leu Thr Asp Tyr Thr Asn Gln Leu Leu Gln Ala Met Gln Arg Val Tyr
        35                  40                  45

Gly Ala Gln Asn Glu Met Cys Leu Ala Thr Gln Gln Leu Ser Lys Gln
    50                  55                  60

Leu Leu Ala Tyr Glu Lys Gln Asn Phe Ala Leu Gly Lys Gly Asp Glu
65                  70                  75                  80

Glu Val Ile Ser Thr Leu His Tyr Phe Ser Lys Val Val Asp Glu Leu
                85                  90                  95

Asn Leu Leu His Thr Glu Leu Ala Lys Gln Leu Ala Asp Thr Met Val
            100                 105                 110

Leu Pro Ile Ile Gln Phe Arg Glu Lys Asp Leu Thr Glu Val Ser Thr
        115                 120                 125

Leu Lys Asp Leu Phe Gly Leu Ala Ser Asn Asp Val Cys Leu Phe Leu
    130                 135                 140

Glu His Asp Leu Ser Met Ala Lys Tyr Ser Arg Leu Pro Lys Lys Lys
145                 150                 155                 160

Glu Asn Glu Lys Val Lys Thr Glu Val Gly Lys Glu Val Ala Ala Ala
                165                 170                 175

Arg Arg Lys Gln His Leu Ser Ser Leu Gln Tyr Tyr Cys Ala Leu Asn
            180                 185                 190

Ala Leu Gln Tyr Arg Lys Gln Met Ala Met Met Glu Pro Met Ile Gly
        195                 200                 205
```

```
Phe Ala His Gly Gln Ile Asn Phe Phe Lys Lys Gly Ala Glu Met Phe
    210                 215                 220

Ser Lys Arg Met Asp Ser Phe Leu Ser Ser Val Ala Asp Met Val Gln
225                 230                 235                 240

Ser Ile Gln Val Glu Leu Glu Ala Glu Ala Glu Lys Met Arg Val Ser
                245                 250                 255

Gln Gln Glu Leu Leu Ser Val Asp Glu Ser Val Tyr Thr Pro Asp Ser
            260                 265                 270

Asp Val Ala Ala Pro Gln Ile Asn Arg Asn Leu Ile Gln Lys Ala Gly
        275                 280                 285

Tyr Leu Asn Leu Arg Asn Lys Thr Gly Leu Val Thr Thr Thr Trp Glu
    290                 295                 300

Arg Leu Tyr Phe Phe Thr Gln Gly Gly Asn Leu Met Cys Gln Pro Arg
305                 310                 315                 320

Gly Ala Val Ala Gly Gly Leu Ile Gln Asp Leu Asp Asn Cys Ser Val
                325                 330                 335

Met Ala Val Asp Cys Glu Asp Arg Arg Tyr Cys Phe Gln Ile Thr Thr
            340                 345                 350

Pro Asn Gly Lys Ser Gly Ile Ile Leu Gln Ala Glu Ser Arg Lys Glu
        355                 360                 365

Asn Glu Glu Trp Ile Cys Ala Ile Asn Asn Ile Ser Arg Gln Ile Tyr
    370                 375                 380

Leu Thr Asp Asn Pro Glu Ala Val Ala Ile Lys Leu Asn Gln Thr Ala
385                 390                 395                 400

Leu Gln Ala Val Thr Pro Ile Thr Ser Phe Gly Lys Lys Gln Glu Ser
                405                 410                 415

Ser Cys Pro Ser Gln Asn Leu Lys Asn Ser Glu Met Glu Asn Glu Asn
            420                 425                 430
```

```
Asp Lys Ile Val Pro Lys Ala Thr Ala Ser Leu Pro Glu Ala Glu Glu
        435                 440                 445

Leu Ile Ala Pro Gly Thr Pro Ile Gln Phe Asp Ile Val Leu Pro Ala
    450                 455                 460

Thr Glu Phe Leu Asp Gln Asn Arg Gly Ser Arg Arg Thr Asn Pro Phe
465                 470                 475                 480

Gly Glu Thr Glu Asp Glu Ser Phe Pro Glu Ala Glu Asp Ser Leu Leu
                485                 490                 495

Gln Gln Met Phe Ile Val Arg Phe Leu Gly Ser Met Ala Val Lys Thr
            500                 505                 510

Asp Ser Thr Thr Glu Val Ile Tyr Glu Ala Met Arg Gln Val Leu Ala
        515                 520                 525

Ala Arg Ala Ile His Asn Ile Phe Arg Met Thr Glu Ser His Leu Met
    530                 535                 540

Val Thr Ser Gln Ser Leu Arg Leu Ile Asp Pro Gln Thr Gln Val Ser
545                 550                 555                 560

Arg Ala Asn Phe Glu Leu Thr Ser Val Thr Gln Phe Ala Ala His Gln
                565                 570                 575

Glu Asn Lys Arg Leu Val Gly Phe Val Ile Arg Val Pro Glu Ser Thr
            580                 585                 590

Gly Glu Glu Ser Leu Ser Thr Tyr Ile Phe Glu Ser Asn Ser Glu Gly
        595                 600                 605

Glu Lys Ile Cys Tyr Ala Ile Asn Leu Gly Lys Glu Ile Ile Glu Val
    610                 615                 620

Gln Lys Asp Pro Glu Ala Leu Ala Gln Leu Met Leu Ser Ile Pro Leu
625                 630                 635                 640

Thr Asn Asp Gly Lys Tyr Val Leu Leu Asn Asp Gln Pro Asp Asp Asp
                645                 650                 655
```

```
Asp Gly Asn Pro Asn Glu His Arg Gly Ala Glu Ser Glu Ala
            660                 665                 670


<210> 2352
<211> 61
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: APPL2; "

<220>
<221> source
<223> /note="Gene Name:
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      zipper containing 2; "

<220>
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<223> /note="ENSP ID: ENSP00000447520"

<400> 2352
Met Gln Arg Val Tyr Gly Ala Gln Asn Glu Met Cys Leu Ala Thr Gln
1               5                   10                  15


Gln Leu Ser Lys Gln Leu Leu Ala Tyr Glu Lys Gln Asn Phe Ala Leu
            20                  25                  30


Gly Lys Gly Asp Glu Glu Val Ile Ser Thr Leu His Tyr Phe Ser Lys
        35                  40                  45


Val Val Asp Glu Leu Asn Leu Leu His Thr Glu Leu Ala
    50                  55                  60


<210> 2353
<211> 107
<212> PRT
<213> Homo sapiens

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leu
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<220>
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<400> 2353
Met Ser Leu Leu Gln Pro Gly Pro Val Phe Pro Ser Gly Asn Ser Glu
1 5 10 15

Asn Ser Asp Leu Thr Val Leu Pro Asn His Ile Cys Ser Lys Ile Leu
20 25 30

Ser Phe Ser Thr Phe Ala Asn His Tyr Phe Ser Cys Leu Leu Gln Ile
35 40 45

Cys Tyr Ala Ile Asn Leu Gly Lys Glu Ile Ile Glu Val Gln Lys Asp
50 55 60

Pro Glu Ala Leu Ala Gln Leu Met Leu Ser Ile Pro Leu Thr Asn Asp
65 70 75 80

Gly Lys Tyr Val Leu Leu Asn Asp Gln Pro Asp Asp Asp Asp Gly Asn
85 90 95

Pro Asn Glu His Arg Gly Ala Glu Ser Glu Ala
100 105

<210> 2354
<211> 39
<212> PRT
<213> Homo sapiens

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<220>
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<223> /note="Gene Symbol: APPL2; "

<220>
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adaptor prt, phosphotyr interaction, PH domain and leu
zipper containing 2; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000448569"

<400> 2354
Met Val Leu Pro Ile Ile Gln Phe Arg Glu Lys Asp Leu Thr Glu Val
1 5 10 15

Ser Thr Leu Lys Asp Leu Phe Gly Leu Ala Ser Asn Ala Gly Cys Leu
20 25 30

Arg Lys Arg Arg Met Arg Arg
35

<210> 2355
<211> 235
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: APPL2; "

<220>
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<223> /note="Gene Name:
adaptor prt, phosphotyr interaction, PH domain and leu
zipper containing 2; "

<220>
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<223> /note="ENSP ID: ENSP00000449410"

<400> 2355
Met Pro Ala Val Asp Lys Leu Leu Leu Glu Glu Ala Leu Gln Asp Ser
1 5 10 15

Pro Gln Thr Arg Ser Leu Leu Ser Val Phe Glu Glu Asp Ala Gly Thr
20 25 30

Leu Thr Asp Tyr Thr Asn Gln Leu Leu Gln Ala Met Gln Arg Val Tyr
35 40 45

Gly Ala Gln Asn Glu Met Cys Leu Ala Thr Gln Gln Leu Ser Lys Gln

```
    50                  55                  60

Leu Leu Ala Tyr Glu Lys Gln Asn Phe Ala Leu Gly Lys Gly Asp Glu
65                  70                  75                  80

Glu Val Ile Ser Thr Leu His Tyr Phe Ser Lys Val Val Asp Glu Leu
                85                  90                  95

Asn Leu Leu His Thr Glu Leu Ala Lys Gln Leu Ala Asp Thr Met Val
            100                 105                 110

Leu Pro Ile Ile Gln Phe Arg Glu Lys Asp Leu Thr Glu Val Ser Thr
        115                 120                 125

Leu Lys Asp Leu Phe Gly Leu Ala Ser Asn Glu His Asp Leu Ser Met
    130                 135                 140

Ala Lys Tyr Ser Arg Leu Pro Lys Lys Lys Glu Asn Glu Lys Val Lys
145                 150                 155                 160

Thr Glu Val Gly Lys Glu Val Ala Ala Ala Arg Arg Lys Gln His Leu
                165                 170                 175

Ser Ser Leu Gln Tyr Tyr Cys Ala Leu Asn Ala Leu Gln Tyr Arg Lys
            180                 185                 190

Gln Met Ala Met Met Glu Pro Met Ile Gly Phe Ala His Gly Gln Ile
        195                 200                 205

Asn Phe Phe Lys Lys Gly Ala Glu Met Phe Ser Lys Arg Met Asp Ser
    210                 215                 220

Phe Leu Ser Ser Val Ala Asp Met Val Gln Arg
225                 230                 235


<210> 2356
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<221> source
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<220>
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adaptor prt, phosphotyr interaction, PH domain and leu
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000449767"

<400> 2356
Met Pro Ala Val Asp Lys Leu Leu Leu Glu Glu Ala Leu Gln Asp Ser
1 5 10 15

Pro Gln Asn Glu Met Cys Leu Ala Thr Gln Gln Leu Ser Lys Gln Leu
20 25 30

Leu Ala Tyr Glu Lys Gln Asn Phe Ala Leu Gly Lys Gly Asp Glu Glu
35 40 45

Val Ile Ser Thr Leu His Tyr Phe Ser Lys Val Val Asp Glu Leu Asn
50 55 60

Leu Leu His Thr Glu Leu Ala Lys Gln Leu Ala Asp Thr Met Val Leu
65 70 75 80

Pro Ile Ile Gln Phe Arg Glu Lys Asp Leu Thr Glu Val Ser Thr Leu
85 90 95

Lys Asp Leu Phe Gly Leu Ala Ser Asn Glu His Asp Leu Ser Met Ala
100 105 110

Lys Tyr Ser Arg Leu Pro Lys Lys Lys Glu Asn Glu Lys Val Lys Thr
115 120 125

Glu Val Gly Lys Glu Val Ala Ala Ala Arg Arg Lys Gln His Leu Ser
130 135 140

<210> 2357
<211> 302
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 584; "

<220>
<221> source
<223> /note="Gene Symbol: AP1AR; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1 associated regulatory prt;
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<220>
<221> source
<223> /note="Uniprot ID: Q63HQ0; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000274000"

<400> 2357

Met	Gly	Asn	Cys	Cys	Trp	Thr	Gln	Cys	Phe	Gly	Leu	Leu	Arg	Lys	Glu
1				5				10						15	

Ala	Gly	Arg	Leu	Gln	Arg	Val	Gly	Gly	Gly	Gly	Gly	Ser	Lys	Tyr	Phe
			20					25					30		

Arg	Thr	Cys	Ser	Arg	Gly	Glu	His	Leu	Thr	Ile	Glu	Phe	Glu	Asn	Leu
		35					40					45			

Val	Glu	Ser	Asp	Glu	Gly	Glu	Ser	Pro	Gly	Ser	Ser	His	Arg	Pro	Leu
	50					55					60				

Thr	Glu	Glu	Glu	Ile	Val	Asp	Leu	Arg	Glu	Arg	His	Tyr	Asp	Ser	Ile
65					70					75					80

Ala	Glu	Lys	Gln	Lys	Asp	Leu	Asp	Lys	Lys	Ile	Gln	Lys	Glu	Leu	Ala
				85					90					95	

Leu	Gln	Glu	Glu	Lys	Leu	Arg	Leu	Glu	Glu	Glu	Ala	Leu	Tyr	Ala	Ala
			100					105					110		

Gln	Arg	Glu	Ala	Ala	Arg	Ala	Ala	Lys	Gln	Arg	Lys	Leu	Leu	Glu	Gln
		115					120					125			

Glu	Arg	Gln	Arg	Ile	Val	Gln	Gln	Tyr	His	Pro	Ser	Asn	Asn	Gly	Glu
	130					135					140				

```
Tyr Gln Ser Ser Gly Pro Glu Asp Asp Phe Glu Ser Cys Leu Arg Asn
145                 150                 155                 160

Met Lys Ser Gln Tyr Glu Val Phe Arg Ser Ser Arg Leu Ser Ser Asp
                165                 170                 175

Ala Thr Val Leu Thr Pro Asn Thr Glu Ser Ser Cys Asp Leu Met Thr
            180                 185                 190

Lys Thr Lys Ser Thr Ser Gly Asn Asp Asp Ser Thr Ser Leu Asp Leu
        195                 200                 205

Glu Trp Glu Asp Glu Glu Gly Met Asn Arg Met Leu Pro Met Arg Glu
    210                 215                 220

Arg Ser Lys Thr Glu Glu Asp Ile Leu Arg Ala Ala Leu Lys Tyr Ser
225                 230                 235                 240

Asn Lys Lys Thr Gly Ser Asn Pro Thr Ser Ala Ser Asp Asp Ser Asn
                245                 250                 255

Gly Leu Glu Trp Glu Asn Asp Phe Val Ser Ala Glu Met Asp Asp Asn
            260                 265                 270

Gly Asn Ser Glu Tyr Ser Gly Phe Val Asn Pro Val Leu Glu Leu Ser
        275                 280                 285

Asp Ser Gly Ile Arg His Ser Asp Thr Asp Gln Gln Thr Arg
    290                 295                 300


<210> 2358
<211> 269
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Symbol: AP1AR; "

<220>
<221> source
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      adaptor-related prt complex 1 associated regulatory prt;
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<220>
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<400> 2358
Met Gly Asn Cys Cys Trp Thr Gln Cys Phe Gly Leu Leu Arg Lys Glu
1   5   10   15

Ala Gly Arg Leu Gln Arg Val Gly Gly Gly Gly Gly Ser Lys Tyr Phe
            20   25   30

Arg Thr Cys Ser Arg Gly Glu His Leu Thr Ile Glu Phe Glu Asn Leu
        35   40   45

Val Glu Ser Asp Glu Gly Glu Ser Pro Gly Ser Ser His Arg Pro Leu
    50   55   60

Thr Glu Glu Glu Ile Val Asp Leu Arg Glu Arg His Tyr Asp Ser Ile
65   70   75   80

Ala Glu Lys Gln Lys Asp Leu Asp Lys Lys Ile Gln Lys Glu Gln Glu
                85   90   95

Arg Gln Arg Ile Val Gln Gln Tyr His Pro Ser Asn Asn Gly Glu Tyr
            100   105   110

Gln Ser Ser Gly Pro Glu Asp Asp Phe Glu Ser Cys Leu Arg Asn Met
        115   120   125

Lys Ser Gln Tyr Glu Val Phe Arg Ser Ser Arg Leu Ser Ser Asp Ala
    130   135   140

Thr Val Leu Thr Pro Asn Thr Glu Ser Ser Cys Asp Leu Met Thr Lys
145   150   155   160

Thr Lys Ser Thr Ser Gly Asn Asp Asp Ser Thr Ser Leu Asp Leu Glu
                165   170   175

Trp Glu Asp Glu Glu Gly Met Asn Arg Met Leu Pro Met Arg Glu Arg
            180   185   190

Ser Lys Thr Glu Glu Asp Ile Leu Arg Ala Ala Leu Lys Tyr Ser Asn
195 200 205

Lys Lys Thr Gly Ser Asn Pro Thr Ser Ala Ser Asp Asp Ser Asn Gly
210 215 220

Leu Glu Trp Glu Asn Asp Phe Val Ser Ala Glu Met Asp Asp Asn Gly
225 230 235 240

Asn Ser Glu Tyr Ser Gly Phe Val Asn Pro Val Leu Glu Leu Ser Asp
245 250 255

Ser Gly Ile Arg His Ser Asp Thr Asp Gln Gln Thr Arg
260 265

<210> 2359
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<223> /note="Gene Symbol: AP1AR; "

<220>
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adaptor-related prt complex 1 associated regulatory prt;
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000422529"

<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 2359
Xaa Gly Glu Tyr Gln Ser Ser Gly Pro Glu Asp Asp Phe Glu Ser Cys
1 5 10 15

Leu Arg Asn Met Lys Ser Gln Tyr Glu Val Phe Arg Ser Ser Arg Leu

```
            20                  25                  30

Ser Ser Asp Ala Thr Val Leu Thr Pro Asn Thr Glu Ser Ser Cys Asp
        35                  40                  45

Leu Met Thr Lys Thr Lys Ser Thr Ser Gly Asn Asp Asp Ser Thr Ser
    50                  55                  60

Leu Asp Leu Glu Trp Glu Asp Glu Glu Gly Ile Leu
65                  70                  75


<210> 2360
<211> 919
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 585; "

<220>
<221> source
<223> /note="Gene Symbol: AP1B1; "

<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="Uniprot ID:  Q10567; "

<220>
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<223> /note="ENSP ID: ENSP00000319361"

<400> 2360
Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1               5                   10                  15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
            20                  25                  30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60
```

```
Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro
            180                 185                 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
            260                 265                 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285
```

```
Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305                 310                 315                 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510
```

```
Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Ser Ala Phe Val Glu Gly Gly Arg Gly Val Val His Lys Ser
            580                 585                 590

Leu Pro Pro Arg Thr Ala Ser Ser Glu Ser Ala Glu Ser Pro Glu Thr
        595                 600                 605

Ala Pro Thr Gly Ala Pro Pro Gly Glu Gln Pro Asp Val Ile Pro Ala
    610                 615                 620

Gln Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro
625                 630                 635                 640

Val Ser Gly Pro Pro Leu Ala Thr Ser Ser Val Gln Met Gly Ala Val
                645                 650                 655

Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Ile Gly Gly Thr Asn Phe
            660                 665                 670

Val Ala Pro Pro Thr Ala Ala Val Pro Ala Asn Leu Gly Ala Pro Ile
        675                 680                 685

Gly Ser Gly Leu Ser Asp Leu Phe Asp Leu Thr Ser Gly Val Gly Thr
    690                 695                 700

Leu Ser Gly Ser Tyr Val Ala Pro Lys Ala Val Gly Ser Ile Ser Met
705                 710                 715                 720

Asp Leu Gln Leu Thr Asn Lys Ala Leu Gln Val Met Thr Asp Phe Ala
                725                 730                 735

Ile Gln Phe Asn Arg Asn Ser Phe Gly Leu Ala Pro Ala Ala Pro Leu
```

740 745 750

Gln Val His Ala Pro Leu Ser Pro Asn Gln Thr Val Glu Ile Ser Leu
755 760 765

Pro Leu Ser Thr Val Gly Ser Val Met Lys Met Glu Pro Leu Asn Asn
770 775 780

Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe Tyr Phe Ser Thr
785 790 795 800

Leu Tyr Pro Leu His Ile Leu Phe Val Glu Asp Gly Lys Met Asp Arg
805 810 815

Gln Met Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn Glu Asn Glu Ala
820 825 830

Gln Phe Gln Ile Arg Asp Cys Pro Leu Asn Ala Glu Ala Ala Ser Ser
835 840 845

Lys Leu Gln Ser Ser Asn Ile Phe Thr Val Ala Lys Arg Asn Val Glu
850 855 860

Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr Asn Gly Ile Trp
865 870 875 880

Val Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro Ser Cys Thr Leu
885 890 895

Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln His Val Tyr Gln Ala
900 905 910

Tyr Glu Thr Ile Leu Lys Asn
915

<210> 2361
<211> 949
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 585; "

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<221> source
<223> /note="Gene Symbol: AP1B1; "

<220>
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<223> /note="Gene Name:
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subunit; "

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<223> /note="Uniprot ID: Q10567; "

<220>
<221> source
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<400> 2361

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Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1               5                  10                  15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
            20                  25                  30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly
145                 150                 155                 160
```

```
Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro
            180                 185                 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
            260                 265                 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305                 310                 315                 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380
```

```
Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Ser Ala Phe Val Glu Gly Gly Arg Gly Val Val His Lys Ser
            580                 585                 590

Leu Pro Pro Arg Thr Ala Ser Ser Glu Ser Ala Glu Ser Pro Glu Thr
        595                 600                 605

Ala Pro Thr Gly Ala Pro Pro Gly Glu Gln Pro Asp Val Ile Pro Ala
```

610 615 620

Gln Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro
625 630 635 640

Val Ser Gly Pro Pro Leu Ala Thr Ser Ser Val Gln Met Gly Ala Val
645 650 655

Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Met Gly Asp Glu Pro Glu
660 665 670

Gly Ile Gly Gly Thr Asn Phe Val Ala Pro Pro Thr Ala Ala Val Pro
675 680 685

Ala Asn Leu Gly Ala Pro Ile Gly Ser Gly Leu Ser Asp Leu Phe Asp
690 695 700

Leu Thr Ser Gly Val Gly Thr Leu Ser Gly Ser Tyr Val Ala Pro Lys
705 710 715 720

Ala Val Trp Leu Pro Ala Met Lys Ala Lys Gly Leu Glu Ile Ser Gly
725 730 735

Thr Phe Thr Arg Gln Val Gly Ser Ile Ser Met Asp Leu Gln Leu Thr
740 745 750

Asn Lys Ala Leu Gln Val Met Thr Asp Phe Ala Ile Gln Phe Asn Arg
755 760 765

Asn Ser Phe Gly Leu Ala Pro Ala Ala Pro Leu Gln Val His Ala Pro
770 775 780

Leu Ser Pro Asn Gln Thr Val Glu Ile Ser Leu Pro Leu Ser Thr Val
785 790 795 800

Gly Ser Val Met Lys Met Glu Pro Leu Asn Asn Leu Gln Val Ala Val
805 810 815

Lys Asn Asn Ile Asp Val Phe Tyr Phe Ser Thr Leu Tyr Pro Leu His
820 825 830

Ile Leu Phe Val Glu Asp Gly Lys Met Asp Arg Gln Met Phe Leu Ala
835 840 845

```
Thr Trp Lys Asp Ile Pro Asn Glu Asn Glu Ala Gln Phe Gln Ile Arg
    850                 855                 860

Asp Cys Pro Leu Asn Ala Glu Ala Ala Ser Ser Lys Leu Gln Ser Ser
865                 870                 875                 880

Asn Ile Phe Thr Val Ala Lys Arg Asn Val Glu Gly Gln Asp Met Leu
                885                 890                 895

Tyr Gln Ser Leu Lys Leu Thr Asn Gly Ile Trp Val Leu Ala Glu Leu
            900                 905                 910

Arg Ile Gln Pro Gly Asn Pro Ser Cys Thr Asp Leu Glu Leu Ser Leu
        915                 920                 925

Lys Cys Arg Ala Pro Glu Val Ser Gln His Val Tyr Gln Ala Tyr Glu
    930                 935                 940

Thr Ile Leu Lys Asn
945
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<210> 2362
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Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65 70 75 80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
85 90 95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
100 105 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
115 120 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
130 135 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly
145 150 155 160

Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
165 170 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro
180 185 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
195 200 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
210 215 220

```
Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
            260                 265                 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305                 310                 315                 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
```

```
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Ser Ala Phe Val Glu Gly Gly Arg Gly Val Val His Lys Ser
            580                 585                 590

Leu Pro Pro Arg Thr Ala Ser Ser Glu Ser Ala Glu Ser Pro Glu Thr
        595                 600                 605

Ala Pro Thr Gly Ala Pro Pro Gly Glu Gln Pro Asp Val Ile Pro Ala
    610                 615                 620

Gln Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro
625                 630                 635                 640

Val Ser Gly Pro Pro Leu Ala Thr Ser Ser Val Gln Met Gly Ala Val
                645                 650                 655

Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Met Gly Asp Glu Pro Glu
            660                 665                 670

Gly Ile Gly Gly Thr Asn Phe Val Ala Pro Pro Thr Ala Ala Val Pro
        675                 680                 685
```

```
Ala Asn Leu Gly Ala Pro Ile Gly Ser Gly Leu Ser Asp Leu Phe Asp
    690                 695                 700

Leu Thr Ser Gly Val Gly Thr Leu Ser Gly Ser Tyr Val Ala Pro Lys
705                 710                 715                 720

Ala Val Trp Leu Pro Ala Met Lys Ala Lys Gly Leu Glu Ile Ser Gly
                725                 730                 735

Thr Phe Thr Arg Gln Val Gly Ser Ile Ser Met Asp Leu Gln Leu Thr
            740                 745                 750

Asn Lys Ala Leu Gln Val Met Thr Asp Phe Ala Ile Gln Phe Asn Arg
        755                 760                 765

Asn Ser Phe Gly Leu Ala Pro Ala Ala Pro Leu Gln Val His Ala Pro
    770                 775                 780

Leu Ser Pro Asn Gln Thr Val Glu Ile Ser Leu Pro Leu Ser Thr Val
785                 790                 795                 800

Gly Ser Val Met Lys Met Glu Pro Leu Asn Asn Leu Gln Val Ala Val
                805                 810                 815

Lys Asn Asn Ile Asp Val Phe Tyr Phe Ser Thr Leu Tyr Pro Leu His
            820                 825                 830

Ile Leu Phe Val Glu Asp Gly Lys Met Asp Arg Gln Met Phe Leu Ala
        835                 840                 845

Thr Trp Lys Asp Ile Pro Asn Glu Asn Glu Ala Gln Phe Gln Ile Arg
    850                 855                 860

Asp Cys Pro Leu Asn Ala Glu Ala Ala Ser Ser Lys Leu Gln Ser Ser
865                 870                 875                 880

Asn Ile Phe Thr Val Ala Lys Arg Asn Val Glu Gly Gln Asp Met Leu
                885                 890                 895

Tyr Gln Ser Leu Lys Leu Thr Asn Gly Ile Trp Val Leu Ala Glu Leu
            900                 905                 910
```

Arg Ile Gln Pro Gly Asn Pro Ser Cys Thr Asp Leu Glu Leu Ser Leu
915 920 925

Lys Cys Arg Ala Pro Glu Val Ser Gln His Val Tyr Gln Ala Tyr Glu
930 935 940

Thr Ile Leu Lys Asn
945

<210> 2363
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<400> 2363
Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

```
Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro
            180                 185                 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
            260                 265                 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
```

```
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305                 310                 315                 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525
```

```
Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Ser Ala Phe Val Glu Gly Gly Arg Gly Val Val His Lys Ser
            580                 585                 590

Leu Pro Pro Arg Thr Ala Ser Ser Glu Ser Ala Glu Ser Pro Glu Thr
        595                 600                 605

Ala Pro Thr Gly Ala Pro Pro Gly Glu Gln Pro Asp Val Ile Pro Ala
    610                 615                 620

Gln Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro
625                 630                 635                 640

Val Ser Gly Pro Pro Leu Ala Thr Ser Ser Val Gln Met Gly Ala Val
                645                 650                 655

Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Ile Gly Gly Thr Asn Phe
            660                 665                 670

Val Ala Pro Pro Thr Ala Ala Val Pro Ala Asn Leu Gly Ala Pro Ile
        675                 680                 685

Gly Ser Gly Leu Ser Asp Leu Phe Asp Leu Thr Ser Gly Val Gly Thr
    690                 695                 700

Leu Ser Gly Ser Tyr Val Ala Pro Lys Ala Val Trp Leu Pro Ala Met
705                 710                 715                 720

Lys Ala Lys Gly Leu Glu Ile Ser Gly Thr Phe Thr Arg Gln Val Gly
                725                 730                 735

Ser Ile Ser Met Asp Leu Gln Leu Thr Asn Lys Ala Leu Gln Val Met
            740                 745                 750
```

```
Thr Asp Phe Ala Ile Gln Phe Asn Arg Asn Ser Phe Gly Leu Ala Pro
        755                 760                 765

Ala Ala Pro Leu Gln Val His Ala Pro Leu Ser Pro Asn Gln Thr Val
    770                 775                 780

Glu Ile Ser Leu Pro Leu Ser Thr Val Gly Ser Val Met Lys Met Glu
785                 790                 795                 800

Pro Leu Asn Asn Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe
                805                 810                 815

Tyr Phe Ser Thr Leu Tyr Pro Leu His Ile Leu Phe Val Glu Asp Gly
            820                 825                 830

Lys Met Asp Arg Gln Met Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn
        835                 840                 845

Glu Asn Glu Ala Gln Phe Gln Ile Arg Asp Cys Pro Leu Asn Ala Glu
    850                 855                 860

Ala Ala Ser Ser Lys Leu Gln Ser Ser Asn Ile Phe Thr Val Ala Lys
865                 870                 875                 880

Arg Asn Val Glu Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr
                885                 890                 895

Asn Gly Ile Trp Val Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro
            900                 905                 910

Ser Cys Thr Leu Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln His
        915                 920                 925

Val Tyr Gln Ala Tyr Glu Thr Ile Leu Lys Asn
    930                 935


<210> 2364
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Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1   5   10   15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
            20   25   30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
        35   40   45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50   55   60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65   70   75   80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
                85   90   95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100   105   110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115   120   125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130   135   140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly

145 150 155 160

Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
165 170 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro
180 185 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
195 200 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
210 215 220

Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225 230 235 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
245 250 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
260 265 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
275 280 285

Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
290 295 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305 310 315 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
325 330 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
340 345 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
355 360 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
370 375 380

```
Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Ser Ala Phe Val Glu Gly Gly Arg Gly Val Val His Lys Ser
            580                 585                 590

Leu Pro Pro Arg Thr Ala Ser Ser Glu Ser Ala Glu Ser Pro Glu Thr
        595                 600                 605
```

```
Ala Pro Thr Gly Ala Pro Pro Gly Glu Gln Pro Asp Val Ile Pro Ala
    610                 615                 620

Gln Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro
625                 630                 635                 640

Val Ser Gly Pro Pro Leu Ala Thr Ser Ser Val Gln Met Gly Ala Val
                645                 650                 655

Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Ile Gly Gly Thr Asn Phe
            660                 665                 670

Val Ala Pro Pro Thr Ala Ala Val Pro Ala Asn Leu Gly Ala Pro Ile
        675                 680                 685

Gly Ser Gly Leu Ser Asp Leu Phe Asp Leu Thr Ser Gly Val Gly Thr
    690                 695                 700

Leu Ser Gly Ser Tyr Val Ala Pro Lys Ala Val Trp Leu Pro Ala Met
705                 710                 715                 720

Lys Ala Lys Gly Leu Glu Ile Ser Gly Thr Phe Thr Arg Gln Val Gly
                725                 730                 735

Ser Ile Ser Met Asp Leu Gln Leu Thr Asn Lys Ala Leu Gln Val Met
            740                 745                 750

Thr Asp Phe Ala Ile Gln Phe Asn Arg Asn Ser Phe Gly Leu Ala Pro
        755                 760                 765

Ala Ala Pro Leu Gln Val His Ala Pro Leu Ser Pro Asn Gln Thr Val
    770                 775                 780

Glu Ile Ser Leu Pro Leu Ser Thr Val Gly Ser Val Met Lys Met Glu
785                 790                 795                 800

Pro Leu Asn Asn Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe
                805                 810                 815

Tyr Phe Ser Thr Leu Tyr Pro Leu His Ile Leu Phe Val Glu Asp Gly
            820                 825                 830
```

```
Lys Met Asp Arg Gln Met Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn
        835                 840                 845

Glu Asn Glu Ala Gln Phe Gln Ile Arg Asp Cys Pro Leu Asn Ala Glu
    850                 855                 860

Ala Ala Ser Ser Lys Leu Gln Ser Ser Asn Ile Phe Thr Val Ala Lys
865                 870                 875                 880

Arg Asn Val Glu Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr
                885                 890                 895

Asn Gly Ile Trp Val Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro
            900                 905                 910

Ser Cys Thr Leu Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln His
        915                 920                 925

Val Tyr Gln Ala Tyr Glu Thr Ile Leu Lys Asn
    930                 935


<210> 2365
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<213> Homo sapiens

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      subunit; "

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<223> /note="ENSP ID: ENSP00000392735"


<220>
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<222> (1)..(1)
<223> Any amino acid
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<400> 2365
Xaa Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala Gln Ala
1 5 10 15

Pro Ala Ser Ser Leu Pro Trp Ala Phe Tyr Leu Glu Gln Glu Ala Glu
20 25 30

Ser His Ser Pro Arg Glu Ser Val Tyr Ile His Cys Pro Gly Val Phe
35 40 45

Gln Gln Ile Ala Pro Ser Gly Ala Pro Ala Pro Ser Phe Leu Phe Gly
50 55 60

Pro Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val
65 70 75 80

Asp Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys
85 90 95

Val Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile
100 105 110

Gln Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys
115 120 125

Asp Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr
130 135 140

Leu Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala
145 150 155 160

Met Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp
165 170

<210> 2366
<211> 578
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
adaptor-related prt complex 1, beta 1
subunit; "

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<400> 2366
Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65 70 75 80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
85 90 95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
100 105 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
115 120 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
130 135 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly
145 150 155 160

Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
165 170 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro

```
            180                 185                 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
            260                 265                 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305                 310                 315                 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
                405                 410                 415
```

```
Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro
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<210> 2367
<211> 939
<212> PRT
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<223> /note="ENSP ID: ENSP00000400065"

<400> 2367

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Met Thr Asp Ser Lys Tyr Phe Thr Thr Thr Lys Lys Gly Glu Ile Phe
1               5                  10                  15

Glu Leu Lys Ala Glu Leu Asn Ser Asp Lys Lys Glu Lys Lys Lys Glu
            20                  25                  30

Ala Val Lys Lys Val Ile Ala Ser Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ala Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Thr Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Leu Val Glu Asp Gln Gly
145                 150                 155                 160
```

```
Phe Leu Asp Thr Leu Lys Asp Leu Ile Ser Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ala Glu Ser His Pro
            180                 185                 190

Ser Ser Asn Leu Leu Asp Leu Asn Pro Gln Ser Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ala Asn Tyr Met Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Met Glu Met Leu Ser Lys
            260                 265                 270

Asp Leu Asp Tyr Tyr Gly Thr Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Ala Glu Pro Glu Leu Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys His Glu
305                 310                 315                 320

Met Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
```

385 390 395 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Lys Asp
405 410 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Val Ile Ala Thr Leu
420 425 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Glu Ala Arg Ala Ala Met
435 440 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
450 455 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465 470 475 480

Gln Leu Gln Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
485 490 495

Thr Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
500 505 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
515 520 525

Leu Leu Ser Thr Asp Pro Val Ala Ala Lys Glu Val Val Leu Ala Glu
530 535 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545 550 555 560

Asp Glu Leu Ile Cys Tyr Ile Gly Thr Leu Ala Ser Val Tyr His Lys
565 570 575

Pro Pro Ser Ala Phe Val Glu Gly Gly Arg Gly Val Val His Lys Ser
580 585 590

Leu Pro Pro Arg Thr Ala Ser Ser Glu Ser Ala Glu Ser Pro Glu Thr
595 600 605

Ala Pro Thr Gly Ala Pro Pro Gly Glu Gln Pro Asp Val Ile Pro Ala
610 615 620

```
Gln Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro
625                 630                 635                 640

Val Ser Gly Pro Pro Leu Ala Thr Ser Ser Val Gln Met Gly Ala Val
                645                 650                 655

Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Ile Gly Gly Thr Asn Phe
            660                 665                 670

Val Ala Pro Pro Thr Ala Ala Val Pro Ala Asn Leu Gly Ala Pro Ile
        675                 680                 685

Gly Ser Gly Leu Ser Asp Leu Phe Asp Leu Thr Ser Gly Val Gly Thr
    690                 695                 700

Leu Ser Gly Ser Tyr Val Ala Pro Lys Ala Val Trp Leu Pro Ala Met
705                 710                 715                 720

Lys Ala Lys Gly Leu Glu Ile Ser Gly Thr Phe Thr Arg Gln Val Gly
                725                 730                 735

Ser Ile Ser Met Asp Leu Gln Leu Thr Asn Lys Ala Leu Gln Val Met
            740                 745                 750

Thr Asp Phe Ala Ile Gln Phe Asn Arg Asn Ser Phe Gly Leu Ala Pro
        755                 760                 765

Ala Ala Pro Leu Gln Val His Ala Pro Leu Ser Pro Asn Gln Thr Val
    770                 775                 780

Glu Ile Ser Leu Pro Leu Ser Thr Val Gly Ser Val Met Lys Met Glu
785                 790                 795                 800

Pro Leu Asn Asn Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe
                805                 810                 815

Tyr Phe Ser Thr Leu Tyr Pro Leu His Ile Leu Phe Val Glu Asp Gly
            820                 825                 830

Lys Met Asp Arg Gln Met Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn
        835                 840                 845
```

```
Glu Asn Glu Ala Gln Phe Gln Ile Arg Asp Cys Pro Leu Asn Ala Glu
    850                 855                 860

Ala Ala Ser Ser Lys Leu Gln Ser Ser Asn Ile Phe Thr Val Ala Lys
865                 870                 875                 880

Arg Asn Val Glu Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr
                885                 890                 895

Asn Gly Ile Trp Val Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro
            900                 905                 910

Ser Cys Thr Leu Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln His
        915                 920                 925

Val Tyr Gln Ala Tyr Glu Thr Ile Leu Lys Asn
    930                 935


<210> 2368
<211> 822
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="Uniprot ID:  O43747; "

<220>
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<400> 2368
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15
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```
Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85                  90                  95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100                 105                 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115                 120                 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130                 135                 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Ala Ala Leu Cys
145                 150                 155                 160

Ala Val His Val Ile Arg Lys Val Pro Glu Leu Met Glu Met Phe Leu
                165                 170                 175

Pro Ala Thr Lys Asn Leu Leu Asn Glu Lys Asn His Gly Val Leu His
            180                 185                 190

Thr Ser Val Val Leu Leu Thr Glu Met Cys Glu Arg Ser Pro Asp Met
        195                 200                 205

Leu Ala His Phe Arg Lys Leu Val Pro Gln Leu Val Arg Ile Leu Lys
    210                 215                 220

Asn Leu Ile Met Ser Gly Tyr Ser Pro Glu His Asp Val Ser Gly Ile
225                 230                 235                 240

Ser Asp Pro Phe Leu Gln Val Arg Ile Leu Arg Leu Leu Arg Ile Leu
```

```
                245                 250                 255

Gly Arg Asn Asp Asp Asp Ser Ser Glu Ala Met Asn Asp Ile Leu Ala
            260                 265                 270

Gln Val Ala Thr Asn Thr Glu Thr Ser Lys Asn Val Gly Asn Ala Ile
        275                 280                 285

Leu Tyr Glu Thr Val Leu Thr Ile Met Asp Ile Lys Ser Glu Ser Gly
    290                 295                 300

Leu Arg Val Leu Ala Ile Asn Ile Leu Gly Arg Phe Leu Leu Asn Asn
305                 310                 315                 320

Asp Lys Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Lys Thr Val
                325                 330                 335

Gln Thr Asp His Asn Ala Val Gln Arg His Arg Ser Thr Ile Val Asp
            340                 345                 350

Cys Leu Lys Asp Leu Asp Val Ser Ile Lys Arg Arg Ala Met Glu Leu
        355                 360                 365

Ser Phe Ala Leu Val Asn Gly Asn Asn Ile Arg Gly Met Met Lys Glu
    370                 375                 380

Leu Leu Tyr Phe Leu Asp Ser Cys Glu Pro Glu Phe Lys Ala Asp Cys
385                 390                 395                 400

Ala Ser Gly Ile Phe Leu Ala Ala Glu Lys Tyr Ala Pro Ser Lys Arg
                405                 410                 415

Trp His Ile Asp Thr Ile Met Arg Val Leu Thr Thr Ala Gly Ser Tyr
            420                 425                 430

Val Arg Asp Asp Ala Val Pro Asn Leu Ile Gln Leu Ile Thr Asn Ser
        435                 440                 445

Val Glu Met His Ala Tyr Thr Val Gln Arg Leu Tyr Lys Ala Ile Leu
    450                 455                 460

Gly Asp Tyr Ser Gln Gln Pro Leu Val Gln Val Ala Ala Trp Cys Ile
465                 470                 475                 480
```

```
Gly Glu Tyr Gly Asp Leu Leu Val Ser Gly Gln Cys Glu Glu Glu Glu
                485                 490                 495

Pro Ile Gln Val Thr Glu Asp Glu Val Leu Asp Ile Leu Glu Ser Val
            500                 505                 510

Leu Ile Ser Asn Met Ser Thr Ser Val Thr Arg Gly Tyr Ala Leu Thr
        515                 520                 525

Ala Ile Met Lys Leu Ser Thr Arg Phe Thr Cys Thr Val Asn Arg Ile
    530                 535                 540

Lys Lys Val Val Ser Ile Tyr Gly Ser Ser Ile Asp Val Glu Leu Gln
545                 550                 555                 560

Gln Arg Ala Val Glu Tyr Asn Ala Leu Phe Lys Lys Tyr Asp His Met
                565                 570                 575

Arg Ser Ala Leu Leu Glu Arg Met Pro Val Met Glu Lys Val Thr Thr
            580                 585                 590

Asn Gly Pro Thr Glu Ile Val Gln Thr Asn Gly Glu Thr Glu Pro Ala
        595                 600                 605

Pro Leu Glu Thr Lys Pro Pro Pro Ser Gly Pro Gln Pro Thr Ser Gln
    610                 615                 620

Ala Asn Asp Leu Leu Asp Leu Leu Gly Gly Asn Asp Ile Thr Pro Val
625                 630                 635                 640

Ile Pro Thr Ala Pro Thr Ser Lys Pro Ser Ser Ala Gly Gly Glu Leu
                645                 650                 655

Leu Asp Leu Leu Gly Asp Ile Asn Leu Thr Gly Ala Pro Ala Ala Ala
            660                 665                 670

Pro Ala Pro Ala Ser Val Pro Gln Ile Ser Gln Pro Pro Phe Leu Leu
        675                 680                 685

Asp Gly Leu Ser Ser Gln Pro Leu Phe Asn Asp Ile Ala Ala Gly Ile
    690                 695                 700
```

```
Pro Ser Ile Thr Ala Tyr Ser Lys Asn Gly Leu Lys Ile Glu Phe Thr
705                 710                 715                 720

Phe Glu Arg Ser Asn Thr Asn Pro Ser Val Thr Val Ile Thr Ile Gln
                725                 730                 735

Ala Ser Asn Ser Thr Glu Leu Asp Met Thr Asp Phe Val Phe Gln Ala
            740                 745                 750

Ala Val Pro Lys Thr Phe Gln Leu Gln Leu Leu Ser Pro Ser Ser Ser
        755                 760                 765

Ile Val Pro Ala Phe Asn Thr Gly Thr Ile Thr Gln Val Ile Lys Val
    770                 775                 780

Leu Asn Pro Gln Lys Gln Gln Leu Arg Met Arg Ile Lys Leu Thr Tyr
785                 790                 795                 800

Asn His Lys Gly Ser Ala Met Gln Asp Leu Ala Glu Val Asn Asn Phe
                805                 810                 815

Pro Pro Gln Ser Trp Gln
            820
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<210> 2369
<211> 825
<212> PRT
<213> Homo sapiens

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subunit; "

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<223> /note="Uniprot ID: O43747; "

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<223> /note="ENSP ID: ENSP00000377148"

<400> 2369

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Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                  10                  15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85                  90                  95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100                 105                 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115                 120                 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130                 135                 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Ala Ala Leu Cys
145                 150                 155                 160

Ala Val His Val Ile Arg Lys Val Pro Glu Leu Met Glu Met Phe Leu
                165                 170                 175

Pro Ala Thr Lys Asn Leu Leu Asn Glu Lys Asn His Gly Val Leu His
            180                 185                 190

Thr Ser Val Val Leu Leu Thr Glu Met Cys Glu Arg Ser Pro Asp Met
        195                 200                 205

Leu Ala His Phe Arg Lys Asn Glu Lys Leu Val Pro Gln Leu Val Arg
```

```
    210                 215                 220

Ile Leu Lys Asn Leu Ile Met Ser Gly Tyr Ser Pro Glu His Asp Val
225                 230                 235                 240

Ser Gly Ile Ser Asp Pro Phe Leu Gln Val Arg Ile Leu Arg Leu Leu
                245                 250                 255

Arg Ile Leu Gly Arg Asn Asp Asp Asp Ser Ser Glu Ala Met Asn Asp
            260                 265                 270

Ile Leu Ala Gln Val Ala Thr Asn Thr Glu Thr Ser Lys Asn Val Gly
        275                 280                 285

Asn Ala Ile Leu Tyr Glu Thr Val Leu Thr Ile Met Asp Ile Lys Ser
    290                 295                 300

Glu Ser Gly Leu Arg Val Leu Ala Ile Asn Ile Leu Gly Arg Phe Leu
305                 310                 315                 320

Leu Asn Asn Asp Lys Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu
                325                 330                 335

Lys Thr Val Gln Thr Asp His Asn Ala Val Gln Arg His Arg Ser Thr
            340                 345                 350

Ile Val Asp Cys Leu Lys Asp Leu Asp Val Ser Ile Lys Arg Arg Ala
        355                 360                 365

Met Glu Leu Ser Phe Ala Leu Val Asn Gly Asn Asn Ile Arg Gly Met
    370                 375                 380

Met Lys Glu Leu Leu Tyr Phe Leu Asp Ser Cys Glu Pro Glu Phe Lys
385                 390                 395                 400

Ala Asp Cys Ala Ser Gly Ile Phe Leu Ala Ala Glu Lys Tyr Ala Pro
                405                 410                 415

Ser Lys Arg Trp His Ile Asp Thr Ile Met Arg Val Leu Thr Thr Ala
            420                 425                 430

Gly Ser Tyr Val Arg Asp Asp Ala Val Pro Asn Leu Ile Gln Leu Ile
        435                 440                 445
```

```
Thr Asn Ser Val Glu Met His Ala Tyr Thr Val Gln Arg Leu Tyr Lys
    450                 455                 460

Ala Ile Leu Gly Asp Tyr Ser Gln Gln Pro Leu Val Gln Val Ala Ala
465                 470                 475                 480

Trp Cys Ile Gly Glu Tyr Gly Asp Leu Leu Val Ser Gly Gln Cys Glu
                485                 490                 495

Glu Glu Glu Pro Ile Gln Val Thr Glu Asp Glu Val Leu Asp Ile Leu
            500                 505                 510

Glu Ser Val Leu Ile Ser Asn Met Ser Thr Ser Val Thr Arg Gly Tyr
        515                 520                 525

Ala Leu Thr Ala Ile Met Lys Leu Ser Thr Arg Phe Thr Cys Thr Val
    530                 535                 540

Asn Arg Ile Lys Lys Val Val Ser Ile Tyr Gly Ser Ser Ile Asp Val
545                 550                 555                 560

Glu Leu Gln Gln Arg Ala Val Glu Tyr Asn Ala Leu Phe Lys Lys Tyr
                565                 570                 575

Asp His Met Arg Ser Ala Leu Leu Glu Arg Met Pro Val Met Glu Lys
            580                 585                 590

Val Thr Thr Asn Gly Pro Thr Glu Ile Val Gln Thr Asn Gly Glu Thr
        595                 600                 605

Glu Pro Ala Pro Leu Glu Thr Lys Pro Pro Pro Ser Gly Pro Gln Pro
    610                 615                 620

Thr Ser Gln Ala Asn Asp Leu Leu Asp Leu Leu Gly Gly Asn Asp Ile
625                 630                 635                 640

Thr Pro Val Ile Pro Thr Ala Pro Thr Ser Lys Pro Ser Ser Ala Gly
                645                 650                 655

Gly Glu Leu Leu Asp Leu Leu Gly Asp Ile Asn Leu Thr Gly Ala Pro
            660                 665                 670
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```
Ala Ala Ala Pro Ala Pro Ala Ser Val Pro Gln Ile Ser Gln Pro Pro
        675                 680                 685

Phe Leu Leu Asp Gly Leu Ser Ser Gln Pro Leu Phe Asn Asp Ile Ala
    690                 695                 700

Ala Gly Ile Pro Ser Ile Thr Ala Tyr Ser Lys Asn Gly Leu Lys Ile
705                 710                 715                 720

Glu Phe Thr Phe Glu Arg Ser Asn Thr Asn Pro Ser Val Thr Val Ile
                725                 730                 735

Thr Ile Gln Ala Ser Asn Ser Thr Glu Leu Asp Met Thr Asp Phe Val
            740                 745                 750

Phe Gln Ala Ala Val Pro Lys Thr Phe Gln Leu Gln Leu Leu Ser Pro
        755                 760                 765

Ser Ser Ser Ile Val Pro Ala Phe Asn Thr Gly Thr Ile Thr Gln Val
    770                 775                 780

Ile Lys Val Leu Asn Pro Gln Lys Gln Gln Leu Arg Met Arg Ile Lys
785                 790                 795                 800

Leu Thr Tyr Asn His Lys Gly Ser Ala Met Gln Asp Leu Ala Glu Val
                805                 810                 815

Asn Asn Phe Pro Pro Gln Ser Trp Gln
            820                 825
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<210> 2370
<211> 176
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<220>
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<220>
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<223> /note="Gene Name:

adaptor-related prt complex 1, gamma 1
subunit; "

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<223> /note="ENSP ID: ENSP00000405836"

<400> 2370
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1 5 10 15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
20 25 30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
35 40 45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
50 55 60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65 70 75 80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
85 90 95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
100 105 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
115 120 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
130 135 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Glu Met Ile Tyr
145 150 155 160

Lys Gln Thr Asn Val Thr Gly Tyr Ile Leu Gly Gly Ile Pro Asn Ser
165 170 175

<210> 2371
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
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<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454219"

<400> 2371
Met Arg Ser Ala Leu Leu Glu Arg Met Pro Val Met Glu Lys Val Thr
1 5 10 15

Thr Asn Gly Pro Thr Glu Ile Val Gln Thr Asn Gly Glu Thr Glu Pro
20 25 30

Ala Pro Leu Glu Thr Lys Pro Pro Pro Ser Gly Pro Gln Pro Thr Ser
35 40 45

Gln Ala Asn Asp Leu Leu Asp Leu Leu Gly Gly Asn Asp Ile Thr Pro
50 55 60

Val Ile Pro Thr Ala Pro Thr Ser Lys Pro Ser Ser Ala Gly Gly Glu
65 70 75 80

Leu Leu Asp Leu Leu Gly Asp Ile Asn Leu Thr Gly Ala Pro Ala Ala
85 90 95

Ala Pro Ala Pro Ala Ser Val Pro Gln Ile Ser Gln Pro Pro Phe Leu
100 105 110

Leu Asp Gly Leu Ser Ser Gln Pro Leu Phe Asn Asp Ile Ala Ala Gly
115 120 125

Ile Pro Ser Ile Thr Ala Tyr Ser Lys Asn Gly Leu Lys Ile Glu Phe
130 135 140

Thr Phe Glu Arg Ser Asn Thr Asn Pro Ser Val Thr Val Ile Thr Ile
145 150 155 160

```
Gln Ala Ser Asn Ser Thr Glu Leu Asp Met Thr Asp Phe Val Phe Gln
                165                 170                 175

Ala Ala Val Pro Lys Thr Phe Gln Leu Gln Leu Leu Ser Pro Ser Ser
            180                 185                 190

Ser Ile Val Pro Ala Phe Asn Thr Gly Thr Ile Thr Gln Val Ile Lys
        195                 200                 205

Val Leu Asn Pro Gln Lys Gln Gln Leu Arg Met Arg Ile Lys Leu Thr
    210                 215                 220

Tyr Asn His Lys Gly Ser Ala Met Gln Asp Leu Ala Glu Val Asn Asn
225                 230                 235                 240

Phe Pro Pro Gln Ser Trp Gln
                245
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<210> 2372
<211> 822
<212> PRT
<213> Homo sapiens

<220>
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subunit; "

<220>
<221> source
<223> /note="Uniprot ID: O43747; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454523"

<400> 2372

```
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15
```

```
Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85                  90                  95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100                 105                 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115                 120                 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130                 135                 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Ala Ala Leu Cys
145                 150                 155                 160

Ala Val His Val Ile Arg Lys Val Pro Glu Leu Met Glu Met Phe Leu
                165                 170                 175

Pro Ala Thr Lys Asn Leu Leu Asn Glu Lys Asn His Gly Val Leu His
            180                 185                 190

Thr Ser Val Val Leu Leu Thr Glu Met Cys Glu Arg Ser Pro Asp Met
        195                 200                 205

Leu Ala His Phe Arg Lys Leu Val Pro Gln Leu Val Arg Ile Leu Lys
    210                 215                 220

Asn Leu Ile Met Ser Gly Tyr Ser Pro Glu His Asp Val Ser Gly Ile
225                 230                 235                 240
```

```
Ser Asp Pro Phe Leu Gln Val Arg Ile Leu Arg Leu Leu Arg Ile Leu
                245                 250                 255

Gly Arg Asn Asp Asp Asp Ser Ser Glu Ala Met Asn Asp Ile Leu Ala
            260                 265                 270

Gln Val Ala Thr Asn Thr Glu Thr Ser Lys Asn Val Gly Asn Ala Ile
        275                 280                 285

Leu Tyr Glu Thr Val Leu Thr Ile Met Asp Ile Lys Ser Glu Ser Gly
    290                 295                 300

Leu Arg Val Leu Ala Ile Asn Ile Leu Gly Arg Phe Leu Leu Asn Asn
305                 310                 315                 320

Asp Lys Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Lys Thr Val
                325                 330                 335

Gln Thr Asp His Asn Ala Val Gln Arg His Arg Ser Thr Ile Val Asp
            340                 345                 350

Cys Leu Lys Asp Leu Asp Val Ser Ile Lys Arg Arg Ala Met Glu Leu
        355                 360                 365

Ser Phe Ala Leu Val Asn Gly Asn Asn Ile Arg Gly Met Met Lys Glu
    370                 375                 380

Leu Leu Tyr Phe Leu Asp Ser Cys Glu Pro Glu Phe Lys Ala Asp Cys
385                 390                 395                 400

Ala Ser Gly Ile Phe Leu Ala Ala Glu Lys Tyr Ala Pro Ser Lys Arg
                405                 410                 415

Trp His Ile Asp Thr Ile Met Arg Val Leu Thr Thr Ala Gly Ser Tyr
            420                 425                 430

Val Arg Asp Asp Ala Val Pro Asn Leu Ile Gln Leu Ile Thr Asn Ser
        435                 440                 445

Val Glu Met His Ala Tyr Thr Val Gln Arg Leu Tyr Lys Ala Ile Leu
    450                 455                 460

Gly Asp Tyr Ser Gln Gln Pro Leu Val Gln Val Ala Ala Trp Cys Ile
```

```
465                 470                 475                 480

Gly Glu Tyr Gly Asp Leu Leu Val Ser Gly Gln Cys Glu Glu Glu Glu
                485                 490                 495

Pro Ile Gln Val Thr Glu Asp Glu Val Leu Asp Ile Leu Glu Ser Val
            500                 505                 510

Leu Ile Ser Asn Met Ser Thr Ser Val Thr Arg Gly Tyr Ala Leu Thr
        515                 520                 525

Ala Ile Met Lys Leu Ser Thr Arg Phe Thr Cys Thr Val Asn Arg Ile
    530                 535                 540

Lys Lys Val Val Ser Ile Tyr Gly Ser Ser Ile Asp Val Glu Leu Gln
545                 550                 555                 560

Gln Arg Ala Val Glu Tyr Asn Ala Leu Phe Lys Lys Tyr Asp His Met
                565                 570                 575

Arg Ser Ala Leu Leu Glu Arg Met Pro Val Met Glu Lys Val Thr Thr
            580                 585                 590

Asn Gly Pro Thr Glu Ile Val Gln Thr Asn Gly Glu Thr Glu Pro Ala
        595                 600                 605

Pro Leu Glu Thr Lys Pro Pro Pro Ser Gly Pro Gln Pro Thr Ser Gln
    610                 615                 620

Ala Asn Asp Leu Leu Asp Leu Leu Gly Gly Asn Asp Ile Thr Pro Val
625                 630                 635                 640

Ile Pro Thr Ala Pro Thr Ser Lys Pro Ser Ser Ala Gly Gly Glu Leu
                645                 650                 655

Leu Asp Leu Leu Gly Asp Ile Asn Leu Thr Gly Ala Pro Ala Ala Ala
            660                 665                 670

Pro Ala Pro Ala Ser Val Pro Gln Ile Ser Gln Pro Pro Phe Leu Leu
        675                 680                 685

Asp Gly Leu Ser Ser Gln Pro Leu Phe Asn Asp Ile Ala Ala Gly Ile
    690                 695                 700
```

```
Pro Ser Ile Thr Ala Tyr Ser Lys Asn Gly Leu Lys Ile Glu Phe Thr
705                 710                 715                 720

Phe Glu Arg Ser Asn Thr Asn Pro Ser Val Thr Val Ile Thr Ile Gln
                725                 730                 735

Ala Ser Asn Ser Thr Glu Leu Asp Met Thr Asp Phe Val Phe Gln Ala
            740                 745                 750

Ala Val Pro Lys Thr Phe Gln Leu Gln Leu Leu Ser Pro Ser Ser Ser
        755                 760                 765

Ile Val Pro Ala Phe Asn Thr Gly Thr Ile Thr Gln Val Ile Lys Val
    770                 775                 780

Leu Asn Pro Gln Lys Gln Gln Leu Arg Met Arg Ile Lys Leu Thr Tyr
785                 790                 795                 800

Asn His Lys Gly Ser Ala Met Gln Asp Leu Ala Glu Val Asn Asn Phe
                805                 810                 815

Pro Pro Gln Ser Trp Gln
            820


<210> 2373
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 1, gamma 1
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454713"
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<400> 2373
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1   5   10   15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20   25   30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35   40   45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50   55   60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65   70   75   80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85   90   95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100   105   110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115   120   125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130   135   140

<210> 2374
<211> 53
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000454717"

<400> 2374
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1   5   10   15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20   25   30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35   40   45

Asn Val Ala Lys Leu
    50

<210> 2375
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 1, gamma 1
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454932"

<400> 2375
Ser Glu Ala Met Asn Asp Ile Leu Ala Gln Val Ala Thr Asn Thr Glu
1   5   10   15

Thr Ser Lys Asn Val Gly Asn Ala Ile Leu Tyr Glu Thr Val Leu Thr
            20   25   30

Ile Met Asp Ile Lys Ser Glu Ser Gly Leu Arg Ile Cys Gly Ser Asp
        35   40   45

Ile Phe Val Glu Asp Cys Thr Asp Arg Ser

50 55

<210> 2376
<211> 236
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1, gamma 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000454970"

<400> 2376
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1 5 10 15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
20 25 30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
35 40 45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
50 55 60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65 70 75 80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
85 90 95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
100 105 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
115 120 125

```
Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130                 135                 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Ala Ala Leu Cys
145                 150                 155                 160

Ala Val His Val Ile Arg Lys Val Pro Glu Leu Met Glu Met Phe Leu
                165                 170                 175

Pro Ala Thr Lys Asn Leu Leu Asn Glu Lys Asn His Gly Val Leu His
            180                 185                 190

Thr Ser Val Val Leu Leu Thr Glu Met Cys Glu Arg Ser Pro Asp Met
        195                 200                 205

Leu Ala His Phe Arg Lys Val Ala Cys Ala Pro Ile Ser Ser Tyr Phe
    210                 215                 220

Lys Glu Pro His His Val Arg Ile Phe Thr Arg Thr
225                 230                 235


<210> 2377
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000455400"

<400> 2377
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15
```

```
Ala Arg Thr Gln Ala Glu Glu Arg Glu Met
            20                  25


<210> 2378
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
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<223> /note="Gene Symbol: AP1G1; "

<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456058"

<400> 2378
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15


Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30


Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45


Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60


Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80


Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85                  90                  95


Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100                 105                 110
```

```
His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115                 120                 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130                 135                 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Ala Ala Leu Cys
145                 150                 155                 160

Ala Val His Val Ile Arg Lys Val Pro Glu Leu Met Glu Met Phe Leu
                165                 170                 175

Pro Ala Thr Lys Asn Leu Leu Asn Glu Lys Asn
            180                 185


<210> 2379
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456316"

<400> 2379
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
```

```
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85                  90                  95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100                 105                 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115                 120                 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala
    130                 135


<210> 2380
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 1, gamma 1
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000456493"

<400> 2380
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45
```

```
Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80

Asp Lys Arg Ile Gly
                85
```

<210> 2381
<211> 208
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1, gamma 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457726"

<400> 2381

```
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80
```

```
Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu Arg
                85                  90                  95

Gln Asp Val His Leu Leu Met Thr Asn Cys Ile Lys Asn Asp Leu Asn
            100                 105                 110

His Ser Thr Gln Phe Val Gln Gly Leu Ala Leu Cys Thr Leu Gly Cys
        115                 120                 125

Met Gly Ser Ser Glu Met Cys Arg Asp Leu Ala Gly Glu Val Glu Lys
    130                 135                 140

Leu Leu Lys Thr Ser Asn Ser Tyr Leu Arg Lys Lys Ala Ala Leu Cys
145                 150                 155                 160

Ala Val His Val Ile Arg Lys Val Pro Glu Leu Met Glu Met Phe Leu
                165                 170                 175

Pro Ala Thr Lys Asn Leu Leu Asn Glu Lys Asn His Gly Asn Val Ile
            180                 185                 190

Trp Met Thr Cys Leu Phe Met Arg His Ser Ser Ile Phe Thr Val Phe
        195                 200                 205


<210> 2382
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 586; "

<220>
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<223> /note="Gene Symbol: AP1G1; "

<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000457927"

<400> 2382
```

```
Met Pro Ala Pro Ile Arg Leu Arg Glu Leu Ile Arg Thr Ile Arg Thr
1               5                   10                  15

Ala Arg Thr Gln Ala Glu Glu Arg Glu Met Ile Gln Lys Glu Cys Ala
            20                  25                  30

Ala Ile Arg Ser Ser Phe Arg Glu Glu Asp Asn Thr Tyr Arg Cys Arg
        35                  40                  45

Asn Val Ala Lys Leu Leu Tyr Met His Met Leu Gly Tyr Pro Ala His
    50                  55                  60

Phe Gly Gln Leu Glu Cys Leu Lys Leu Ile Ala Ser Gln Lys Phe Thr
65                  70                  75                  80

Asp Lys Arg Ile Gly Tyr Leu Gly Ala Met Leu
                85                  90
```

<210> 2383
<211> 785
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 587; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1, gamma 2
subunit; "

<220>
<221> source
<223> /note="Uniprot ID: O75843; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000312442"

<400> 2383

```
Met Val Val Pro Ser Leu Lys Leu Gln Asp Leu Ile Glu Glu Ile Arg
1               5                   10                  15

Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
```

```
            20                  25                  30

Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
        35                  40                  45

Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
    50                  55                  60

His Phe Gly Gln Met Glu Cys Leu Lys Leu Ile Ala Ser Ser Arg Phe
65                  70                  75                  80

Thr Asp Lys Arg Val Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu
                85                  90                  95

Arg His Asp Ala His Leu Leu Ile Thr Asn Ser Ile Lys Asn Asp Leu
            100                 105                 110

Ser Gln Gly Ile Gln Pro Val Gln Gly Leu Ala Leu Cys Thr Leu Ser
        115                 120                 125

Thr Met Gly Ser Ala Glu Met Cys Arg Asp Leu Ala Pro Glu Val Glu
    130                 135                 140

Lys Leu Leu Leu Gln Pro Ser Pro Tyr Val Arg Lys Lys Ala Ile Leu
145                 150                 155                 160

Thr Ala Val His Met Ile Arg Lys Val Pro Glu Leu Ser Ser Val Phe
                165                 170                 175

Leu Pro Pro Cys Ala Gln Leu Leu His Glu Arg His His Gly Ile Leu
            180                 185                 190

Leu Gly Thr Ile Thr Leu Ile Thr Glu Leu Cys Glu Arg Ser Pro Ala
        195                 200                 205

Ala Leu Arg His Phe Arg Lys Val Val Pro Gln Leu Val His Ile Leu
    210                 215                 220

Arg Thr Leu Val Thr Met Gly Tyr Ser Thr Glu His Ser Ile Ser Gly
225                 230                 235                 240

Val Ser Asp Pro Phe Leu Gln Val Gln Ile Leu Arg Leu Leu Arg Ile
                245                 250                 255
```

```
Leu Gly Arg Asn His Glu Glu Ser Ser Glu Thr Met Asn Asp Leu Leu
            260                 265                 270

Ala Gln Val Ala Thr Asn Thr Asp Thr Ser Arg Asn Ala Gly Asn Ala
        275                 280                 285

Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
    290                 295                 300

Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
305                 310                 315                 320

Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
                325                 330                 335

Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
            340                 345                 350

Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg Arg Ala Leu Glu
        355                 360                 365

Leu Ser Leu Ala Leu Val Asn Ser Ser Asn Val Arg Ala Met Met Gln
    370                 375                 380

Glu Leu Gln Ala Phe Leu Glu Ser Cys Pro Pro Asp Leu Arg Ala Asp
385                 390                 395                 400

Cys Ala Ser Gly Ile Leu Leu Ala Ala Glu Arg Phe Ala Pro Thr Lys
                405                 410                 415

Arg Trp His Ile Asp Thr Ile Leu His Val Leu Thr Thr Ala Gly Thr
            420                 425                 430

His Val Arg Asp Asp Ala Val Ala Asn Leu Thr Gln Leu Ile Gly Gly
        435                 440                 445

Ala Gln Glu Leu His Ala Tyr Ser Val Arg Arg Leu Tyr Asn Ala Leu
    450                 455                 460

Ala Glu Asp Ile Ser Gln Gln Pro Leu Val Gln Val Ala Ala Trp Cys
465                 470                 475                 480
```

```
Ile Gly Glu Tyr Gly Asp Leu Leu Leu Ala Gly Asn Cys Glu Glu Ile
                485                 490                 495

Glu Pro Leu Gln Val Asp Glu Glu Glu Val Leu Ala Leu Leu Glu Lys
            500                 505                 510

Val Leu Gln Ser His Met Ser Leu Pro Ala Thr Arg Gly Tyr Ala Leu
        515                 520                 525

Thr Ala Leu Met Lys Leu Ser Thr Arg Leu Cys Gly Asp Asn Asn Arg
    530                 535                 540

Ile Arg Gln Val Val Ser Ile Tyr Gly Ser Cys Leu Asp Val Glu Leu
545                 550                 555                 560

Gln Gln Arg Ala Val Glu Tyr Asp Thr Leu Phe Arg Lys Tyr Asp His
                565                 570                 575

Met Arg Ala Ala Ile Leu Glu Lys Met Pro Leu Val Glu Arg Asp Gly
            580                 585                 590

Pro Gln Ala Asp Glu Glu Ala Lys Glu Ser Lys Glu Ala Ala Gln Leu
        595                 600                 605

Ser Glu Ala Ala Pro Val Pro Thr Glu Pro Gln Ala Ser Gln Leu Leu
    610                 615                 620

Asp Leu Leu Asp Leu Leu Asp Gly Ala Ser Gly Asp Val Gln His Pro
625                 630                 635                 640

Pro His Leu Asp Pro Ser Pro Gly Gly Ala Leu Val His Leu Leu Asp
                645                 650                 655

Leu Pro Cys Val Pro Pro Pro Pro Ala Pro Ile Pro Asp Leu Lys Val
            660                 665                 670

Phe Glu Arg Glu Gly Val Gln Leu Asn Leu Ser Phe Ile Arg Pro Pro
        675                 680                 685

Glu Asn Pro Ala Leu Leu Leu Ile Thr Ile Thr Ala Thr Asn Phe Ser
    690                 695                 700
```

```
Glu Gly Asp Val Thr His Phe Ile Cys Gln Ala Ala Val Pro Lys Ser
705                 710                 715                 720


Leu Gln Leu Gln Leu Gln Ala Pro Ser Gly Asn Thr Val Pro Ala Arg
                725                 730                 735


Gly Gly Leu Pro Ile Thr Gln Leu Phe Arg Ile Leu Asn Pro Asn Lys
            740                 745                 750


Ala Pro Leu Arg Leu Lys Leu Arg Leu Thr Tyr Asp His Phe His Gln
        755                 760                 765


Ser Val Gln Glu Ile Phe Glu Val Asn Asn Leu Pro Val Glu Ser Trp
    770                 775                 780


Gln
785


<210> 2384
<211> 785
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 587; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G2; "

<220>
<221> source
<223> /note="Gene Name:
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<220>
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<223> /note="Uniprot ID:  O75843; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000380309"

<400> 2384
Met Val Val Pro Ser Leu Lys Leu Gln Asp Leu Ile Glu Glu Ile Arg
1               5                   10                  15


Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
```

```
            20                  25                  30

Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
        35                  40                  45

Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
    50                  55                  60

His Phe Gly Gln Met Glu Cys Leu Lys Leu Ile Ala Ser Ser Arg Phe
65                  70                  75                  80

Thr Asp Lys Arg Val Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu
                85                  90                  95

Arg His Asp Ala His Leu Leu Ile Thr Asn Ser Ile Lys Asn Asp Leu
            100                 105                 110

Ser Gln Gly Ile Gln Pro Val Gln Gly Leu Ala Leu Cys Thr Leu Ser
        115                 120                 125

Thr Met Gly Ser Ala Glu Met Cys Arg Asp Leu Ala Pro Glu Val Glu
    130                 135                 140

Lys Leu Leu Leu Gln Pro Ser Pro Tyr Val Arg Lys Lys Ala Ile Leu
145                 150                 155                 160

Thr Ala Val His Met Ile Arg Lys Val Pro Glu Leu Ser Ser Val Phe
                165                 170                 175

Leu Pro Pro Cys Ala Gln Leu Leu His Glu Arg His His Gly Ile Leu
            180                 185                 190

Leu Gly Thr Ile Thr Leu Ile Thr Glu Leu Cys Glu Arg Ser Pro Ala
        195                 200                 205

Ala Leu Arg His Phe Arg Lys Val Val Pro Gln Leu Val His Ile Leu
    210                 215                 220

Arg Thr Leu Val Thr Met Gly Tyr Ser Thr Glu His Ser Ile Ser Gly
225                 230                 235                 240

Val Ser Asp Pro Phe Leu Gln Val Gln Ile Leu Arg Leu Leu Arg Ile
                245                 250                 255
```

```
Leu Gly Arg Asn His Glu Glu Ser Ser Glu Thr Met Asn Asp Leu Leu
            260                 265                 270

Ala Gln Val Ala Thr Asn Thr Asp Thr Ser Arg Asn Ala Gly Asn Ala
        275                 280                 285

Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
    290                 295                 300

Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
305                 310                 315                 320

Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
                325                 330                 335

Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
            340                 345                 350

Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg Arg Ala Leu Glu
        355                 360                 365

Leu Ser Leu Ala Leu Val Asn Ser Ser Asn Val Arg Ala Met Met Gln
    370                 375                 380

Glu Leu Gln Ala Phe Leu Glu Ser Cys Pro Pro Asp Leu Arg Ala Asp
385                 390                 395                 400

Cys Ala Ser Gly Ile Leu Leu Ala Ala Glu Arg Phe Ala Pro Thr Lys
                405                 410                 415

Arg Trp His Ile Asp Thr Ile Leu His Val Leu Thr Thr Ala Gly Thr
            420                 425                 430

His Val Arg Asp Asp Ala Val Ala Asn Leu Thr Gln Leu Ile Gly Gly
        435                 440                 445

Ala Gln Glu Leu His Ala Tyr Ser Val Arg Arg Leu Tyr Asn Ala Leu
    450                 455                 460

Ala Glu Asp Ile Ser Gln Gln Pro Leu Val Gln Val Ala Ala Trp Cys
465                 470                 475                 480
```

```
Ile Gly Glu Tyr Gly Asp Leu Leu Leu Ala Gly Asn Cys Glu Glu Ile
                485                 490                 495

Glu Pro Leu Gln Val Asp Glu Glu Glu Val Leu Ala Leu Leu Glu Lys
            500                 505                 510

Val Leu Gln Ser His Met Ser Leu Pro Ala Thr Arg Gly Tyr Ala Leu
        515                 520                 525

Thr Ala Leu Met Lys Leu Ser Thr Arg Leu Cys Gly Asp Asn Asn Arg
    530                 535                 540

Ile Arg Gln Val Val Ser Ile Tyr Gly Ser Cys Leu Asp Val Glu Leu
545                 550                 555                 560

Gln Gln Arg Ala Val Glu Tyr Asp Thr Leu Phe Arg Lys Tyr Asp His
                565                 570                 575

Met Arg Ala Ala Ile Leu Glu Lys Met Pro Leu Val Glu Arg Asp Gly
            580                 585                 590

Pro Gln Ala Asp Glu Glu Ala Lys Glu Ser Lys Glu Ala Ala Gln Leu
        595                 600                 605

Ser Glu Ala Ala Pro Val Pro Thr Glu Pro Gln Ala Ser Gln Leu Leu
    610                 615                 620

Asp Leu Leu Asp Leu Leu Asp Gly Ala Ser Gly Asp Val Gln His Pro
625                 630                 635                 640

Pro His Leu Asp Pro Ser Pro Gly Gly Ala Leu Val His Leu Leu Asp
                645                 650                 655

Leu Pro Cys Val Pro Pro Pro Pro Ala Pro Ile Pro Asp Leu Lys Val
            660                 665                 670

Phe Glu Arg Glu Gly Val Gln Leu Asn Leu Ser Phe Ile Arg Pro Pro
        675                 680                 685

Glu Asn Pro Ala Leu Leu Leu Ile Thr Ile Thr Ala Thr Asn Phe Ser
    690                 695                 700
```

```
Glu Gly Asp Val Thr His Phe Ile Cys Gln Ala Ala Val Pro Lys Ser
705                 710                 715                 720

Leu Gln Leu Gln Leu Gln Ala Pro Ser Gly Asn Thr Val Pro Ala Arg
                725                 730                 735

Gly Gly Leu Pro Ile Thr Gln Leu Phe Arg Ile Leu Asn Pro Asn Lys
            740                 745                 750

Ala Pro Leu Arg Leu Lys Leu Arg Leu Thr Tyr Asp His Phe His Gln
        755                 760                 765

Ser Val Gln Glu Ile Phe Glu Val Asn Asn Leu Pro Val Glu Ser Trp
    770                 775                 780

Gln
785


<210> 2385
<211> 143
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 587; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G2; "

<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000450588"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2385
Xaa Ala Gly Asn Ala Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp
1               5                   10                  15
```

```
Ile Arg Ser Ala Ala Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly
            20                  25                  30

Arg Phe Leu Leu Asn Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr
        35                  40                  45

Ser Leu Leu Arg Leu Val Gln Ser Asp His Ser Ala Val Gln Arg His
    50                  55                  60

Arg Pro Thr Val Val Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser
65                  70                  75                  80

Arg Arg Ala Leu Glu Leu Ser Leu Ala Leu Val Asn Ser Ser Asn Val
                85                  90                  95

Arg Ala Met Met Gln Glu Leu Gln Ala Phe Leu Glu Ser Cys Pro Pro
            100                 105                 110

Asp Leu Arg Ala Asp Cys Ala Ser Gly Ile Leu Leu Ala Ala Glu Arg
        115                 120                 125

His His Pro Ala Cys Ala Asp Asn Gly Gly His Pro Cys Ala Gly
    130                 135                 140


<210> 2386
<211> 197
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000450805"

<400> 2386
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Glu Glu Val Leu Ala Leu Leu Glu Lys Val Leu Gln Ser His Met Ser
1               5                  10                  15

Leu Pro Ala Thr Arg Gly Tyr Ala Leu Thr Ala Leu Met Lys Leu Ser
            20                  25                  30

Thr Arg Leu Cys Gly Asp Asn Lys Ala Ala Ile Leu Glu Lys Met Pro
        35                  40                  45

Leu Val Glu Arg Asp Gly Pro Gln Ala Asp Glu Glu Ala Lys Glu Ser
    50                  55                  60

Lys Glu Ala Ala Gln Leu Ser Glu Ala Ala Pro Val Pro Thr Glu Pro
65                  70                  75                  80

Gln Ala Ser Gln Leu Leu Asp Leu Leu Asp Leu Leu Asp Gly Ala Ser
                85                  90                  95

Gly Asp Val Gln His Pro Pro His Leu Asp Pro Ser Pro Gly Gly Ala
            100                 105                 110

Leu Val His Leu Leu Asp Leu Pro Cys Val Pro Pro Pro Pro Ala Pro
        115                 120                 125

Ile Pro Asp Leu Lys Val Phe Glu Arg Glu Gly Val Gln Leu Asn Leu
    130                 135                 140

Ser Phe Ile Arg Pro Pro Glu Asn Pro Ala Leu Leu Leu Ile Thr Ile
145                 150                 155                 160

Thr Ala Thr Asn Phe Ser Glu Gly Asp Val Thr His Phe Ile Cys Gln
                165                 170                 175

Ala Ala Val Pro Lys Ser Leu Gln Leu Gln Leu Gln Ala Pro Ser Gly
            180                 185                 190

Asn Thr Val Pro Ala
        195
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<210> 2387
<211> 68
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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subunit; "

<220>
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<223> /note="ENSP ID: ENSP00000450888"

<400> 2387
Met Val Val Pro Ser Leu Lys Leu Gln Asp Leu Ile Glu Glu Ile Arg
1 5 10 15

Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
20 25 30

Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
35 40 45

Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
50 55 60

His Phe Gly Gln
65

<210> 2388
<211> 68
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 587; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1, gamma 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451343"

<400> 2388
Met Val Val Pro Ser Leu Lys Leu Gln Asp Leu Ile Glu Glu Ile Arg
1   5   10   15

Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
            20   25   30

Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
        35   40   45

Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
    50   55   60

His Phe Gly Gln
65

<210> 2389
<211> 136
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 587; "

<220>
<221> source
<223> /note="Gene Symbol: AP1G2; "

<220>
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000451504"

<400> 2389
Met Val Val Pro Ser Leu Lys Leu Gln Asp Leu Ile Glu Glu Ile Arg
1   5   10   15

Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
            20   25   30

```
Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
        35                  40                  45

Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
    50                  55                  60

His Phe Gly Gln Met Glu Cys Leu Lys Leu Ile Ala Ser Ser Arg Phe
65                  70                  75                  80

Thr Asp Lys Arg Val Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu
                85                  90                  95

Arg His Asp Ala His Leu Leu Ile Thr Asn Ser Ile Lys Asn Asp Leu
            100                 105                 110

Ser Gln Gly Ile Gln Pro Val Gln Gly Leu Ala Leu Cys Thr Leu Ser
        115                 120                 125

Thr Met Gly Ser Ala Glu Met Cys
    130                 135


<210> 2390
<211> 200
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 587; "

<220>
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<220>
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000452153"

<400> 2390
Met Val Val Pro Ser Leu Lys Leu Gln Asp Leu Ile Glu Glu Ile Arg
1               5                   10                  15
```

```
Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
            20                  25                  30

Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
        35                  40                  45

Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
    50                  55                  60

His Phe Gly Gln Met Glu Cys Leu Lys Leu Ile Ala Ser Ser Arg Phe
65                  70                  75                  80

Thr Asp Lys Arg Val Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu
                85                  90                  95

Arg His Asp Ala His Leu Leu Ile Thr Asn Ser Ile Lys Asn Asp Leu
            100                 105                 110

Ser Gln Gly Ile Gln Pro Val Gln Gly Leu Ala Leu Cys Thr Leu Ser
        115                 120                 125

Thr Met Gly Ser Ala Glu Met Cys Arg Asp Leu Ala Pro Glu Val Glu
    130                 135                 140

Lys Leu Leu Leu Gln Pro Ser Pro Tyr Val Arg Lys Lys Ala Ile Leu
145                 150                 155                 160

Thr Ala Val His Met Ile Arg Lys Val Pro Glu Leu Ser Ser Val Phe
                165                 170                 175

Leu Pro Pro Cys Ala Gln Leu Leu His Glu Arg His His Gly Ile Leu
            180                 185                 190

Leu Gly Thr Ile Thr Leu Ile Thr
        195                 200


<210> 2391
<211> 423
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 588; "
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<220>
<221> source
<223> /note="Gene Symbol: AP1M1; "

<220>
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<223> /note="Gene Name:
adaptor-related prt complex 1, mu 1
subunit; "

<220>
<221> source
<223> /note="Uniprot ID: Q9BXS5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000291439"

<400> 2391

```
Met Ser Ala Ser Ala Val Tyr Val Leu Asp Leu Lys Gly Lys Val Leu
1               5                  10                  15

Ile Cys Arg Asn Tyr Arg Gly Asp Val Asp Met Ser Glu Val Glu His
            20                  25                  30

Phe Met Pro Ile Leu Met Glu Lys Glu Glu Glu Gly Met Leu Ser Pro
        35                  40                  45

Ile Leu Ala His Gly Gly Val Arg Phe Met Trp Ile Lys His Asn Asn
    50                  55                  60

Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu Val
65                  70                  75                  80

Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe Lys
                85                  90                  95

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr Glu
            100                 105                 110

Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr Pro Gln Thr Thr Asp Ser
        115                 120                 125

Lys Ile Leu Gln Glu Tyr Ile Thr Gln Glu Gly His Lys Leu Glu Thr
    130                 135                 140

Gly Ala Pro Arg Pro Pro Ala Thr Val Thr Asn Ala Val Ser Trp Arg
145                 150                 155                 160
```

Ser Glu Gly Ile Lys Tyr Arg Lys Asn Glu Val Phe Leu Asp Val Ile
165 170 175

Glu Ser Val Asn Leu Leu Val Ser Ala Asn Gly Asn Val Leu Arg Ser
180 185 190

Glu Ile Val Gly Ser Ile Lys Met Arg Val Phe Leu Ser Gly Met Pro
195 200 205

Glu Leu Arg Leu Gly Leu Asn Asp Lys Val Leu Phe Asp Asn Thr Gly
210 215 220

Arg Gly Lys Ser Lys Ser Val Glu Leu Glu Asp Val Lys Phe His Gln
225 230 235 240

Cys Val Arg Leu Ser Arg Phe Glu Asn Asp Arg Thr Ile Ser Phe Ile
245 250 255

Pro Pro Asp Gly Glu Phe Glu Leu Met Ser Tyr Arg Leu Asn Thr His
260 265 270

Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys His Ser His
275 280 285

Ser Arg Ile Glu Tyr Met Ile Lys Ala Lys Ser Gln Phe Lys Arg Arg
290 295 300

Ser Thr Ala Asn Asn Val Glu Ile His Ile Pro Val Pro Asn Asp Ala
305 310 315 320

Asp Ser Pro Lys Phe Lys Thr Thr Val Gly Ser Val Lys Trp Val Pro
325 330 335

Glu Asn Ser Glu Ile Val Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys
340 345 350

Glu Tyr Leu Met Arg Ala His Phe Gly Leu Pro Ser Val Glu Ala Glu
355 360 365

Asp Lys Glu Gly Lys Pro Pro Ile Ser Val Lys Phe Glu Ile Pro Tyr
370 375 380

```
Phe Thr Thr Ser Gly Ile Gln Val Arg Tyr Leu Lys Ile Ile Glu Lys
385                 390                 395                 400


Ser Gly Tyr Gln Ala Leu Pro Trp Val Arg Tyr Ile Thr Gln Asn Gly
                405                 410                 415


Asp Tyr Gln Leu Arg Thr Gln
            420


<210> 2392
<211> 435
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 588; "

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<221> source
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<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="Uniprot ID:  Q9BXS5; "

<220>
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<223> /note="ENSP ID: ENSP00000388996"

<400> 2392
Met Ser Ala Ser Ala Val Tyr Val Leu Asp Leu Lys Gly Lys Val Leu
1               5                   10                  15


Ile Cys Arg Asn Tyr Arg Gly Asp Val Asp Met Ser Glu Val Glu His
            20                  25                  30


Phe Met Pro Ile Leu Met Glu Lys Glu Glu Glu Gly Met Leu Ser Pro
        35                  40                  45


Ile Leu Ala His Gly Gly Val Arg Phe Met Trp Ile Lys His Asn Asn
    50                  55                  60
```

```
Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu Val
65                  70                  75                  80

Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe Lys
                85                  90                  95

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr Glu
            100                 105                 110

Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr Pro Gln Thr Thr Asp Ser
        115                 120                 125

Lys Ile Leu Gln Glu Tyr Ile Thr Gln Glu Gly His Lys Leu Glu Thr
    130                 135                 140

Gly Ala Pro Arg Pro Pro Ala Thr Val Thr Asn Ala Val Ser Trp Arg
145                 150                 155                 160

Ser Glu Gly Ile Lys Tyr Arg Lys Asn Glu Val Phe Leu Asp Val Ile
                165                 170                 175

Glu Ser Val Asn Leu Leu Gly Lys Tyr Pro Gly Val Gly Trp Leu Gly
            180                 185                 190

His Thr Val Ser Ala Asn Gly Asn Val Leu Arg Ser Glu Ile Val Gly
        195                 200                 205

Ser Ile Lys Met Arg Val Phe Leu Ser Gly Met Pro Glu Leu Arg Leu
    210                 215                 220

Gly Leu Asn Asp Lys Val Leu Phe Asp Asn Thr Gly Arg Gly Lys Ser
225                 230                 235                 240

Lys Ser Val Glu Leu Glu Asp Val Lys Phe His Gln Cys Val Arg Leu
                245                 250                 255

Ser Arg Phe Glu Asn Asp Arg Thr Ile Ser Phe Ile Pro Pro Asp Gly
            260                 265                 270

Glu Phe Glu Leu Met Ser Tyr Arg Leu Asn Thr His Val Lys Pro Leu
        275                 280                 285

Ile Trp Ile Glu Ser Val Ile Glu Lys His Ser His Ser Arg Ile Glu
```

```
    290                 295                 300

Tyr Met Ile Lys Ala Lys Ser Gln Phe Lys Arg Arg Ser Thr Ala Asn
305                 310                 315                 320

Asn Val Glu Ile His Ile Pro Val Pro Asn Asp Ala Asp Ser Pro Lys
                325                 330                 335

Phe Lys Thr Thr Val Gly Ser Val Lys Trp Val Pro Glu Asn Ser Glu
            340                 345                 350

Ile Val Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys Glu Tyr Leu Met
        355                 360                 365

Arg Ala His Phe Gly Leu Pro Ser Val Glu Ala Glu Asp Lys Glu Gly
    370                 375                 380

Lys Pro Pro Ile Ser Val Lys Phe Glu Ile Pro Tyr Phe Thr Thr Ser
385                 390                 395                 400

Gly Ile Gln Val Arg Tyr Leu Lys Ile Ile Glu Lys Ser Gly Tyr Gln
                405                 410                 415

Ala Leu Pro Trp Val Arg Tyr Ile Thr Gln Asn Gly Asp Tyr Gln Leu
            420                 425                 430

Arg Thr Gln
        435


<210> 2393
<211> 370
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 588; "

<220>
<221> source
<223> /note="Gene Symbol: AP1M1; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000411498"

<400> 2393
Met Ser Ala Ser Ala Val Tyr Val Leu Asp Leu Lys Gly Lys Val Leu
1 5 10 15

Ile Cys Arg Asn Tyr Arg Gly Asp Val Asp Met Ser Glu Val Glu His
20 25 30

Phe Met Pro Ile Leu Met Glu Lys Glu Glu Glu Gly Met Leu Ser Pro
35 40 45

Ile Leu Ala His Gly Gly Val Arg Phe Met Trp Ile Lys His Asn Asn
50 55 60

Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu Val
65 70 75 80

Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe Lys
85 90 95

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr Glu
100 105 110

Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr Pro Gln Thr Thr Asp Ser
115 120 125

Lys Ile Leu Gln Glu Tyr Ile Thr Gln Glu Gly His Lys Leu Glu Thr
130 135 140

Gly Ala Pro Arg Pro Pro Ala Thr Val Thr Asn Ala Val Ser Trp Arg
145 150 155 160

Ser Glu Gly Ile Lys Tyr Arg Lys Asn Glu Val Phe Leu Asp Val Ile
165 170 175

Glu Ser Val Asn Leu Leu Val Ser Ala Asn Gly Asn Val Leu Arg Ser
180 185 190

Glu Ile Val Gly Ser Ile Lys Met Arg Val Phe Leu Ser Gly Met Pro
195 200 205

```
Glu Leu Arg Leu Gly Leu Asn Asp Lys Val Leu Phe Asp Asn Thr Gly
    210                 215                 220

Arg Gly Lys Ser Lys Ser Val Glu Leu Glu Asp Val Lys Phe His Gln
225                 230                 235                 240

Cys Val Arg Leu Ser Arg Phe Glu Asn Asp Arg Thr Ile Ser Phe Ile
                245                 250                 255

Pro Pro Asp Gly Glu Phe Glu Leu Met Ser Tyr Arg Leu Asn Thr His
            260                 265                 270

Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys His Ser His
        275                 280                 285

Ser Arg Ile Glu Tyr Met Ile Lys Gly Gly Lys Glu Tyr Leu Met Arg
    290                 295                 300

Ala His Phe Gly Leu Pro Ser Val Glu Ala Glu Asp Lys Glu Gly Lys
305                 310                 315                 320

Pro Pro Ile Ser Val Lys Phe Glu Ile Pro Tyr Phe Thr Thr Ser Gly
                325                 330                 335

Ile Gln Val Arg Tyr Leu Lys Ile Ile Glu Lys Ser Gly Tyr Gln Ala
            340                 345                 350

Leu Pro Trp Val Arg Tyr Ile Thr Gln Asn Gly Asp Tyr Gln Leu Arg
        355                 360                 365

Thr Gln
    370
```

<210> 2394
<211> 351
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 588; "

<220>
<221> source
<223> /note="Gene Symbol: AP1M1; "

<220>
<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465224"

<400> 2394
Met Ser Ala Ser Ala Val Tyr Val Leu Asp Leu Lys Gly Lys Val Leu
1 5 10 15

Arg Val Phe Ser Glu Tyr Phe Lys Glu Leu Glu Glu Glu Ser Ile Arg
20 25 30

Asp Asn Phe Val Ile Ile Tyr Glu Leu Leu Asp Glu Leu Met Asp Phe
35 40 45

Gly Tyr Pro Gln Thr Thr Asp Ser Lys Ile Leu Gln Glu Tyr Ile Thr
50 55 60

Gln Glu Gly His Lys Leu Glu Thr Gly Ala Pro Arg Pro Pro Ala Thr
65 70 75 80

Val Thr Asn Ala Val Ser Trp Arg Ser Glu Gly Ile Lys Tyr Arg Lys
85 90 95

Asn Glu Val Phe Leu Asp Val Ile Glu Ser Val Asn Leu Leu Val Ser
100 105 110

Ala Asn Gly Asn Val Leu Arg Ser Glu Ile Val Gly Ser Ile Lys Met
115 120 125

Arg Val Phe Leu Ser Gly Met Pro Glu Leu Arg Leu Gly Leu Asn Asp
130 135 140

Lys Val Leu Phe Asp Asn Thr Gly Arg Gly Lys Ser Lys Ser Val Glu
145 150 155 160

Leu Glu Asp Val Lys Phe His Gln Cys Val Arg Leu Ser Arg Phe Glu
165 170 175

Asn Asp Arg Thr Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe Glu Leu

```
            180                 185                 190

Met Ser Tyr Arg Leu Asn Thr His Val Lys Pro Leu Ile Trp Ile Glu
        195                 200                 205

Ser Val Ile Glu Lys His Ser His Ser Arg Ile Glu Tyr Met Ile Lys
    210                 215                 220

Ala Lys Ser Gln Phe Lys Arg Arg Ser Thr Ala Asn Asn Val Glu Ile
225                 230                 235                 240

His Ile Pro Val Pro Asn Asp Ala Asp Ser Pro Lys Phe Lys Thr Thr
                245                 250                 255

Val Gly Ser Val Lys Trp Val Pro Glu Asn Ser Glu Ile Val Trp Ser
            260                 265                 270

Ile Lys Ser Phe Pro Gly Gly Lys Glu Tyr Leu Met Arg Ala His Phe
        275                 280                 285

Gly Leu Pro Ser Val Glu Ala Glu Asp Lys Glu Gly Lys Pro Pro Ile
    290                 295                 300

Ser Val Lys Phe Glu Ile Pro Tyr Phe Thr Thr Ser Gly Ile Gln Val
305                 310                 315                 320

Arg Tyr Leu Lys Ile Ile Glu Lys Ser Gly Tyr Gln Ala Leu Pro Trp
                325                 330                 335

Val Arg Tyr Ile Thr Gln Asn Gly Asp Tyr Gln Leu Arg Thr Gln
            340                 345                 350


<210> 2395
<211> 136
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AP1M1; "

<220>
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<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466858"

<400> 2395
Met Ser Ala Ser Ala Val Tyr Val Leu Asp Leu Lys Gly Lys Val Leu
1 5 10 15

Ile Cys Arg Asn Tyr Arg Gly Asp Val Asp Met Ser Glu Val Glu His
20 25 30

Phe Met Pro Ile Leu Met Glu Lys Glu Glu Glu Gly Met Leu Ser Pro
35 40 45

Ile Leu Ala His Gly Gly Val Arg Phe Met Trp Ile Lys His Asn Asn
50 55 60

Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu Val
65 70 75 80

Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe Lys
85 90 95

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr Glu
100 105 110

Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr Pro Gln Thr Thr Asp Ser
115 120 125

Lys Ile Leu Gln Glu Tyr Ile Thr
130 135

<210> 2396
<211> 125
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source

<223> /note="Gene Symbol: AP1M1; "

<220>
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<223> /note="Gene Name:
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subunit; "

<220>
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<223> /note="ENSP ID: ENSP00000467417"

<400> 2396
Met Ser Glu Val Glu His Phe Met Pro Ile Leu Met Glu Lys Glu Glu
1 5 10 15

Glu Gly Met Leu Ser Pro Ile Leu Ala His Gly Gly Val Arg Phe Met
20 25 30

Trp Ile Lys His Asn Asn Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn
35 40 45

Ala Cys Val Ser Leu Val Phe Ser Phe Leu Tyr Lys Val Val Gln Val
50 55 60

Phe Ser Glu Tyr Phe Lys Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn
65 70 75 80

Phe Val Ile Ile Tyr Glu Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr
85 90 95

Pro Gln Thr Thr Asp Ser Lys Ile Leu Gln Glu Tyr Ile Thr Gln Glu
100 105 110

Gly His Lys Leu Glu Thr Gly Ala Pro Arg Pro Pro Ala
115 120 125

<210> 2397
<211> 64
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:
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subunit; "

<220>
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<223> /note="ENSP ID: ENSP00000467721"

<400> 2397
Met Ser Glu Val Glu His Phe Met Pro Ile Leu Met Glu Lys Glu Glu
1 5 10 15

Glu Gly Met Leu Ser Pro Ile Leu Ala His Gly Gly Val Arg Phe Met
20 25 30

Trp Ile Lys His Asn Asn Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn
35 40 45

Ala Cys Val Ser Leu Val Phe Ser Phe Leu Tyr Lys Val Val Gln Val
50 55 60

<210> 2398
<211> 176
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 2398
Xaa Ser Arg Phe Glu Asn Asp Arg Thr Ile Ser Phe Ile Pro Pro Asp
1 5 10 15

Gly Glu Phe Glu Leu Met Ser Tyr Arg Leu Asn Thr His Val Lys Pro
20 25 30

Leu Ile Trp Ile Glu Ser Val Ile Glu Lys His Ser His Ser Arg Ile
35 40 45

Glu Tyr Met Ile Lys Ala Lys Ser Gln Phe Lys Arg Arg Ser Thr Ala
50 55 60

Asn Asn Val Glu Ile His Ile Pro Val Pro Asn Asp Ala Asp Ser Pro
65 70 75 80

Lys Phe Lys Thr Thr Val Gly Ser Val Lys Trp Val Pro Glu Asn Ser
85 90 95

Glu Ile Val Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys Glu Tyr Leu
100 105 110

Met Arg Ala His Phe Gly Leu Pro Ser Val Glu Ala Glu Asp Lys Glu
115 120 125

Gly Lys Pro Pro Ile Ser Val Lys Phe Glu Ile Pro Tyr Phe Thr Thr
130 135 140

Ser Gly Ile Gln Met Leu Ser Leu Ser Gln Ile Ser Ile Asp Pro Pro
145 150 155 160

Gly Glu Val Gly Phe Gly Glu Arg Arg Gln Pro Gln Thr Phe Ser His
165 170 175

<210> 2399
<211> 105
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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subunit; "

<220>
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<400> 2399
Met Ser Glu Val Glu His Phe Met Pro Ile Leu Met Glu Lys Glu Glu
1 5 10 15

Glu Gly Met Leu Ser Pro Ile Leu Ala His Gly Gly Val Arg Phe Met
20 25 30

Trp Ile Lys His Asn Asn Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn
35 40 45

Ala Cys Val Ser Leu Val Phe Ser Phe Leu Tyr Lys Val Val Gln Val
50 55 60

Phe Ser Glu Tyr Phe Lys Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn
65 70 75 80

Phe Val Ile Ile Tyr Glu Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr
85 90 95

Pro Gln Thr Thr Asp Ser Lys Ile Leu
100 105

<210> 2400
<211> 128
<212> PRT
<213> Homo sapiens

<220>
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<220>
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subunit; "

<220>
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<400> 2400
Asn Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu
1   5   10   15

Val Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe
            20   25   30

Lys Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr
        35   40   45

Glu Leu Leu Asp Glu Leu Met Asp Phe Gly Tyr Pro Gln Thr Thr Asp
    50   55   60

Ser Lys Ile Leu Gln Glu Tyr Ile Thr Gln Glu Gly His Lys Leu Glu
65   70   75   80

Thr Gly Ala Pro Arg Pro Pro Ala Thr Val Thr Asn Ala Val Ser Trp
                85   90   95

Arg Ser Glu Gly Ile Lys Tyr Arg Lys Asn Glu Val Phe Leu Asp Val
            100   105   110

Ile Glu Ser Val Asn Leu Leu Val Gly Leu Phe Ser Phe Leu Leu Leu
        115   120   125

<210> 2401
<211> 423
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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subunit; "

<220>
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<223> /note="Uniprot ID: Q9Y6Q5; "

<220>
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<223> /note="ENSP ID: ENSP00000250244"

<400> 2401
Met Ser Ala Ser Ala Val Phe Ile Leu Asp Val Lys Gly Lys Pro Leu
1   5   10   15

Ile Ser Arg Asn Tyr Lys Gly Asp Val Ala Met Ser Lys Ile Glu His
            20   25   30

Phe Met Pro Leu Leu Val Gln Arg Glu Glu Glu Gly Ala Leu Ala Pro
        35   40   45

Leu Leu Ser His Gly Gln Val His Phe Leu Trp Ile Lys His Ser Asn
    50   55   60

Leu Tyr Leu Val Ala Thr Thr Ser Lys Asn Ala Asn Ala Ser Leu Val
65   70   75   80

Tyr Ser Phe Leu Tyr Lys Thr Ile Glu Val Phe Cys Glu Tyr Phe Lys
                85   90   95

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Val Tyr Glu
            100   105   110

Leu Leu Asp Glu Leu Met Asp Phe Gly Phe Pro Gln Thr Thr Asp Ser
        115   120   125

Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln Ser Asn Lys Leu Glu Thr
    130   135   140

Gly Lys Ser Arg Val Pro Pro Thr Val Thr Asn Ala Val Ser Trp Arg
145   150   155   160

Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu Val Phe Ile Asp Val Ile
                165   170   175

Glu Ser Val Asn Leu Leu Val Asn Ala Asn Gly Ser Val Leu Leu Ser
            180   185   190

```
Glu Ile Val Gly Thr Ile Lys Leu Lys Val Phe Leu Ser Gly Met Pro
        195                 200                 205

Glu Leu Arg Leu Gly Leu Asn Asp Arg Val Leu Phe Glu Leu Thr Gly
    210                 215                 220

Arg Ser Lys Asn Lys Ser Val Glu Leu Glu Asp Val Lys Phe His Gln
225                 230                 235                 240

Cys Val Arg Leu Ser Arg Phe Asp Asn Asp Arg Thr Ile Ser Phe Ile
                245                 250                 255

Pro Pro Asp Gly Asp Phe Glu Leu Met Ser Tyr Arg Leu Ser Thr Gln
            260                 265                 270

Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys Phe Ser His
        275                 280                 285

Ser Arg Val Glu Ile Met Val Lys Ala Lys Gly Gln Phe Lys Lys Gln
    290                 295                 300

Ser Val Ala Asn Gly Val Glu Ile Ser Val Pro Val Pro Ser Asp Ala
305                 310                 315                 320

Asp Ser Pro Arg Phe Lys Thr Ser Val Gly Ser Ala Lys Tyr Val Pro
                325                 330                 335

Glu Arg Asn Val Val Ile Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys
            340                 345                 350

Glu Tyr Leu Met Arg Ala His Phe Gly Leu Pro Ser Val Glu Lys Glu
        355                 360                 365

Glu Val Glu Gly Arg Pro Pro Ile Gly Val Lys Phe Glu Ile Pro Tyr
    370                 375                 380

Phe Thr Val Ser Gly Ile Gln Val Arg Tyr Met Lys Ile Ile Glu Lys
385                 390                 395                 400

Ser Gly Tyr Gln Ala Leu Pro Trp Val Arg Tyr Ile Thr Gln Ser Gly
                405                 410                 415
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Asp Tyr Gln Leu Arg Thr Ser
420

<210> 2402
<211> 245
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AP1M2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1, mu 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465193"

<400> 2402
Ala Val Phe Ile Leu Asp Val Lys Gly Lys Val Phe Cys Glu Tyr Phe
1 5 10 15

Lys Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Val Tyr
20 25 30

Glu Leu Leu Asp Glu Leu Met Asp Phe Gly Phe Pro Gln Thr Thr Asp
35 40 45

Ser Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln Ser Asn Lys Leu Glu
50 55 60

Thr Gly Lys Ser Arg Val Pro Pro Thr Val Thr Asn Ala Val Ser Trp
65 70 75 80

Arg Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu Val Phe Ile Asp Val
85 90 95

Ile Glu Ser Val Asn Leu Leu Val Asn Ala Asn Gly Ser Val Leu Leu
100 105 110

Ser Glu Ile Val Gly Thr Ile Lys Leu Lys Val Phe Leu Ser Gly Met

```
        115                 120                 125

Pro Glu Leu Arg Leu Gly Leu Asn Asp Arg Val Leu Phe Glu Leu Thr
    130                 135                 140

Gly Arg Ser Lys Asn Lys Ser Val Glu Leu Glu Asp Val Lys Phe His
145                 150                 155                 160

Gln Cys Val Arg Leu Ser Arg Phe Asp Asn Asp Arg Thr Ile Ser Phe
                165                 170                 175

Ile Pro Pro Asp Gly Asp Phe Glu Leu Met Ser Tyr Arg Leu Ser Thr
            180                 185                 190

Gln Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys Phe Ser
        195                 200                 205

His Ser Arg Val Glu Ile Met Val Lys Ala Lys Gly Gln Phe Lys Lys
    210                 215                 220

Gln Ser Val Ala Asn Gly Val Glu Ile Ser Val Pro Val Pro Ser Asp
225                 230                 235                 240

Ala Asp Ser Pro Arg
                245


<210> 2403
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 589; "

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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000465488"
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<220>
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<223> Any amino acid

<400> 2403
Xaa Asn Val Val Ile Trp Ser Ile Lys Ser Phe Pro Val Arg Tyr Met
1   5   10   15

Lys Ile Ile Glu Lys Ser Gly Tyr Gln Ala Leu Pro Trp Val Arg Tyr
            20   25   30

Ile Thr Gln Ser Gly Asp Tyr Gln Leu Arg Thr Ser
        35   40

<210> 2404
<211> 425
<212> PRT
<213> Homo sapiens

<220>
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<221> source
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<220>
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<220>
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<223> /note="Uniprot ID: Q9Y6Q5; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465685"

<400> 2404
Met Ser Ala Ser Ala Val Phe Ile Leu Asp Val Lys Gly Lys Pro Leu
1   5   10   15

Ile Ser Arg Asn Tyr Lys Gly Asp Val Ala Met Ser Lys Ile Glu His
            20   25   30

Phe Met Pro Leu Leu Val Gln Arg Glu Glu Glu Gly Ala Leu Ala Pro

```
        35                  40                  45

Leu Leu Ser His Gly Gln Val His Phe Leu Trp Ile Lys His Ser Asn
    50                  55                  60

Leu Tyr Leu Val Ala Thr Thr Ser Lys Asn Ala Asn Ala Ser Leu Val
65                  70                  75                  80

Tyr Ser Phe Leu Tyr Lys Thr Ile Glu Val Phe Cys Glu Tyr Phe Lys
                85                  90                  95

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Val Tyr Glu
            100                 105                 110

Leu Leu Asp Glu Leu Met Asp Phe Gly Phe Pro Gln Thr Thr Asp Ser
        115                 120                 125

Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln Ser Asn Lys Leu Glu Thr
    130                 135                 140

Gly Lys Ser Arg Val Pro Pro Thr Val Thr Asn Ala Val Ser Trp Arg
145                 150                 155                 160

Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu Val Phe Ile Asp Val Ile
                165                 170                 175

Glu Ser Val Asn Leu Leu Val Asn Ala Asn Gly Ser Val Leu Leu Ser
            180                 185                 190

Glu Ile Val Gly Thr Ile Lys Leu Lys Val Phe Leu Ser Gly Met Pro
        195                 200                 205

Glu Leu Arg Leu Gly Leu Asn Asp Arg Val Leu Phe Glu Leu Thr Gly
    210                 215                 220

Leu Ser Gly Ser Lys Asn Lys Ser Val Glu Leu Glu Asp Val Lys Phe
225                 230                 235                 240

His Gln Cys Val Arg Leu Ser Arg Phe Asp Asn Asp Arg Thr Ile Ser
                245                 250                 255

Phe Ile Pro Pro Asp Gly Asp Phe Glu Leu Met Ser Tyr Arg Leu Ser
            260                 265                 270
```

```
Thr Gln Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys Phe
        275                 280                 285

Ser His Ser Arg Val Glu Ile Met Val Lys Ala Lys Gly Gln Phe Lys
    290                 295                 300

Lys Gln Ser Val Ala Asn Gly Val Glu Ile Ser Val Pro Val Pro Ser
305                 310                 315                 320

Asp Ala Asp Ser Pro Arg Phe Lys Thr Ser Val Gly Ser Ala Lys Tyr
                325                 330                 335

Val Pro Glu Arg Asn Val Val Ile Trp Ser Ile Lys Ser Phe Pro Gly
            340                 345                 350

Gly Lys Glu Tyr Leu Met Arg Ala His Phe Gly Leu Pro Ser Val Glu
        355                 360                 365

Lys Glu Glu Val Glu Gly Arg Pro Pro Ile Gly Val Lys Phe Glu Ile
    370                 375                 380

Pro Tyr Phe Thr Val Ser Gly Ile Gln Val Arg Tyr Met Lys Ile Ile
385                 390                 395                 400

Glu Lys Ser Gly Tyr Gln Ala Leu Pro Trp Val Arg Tyr Ile Thr Gln
                405                 410                 415

Ser Gly Asp Tyr Gln Leu Arg Thr Ser
            420                 425


<210> 2405
<211> 128
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 589; "

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<223> /note="Gene Symbol: AP1M2; "

<220>
<221> source
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<223> /note="Gene Name:
adaptor-related prt complex 1, mu 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465865"

<400> 2405
Glu Ile Ser Val Pro Val Pro Ser Asp Ala Asp Ser Pro Arg Phe Lys
1 5 10 15

Thr Ser Val Gly Ser Ala Lys Tyr Val Pro Glu Arg Asn Val Val Ile
20 25 30

Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys Glu Tyr Leu Met Arg Ala
35 40 45

His Phe Gly Leu Pro Ser Val Glu Lys Glu Glu Val Glu Gly Arg Pro
50 55 60

Pro Ile Gly Val Lys Phe Glu Ile Pro Tyr Phe Thr Val Ser Gly Ile
65 70 75 80

Gln Val Arg Tyr Met Lys Ile Ile Glu Lys Ser Gly Tyr Gln Ala Leu
85 90 95

Pro Trp Val Arg Tyr Ile Thr Gln Ser Gly Gly Trp Glu Arg Asn Ser
100 105 110

Leu Cys Phe Pro Arg Pro Trp Ser Phe Pro His Pro Pro Asp Phe Ile
115 120 125

<210> 2406
<211> 299
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 589; "

<220>
<221> source
<223> /note="Gene Symbol: AP1M2; "

<220>
<221> source
<223> /note="Gene Name:

adaptor-related prt complex 1, mu 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466494"

<400> 2406

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Met Ser Ala Ser Ala Val Phe Ile Leu Asp Val Lys Gly Lys Pro Leu
1               5                  10                  15

Ile Ser Arg Asn Tyr Lys Gly Asp Val Ala Met Ser Lys Ile Glu His
            20                  25                  30

Phe Met Pro Leu Leu Val Gln Arg Glu Glu Glu Gly Ala Leu Ala Pro
        35                  40                  45

Leu Leu Ser His Gly Gln Val His Phe Leu Trp Ile Lys His Ser Asn
    50                  55                  60

Leu Tyr Cys Ile His Pro Thr Trp Cys Pro Trp Arg Trp Val Trp Gly
65                  70                  75                  80

Leu Ser Ala Met Val Ala Ala Gln Ala Lys Arg Gly Trp Ala Glu Asp
                85                  90                  95

Arg Ser Cys Thr Ala His Leu Cys Gly Leu Gly Trp Gly Ala Gly Ala
            100                 105                 110

Gly Arg Asp Glu Gly Gly Gly Lys Gly Gln Gly Gly Gly Ser Gly Ser
        115                 120                 125

Val Phe His Leu Leu Leu His Lys Trp His Leu Phe Leu Asn Leu Ala
    130                 135                 140

Ala Pro Val Val Ala Thr Thr Ser Lys Asn Ala Asn Ala Ser Leu Val
145                 150                 155                 160

Tyr Ser Phe Leu Tyr Lys Thr Ile Glu Val Phe Cys Glu Tyr Phe Lys
                165                 170                 175

Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Val Tyr Glu
            180                 185                 190

Leu Leu Asp Glu Leu Met Asp Phe Gly Phe Pro Gln Thr Thr Asp Ser
```

```
        195                 200                 205

Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln Ser Asn Lys Leu Glu Thr
    210                 215                 220

Gly Lys Ser Arg Val Pro Pro Thr Val Thr Asn Ala Val Ser Trp Arg
225                 230                 235                 240

Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu Val Phe Ile Asp Val Ile
                245                 250                 255

Glu Ser Val Asn Leu Leu Val Asn Ala Asn Gly Ser Val Leu Leu Ser
            260                 265                 270

Glu Ile Val Gly Thr Ile Lys Leu Lys Val Phe Leu Ser Gly Met Pro
        275                 280                 285

Glu Leu Arg Leu Gly Leu Asn Asp Arg Val Leu
    290                 295


<210> 2407
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 589; "

<220>
<221> source
<223> /note="Gene Symbol: AP1M2; "

<220>
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      adaptor-related prt complex 1, mu 2
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467406"

<400> 2407
Met Ser Ala Ser Ala Val Phe Ile Leu Asp Val Lys Gly Lys Arg Asp
1               5                   10                  15

Pro Ala Met Leu Pro Lys Leu Val Ser Asn Ser Trp Pro Gln Gly Ile
            20                  25                  30
```

Leu Leu Pro Trp Ser Ser
35

<210> 2408
<211> 239
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AP1M2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 1, mu 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467498"

<400> 2408
Met Ser Lys Ile Glu His Phe Met Pro Leu Leu Val Gln Arg Glu Glu
1 5 10 15

Glu Gly Ala Leu Ala Pro Leu Leu Ser His Gly Gln Val His Phe Leu
20 25 30

Trp Ile Lys His Ser Asn Leu Tyr Leu Val Ala Thr Thr Ser Lys Asn
35 40 45

Ala Asn Ala Ser Leu Val Tyr Ser Phe Leu Tyr Lys Thr Ile Glu Val
50 55 60

Phe Cys Glu Tyr Phe Lys Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn
65 70 75 80

Phe Val Ile Val Tyr Glu Leu Leu Asp Glu Leu Met Asp Phe Gly Phe
85 90 95

Pro Gln Thr Thr Asp Ser Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln
100 105 110

```
Ser Asn Lys Leu Glu Thr Gly Lys Ser Arg Val Pro Pro Thr Val Thr
        115                 120                 125

Asn Ala Val Ser Trp Arg Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu
    130                 135                 140

Val Phe Ile Asp Val Ile Glu Ser Val Asn Leu Leu Val Asn Ala Asn
145                 150                 155                 160

Gly Ser Val Leu Leu Ser Glu Ile Val Gly Thr Ile Lys Leu Lys Val
                165                 170                 175

Phe Leu Ser Gly Met Pro Glu Leu Arg Leu Gly Leu Asn Asp Arg Val
            180                 185                 190

Leu Phe Glu Leu Thr Gly Arg Ser Lys Asn Lys Ser Val Glu Leu Glu
        195                 200                 205

Asp Val Lys Phe His Gln Cys Val Arg Leu Ser Arg Phe Asp Asn Asp
    210                 215                 220

Arg Thr Ile Ser Phe Ile Pro Pro Asp Gly Asp Phe Glu Leu Met
225                 230                 235


<210> 2409
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 589; "

<220>
<221> source
<223> /note="Gene Symbol: AP1M2; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468260"

<400> 2409
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Phe Lys Thr Ser Val Gly Ser Ala Lys Tyr Val Pro Glu Arg Asn Val
1               5                   10                  15

Val Ile Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys Glu Tyr Leu Met
            20                  25                  30

Arg Ala His Phe Gly Leu Pro Ser Val Glu Lys Glu Glu Val Glu Gly
        35                  40                  45

Arg Pro Pro Ile Gly Val Lys Phe Glu Ile Pro Tyr Phe Thr Val Ser
    50                  55                  60

Gly Ile Gln Val Arg Tyr Met Lys Ile Ile Glu Lys Ser Gly Tyr Gln
65                  70                  75                  80

Ala Leu Pro Trp Val Arg Tyr Ile Thr Gln Ser Gly Gly Lys Ala Ala
                85                  90                  95

Gln Leu Leu Gly Thr Met Gly
            100


<210> 2410
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 590; "

<220>
<221> source
<223> /note="Gene Symbol: AP1S1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 1, sigma 1
      subunit; "

<220>
<221> source
<223> /note="Uniprot ID:  P61966; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000336666"

<400> 2410
Met Met Arg Phe Met Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
```

```
1               5                   10                  15

Gln Lys Trp Tyr Leu Ala Thr Ser Asp Lys Glu Arg Lys Lys Met Val
            20                  25                  30

Arg Glu Leu Met Gln Val Val Leu Ala Arg Lys Pro Lys Met Cys Ser
        35                  40                  45

Phe Leu Glu Trp Arg Asp Leu Lys Val Val Tyr Lys Arg Tyr Ala Ser
    50                  55                  60

Leu Tyr Phe Cys Cys Ala Ile Glu Gly Gln Asp Asn Glu Leu Ile Thr
65                  70                  75                  80

Leu Glu Leu Ile His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
                85                  90                  95

Ser Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe
            100                 105                 110

Ile Leu Asp Glu Phe Leu Met Gly Gly Asp Val Gln Asp Thr Ser Lys
        115                 120                 125

Lys Ser Val Leu Lys Ala Ile Glu Gln Ala Asp Leu Leu Gln Glu Glu
    130                 135                 140

Asp Glu Ser Pro Arg Ser Val Leu Glu Glu Met Gly Leu Ala
145                 150                 155


<210> 2411
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 590; "

<220>
<221> source
<223> /note="Gene Symbol: AP1S1; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000399902"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2411
Xaa Ala Lys Arg Glu Gly Arg Gly Lys Arg Gly Ala Trp Ala Ala Pro
1 5 10 15

Ala Gly Val Leu Gly Gly Arg Pro Arg Gly Glu Pro Pro Cys Leu Pro
20 25 30

Ser Gly Pro Gln Arg Pro Pro Leu Pro Arg Arg Met Arg Phe Met Leu
35 40 45

Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu Gln Lys Trp Tyr Leu Ala
50 55 60

Thr Ser Asp Lys Glu Arg Lys Lys Met Val Arg Glu Leu Met Gln Val
65 70 75 80

Val Leu Ala Arg Lys Pro Lys Met Cys Ser Phe Leu Glu Trp Arg Asp
85 90 95

Leu Lys Val Val Tyr Lys Arg Tyr Ala Ser Leu Tyr Phe Cys Cys Ala
100 105 110

Ile Glu Gly Gln Asp Asn Glu Leu Ile Thr Leu Glu Leu Ile His Arg
115 120 125

Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly Ser Val Cys Glu Leu Asp
130 135 140

Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe Ile Leu Asp Glu Phe Leu
145 150 155 160

Met Gly Gly Asp Val Gln Asp Thr Ser Lys Lys Ser Val Leu Lys Ala
165 170 175

Ile Glu Gln Ala Asp Leu Leu Gln Glu Glu Asp Glu Ser Pro Arg

180 185 190

<210> 2412
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 590; "

<220>
<221> source
<223> /note="Gene Symbol: AP1S1; "

<220>
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<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="Uniprot ID: P61966; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000410780"

<400> 2412
Met Met Arg Phe Met Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1 5 10 15

Gln Lys Trp Tyr Leu Ala Thr Ser Asp Lys Glu Arg Lys Lys Met Val
20 25 30

Arg Glu Leu Met Gln Val Val Leu Ala Arg Lys Pro Lys Met Cys Ser
35 40 45

Phe Leu Glu Trp Arg Asp Leu Lys Val Val Tyr Lys Arg Tyr Ala Ser
50 55 60

Leu Tyr Phe Cys Cys Ala Ile Glu Gly Gln Asp Asn Glu Leu Ile Thr
65 70 75 80

Leu Glu Leu Ile His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
85 90 95

Ser Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe
100 105 110

Ile Leu Asp Glu Phe Leu Met Gly Gly Asp Val Gln Asp Thr Ser Lys
        115   120   125

Lys Ser Val Leu Lys Ala Ile Glu Gln Ala Asp Leu Leu Gln Glu Glu
    130   135   140

Asp Glu Ser Pro Arg Ser Val Leu Glu Glu Met Gly Leu Ala
145   150   155

<210> 2413
<211> 157
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<213> Homo sapiens

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<223> /note="Uniprot ID: P56377; "

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<400> 2413
Met Gln Phe Met Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu Gln
1   5   10   15

Lys Trp Tyr Val Pro Leu Ser Asp Lys Glu Lys Lys Lys Ile Thr Arg
            20   25   30

Glu Leu Val Gln Thr Val Leu Ala Arg Lys Pro Lys Met Cys Ser Phe
        35   40   45

Leu Glu Trp Arg Asp Leu Lys Ile Val Tyr Lys Arg Tyr Ala Ser Leu
    50   55   60

```
Tyr Phe Cys Cys Ala Ile Glu Asp Gln Asp Asn Glu Leu Ile Thr Leu
65                  70                  75                  80


Glu Ile Ile His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly Ser
                85                  90                  95


Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe Ile
            100                 105                 110


Leu Asp Glu Phe Leu Leu Gly Gly Glu Val Gln Glu Thr Ser Lys Lys
        115                 120                 125


Asn Val Leu Lys Ala Ile Glu Gln Ala Asp Leu Leu Gln Glu Glu Ala
    130                 135                 140


Glu Thr Pro Arg Ser Val Leu Glu Glu Ile Gly Leu Thr
145                 150                 155


<210> 2414
<211> 160
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<400> 2414
Met Gln Phe Met Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu Gln
1               5                   10                  15


Lys Trp Tyr Val Pro Leu Ser Asp Lys Glu Lys Lys Lys Ile Thr Arg
            20                  25                  30
```

```
Glu Leu Val Gln Thr Val Leu Ala Arg Lys Pro Lys Met Cys Ser Phe
        35                  40                  45

Leu Glu Trp Arg Asp Leu Lys Ile Val Tyr Lys Arg Tyr Ala Ser Leu
    50                  55                  60

Tyr Phe Cys Cys Ala Ile Glu Asp Gln Asp Asn Glu Leu Ile Thr Leu
65                  70                  75                  80

Glu Ile Ile His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly Ser
                85                  90                  95

Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe Ile
            100                 105                 110

Leu Asp Glu Phe Leu Leu Gly Gly Glu Val Gln Glu Thr Ser Lys Lys
        115                 120                 125

Asn Val Leu Lys Ala Ile Glu Gln Ala Asp Leu Leu Gln Glu Lys Thr
    130                 135                 140

Glu Thr Met Tyr His Ser Lys Ser Phe Ile Gly Phe Lys Lys Ala Tyr
145                 150                 155                 160
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<210> 2415
<211> 146
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<213> Homo sapiens

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<220>

<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2415
Xaa Arg Gln Gly Lys Leu Arg Leu Gln Lys Trp Tyr Val Pro Leu Ser
1 5 10 15

Asp Lys Glu Lys Lys Lys Ile Thr Arg Glu Leu Val Gln Thr Val Leu
20 25 30

Ala Arg Lys Pro Lys Met Cys Ser Phe Leu Glu Trp Arg Asp Leu Lys
35 40 45

Ile Val Tyr Lys Arg Tyr Ala Ser Leu Tyr Phe Cys Cys Ala Ile Glu
50 55 60

Asp Gln Asp Asn Glu Leu Ile Thr Leu Glu Ile Ile His Arg Tyr Val
65 70 75 80

Glu Leu Leu Asp Lys Tyr Phe Gly Ser Val Cys Glu Leu Asp Ile Ile
85 90 95

Phe Asn Phe Glu Lys Ala Tyr Phe Ile Leu Asp Glu Phe Leu Leu Gly
100 105 110

Gly Glu Val Gln Glu Thr Ser Lys Lys Asn Val Leu Lys Ala Ile Glu
115 120 125

Gln Ala Asp Leu Leu Gln Glu Pro Arg His Glu Tyr Phe Asn Val Pro
130 135 140

Val Tyr
145

<210> 2416
<211> 153
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 2416
Xaa Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu Gln Lys Trp Tyr
1 5 10 15

Val Pro Leu Ser Asp Lys Glu Lys Lys Lys Ile Thr Arg Glu Leu Val
20 25 30

Gln Thr Val Leu Ala Arg Lys Pro Lys Met Cys Ser Phe Leu Glu Trp
35 40 45

Arg Asp Leu Lys Ile Val Tyr Lys Arg Tyr Ala Ser Leu Tyr Phe Cys
50 55 60

Cys Ala Ile Glu Asp Gln Asp Asn Glu Leu Ile Thr Leu Glu Ile Ile
65 70 75 80

His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly Ser Val Cys Glu
85 90 95

Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe Ile Leu Asp Glu
100 105 110

Phe Leu Leu Gly Gly Glu Val Gln Glu Thr Ser Lys Lys Asn Val Leu
115 120 125

Lys Ala Ile Glu Gln Ala Asp Leu Leu Gln Glu Ser Gln Asn Glu Glu
130 135 140

Trp Gly Gly Leu Ser Glu Asp Ile Leu
145 150

<210> 2417
<211> 160
<212> PRT
<213> Homo sapiens

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<220>
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<223> /note="ENSP ID: ENSP00000444957"

<400> 2417
Met Gln Phe Met Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu Gln
1 5 10 15

Lys Trp Tyr Val Pro Leu Ser Asp Lys Glu Lys Lys Lys Ile Thr Arg
20 25 30

Glu Leu Val Gln Thr Val Leu Ala Arg Lys Pro Lys Met Cys Ser Phe
35 40 45

Leu Glu Trp Arg Asp Leu Lys Ile Val Tyr Lys Arg Tyr Ala Ser Leu
50 55 60

Tyr Phe Cys Cys Ala Ile Glu Asp Gln Asp Asn Glu Leu Ile Thr Leu
65 70 75 80

Glu Ile Ile His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly Ser
85 90 95

Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe Ile
100 105 110

Leu Asp Glu Phe Leu Leu Gly Gly Glu Val Gln Glu Thr Ser Lys Lys
115 120 125

Asn Val Leu Lys Ala Ile Glu Gln Ala Asp Leu Leu Gln Glu Asp Ala
130 135 140

Lys Glu Ala Glu Thr Pro Arg Ser Val Leu Glu Glu Ile Gly Leu Thr
145 150 155 160

<210> 2418
<211> 81
<212> PRT
<213> Homo sapiens

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<223> /note="ENSP ID: ENSP00000333888"

<400> 2418
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1 5 10 15

Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
20 25 30

Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
35 40 45

Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Ser Val Ser
50 55 60

Trp Ile Leu Ser Leu Ile Leu Lys Arg Leu Ile Ser Ser Trp Thr Ser
65 70 75 80

Leu

<210> 2419

<211> 63
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000379890"

<400> 2419
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1 5 10 15

Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
20 25 30

Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
35 40 45

Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Cys Leu
50 55 60

<210> 2420
<211> 154
<212> PRT
<213> Homo sapiens

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<220>
<221> source
<223> /note="Uniprot ID: Q96PC3; "

<220>
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<223> /note="ENSP ID: ENSP00000379891"

<400> 2420
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1   5   10   15

Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
            20   25   30

Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
        35   40   45

Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Tyr Ala Ser
    50   55   60

Leu Tyr Phe Cys Cys Ala Ile Glu Asn Gln Asp Asn Glu Leu Leu Thr
65   70   75   80

Leu Glu Ile Val His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
                85   90   95

Asn Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe
            100   105   110

Ile Leu Asp Glu Phe Ile Ile Gly Gly Glu Ile Gln Glu Thr Ser Lys
        115   120   125

Lys Ile Ala Val Lys Ala Ile Glu Asp Ser Asp Met Leu Gln Glu Thr
    130   135   140

Met Glu Glu Tyr Met Asn Lys Pro Thr Phe
145   150

<210> 2421
<211> 137
<212> PRT
<213> Homo sapiens

<220>
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<400> 2421
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1 5 10 15

Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
20 25 30

Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
35 40 45

Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Tyr Ala Ser
50 55 60

Leu Tyr Phe Cys Cys Ala Ile Glu Asn Gln Asp Asn Glu Leu Leu Thr
65 70 75 80

Leu Glu Ile Val His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
85 90 95

Asn Glu Phe Asn Cys Trp Phe Leu Leu Met Arg Leu Leu Ser Val Leu
100 105 110

Asp Ser Trp Ser Thr Pro Ala Leu Asn Ser Glu Val Pro Gln Leu Ala
115 120 125

Thr Ile Thr Pro Asp Phe Cys Leu Phe
130 135

<210> 2422
<211> 154
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000388738"

<400> 2422
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1   5   10   15

Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
            20   25   30

Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
        35   40   45

Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Tyr Ala Ser
    50   55   60

Leu Tyr Phe Cys Cys Ala Ile Glu Asn Gln Asp Asn Glu Leu Leu Thr
65   70   75   80

Leu Glu Ile Val His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
                85   90   95

Asn Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe
            100   105   110

Ile Leu Asp Glu Phe Ile Ile Gly Gly Glu Ile Gln Glu Thr Ser Lys
        115   120   125

Lys Ile Ala Val Lys Ala Ile Glu Asp Ser Asp Met Leu Gln Glu Val

130 135 140

Ser Thr Val Ser Gln Thr Met Gly Glu Arg
145 150

<210> 2423
<211> 164
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Uniprot ID: Q96PC3; "

<220>
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<400> 2423
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1 5 10 15

Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
20 25 30

Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
35 40 45

Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Tyr Ala Ser
50 55 60

Leu Tyr Phe Cys Cys Ala Ile Glu Asn Gln Asp Asn Glu Leu Leu Thr
65 70 75 80

Leu Glu Ile Val His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
85 90 95

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Asn Val Cys Glu Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe
            100                 105                 110

Ile Leu Asp Glu Phe Ile Ile Gly Gly Glu Ile Gln Glu Thr Ser Lys
        115                 120                 125

Lys Ile Ala Val Lys Ala Ile Glu Asp Ser Asp Met Leu Gln Glu Asn
    130                 135                 140

Arg Leu Ser Pro Arg Gly Arg Asp Cys Ser Glu Pro Arg Ser Cys His
145                 150                 155                 160

Cys Thr Leu Ala
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<210> 2424
<211> 56
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<220>
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<220>
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<400> 2424

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Met Ile Ser Phe Leu Asp Glu Glu Arg Leu Gly Gly Gly Gly Gly Asp
1               5                   10                  15

Cys Ile Phe Val Gly Lys Thr Val Ser Arg Leu Leu Asn Val Cys Glu
            20                  25                  30

Leu Asp Ile Ile Phe Asn Phe Glu Lys Ala Tyr Phe Ile Leu Asp Glu
        35                  40                  45
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Phe Ile Ile Gly Gly Glu Ile Gln
    50                  55


<210> 2425
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<212> PRT
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<220>
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000401705"

<400> 2425
Met Ile His Phe Ile Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
1               5                   10                  15


Gln Lys Trp Tyr Ile Thr Leu Pro Asp Lys Glu Arg Lys Lys Ile Thr
            20                  25                  30


Arg Glu Ile Val Gln Ile Ile Leu Ser Arg Gly His Arg Thr Ser Ser
        35                  40                  45


Phe Val Asp Trp Lys Glu Leu Lys Leu Val Tyr Lys Arg Tyr Ala Ser
    50                  55                  60


Leu Tyr Phe Cys Cys Ala Ile Glu Asn Gln Asp Asn Glu Leu Leu Thr
65                  70                  75                  80


Leu Glu Ile Val His Arg Tyr Val Glu Leu Leu Asp Lys Tyr Phe Gly
                85                  90                  95
```

Asn Thr Trp Pro Phe Ala Arg Ala
100

<210> 2426
<211> 955
<212> PRT
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<220>
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<400> 2426
Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1 5 10 15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg
20 25 30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
35 40 45

Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe
50 55 60

Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala Val
65 70 75 80

Asn Leu Leu Ser Ser Asn Lys Tyr Thr Glu Lys Gln Ile Gly Tyr Leu
85 90 95

Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile

```
            100                 105                 110

Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe Met
        115                 120                 125

Cys Leu Ala Leu His Cys Ile Ala Asn Val Gly Ser Arg Glu Met Gly
    130                 135                 140

Glu Ala Phe Ala Ala Asp Ile Pro Arg Ile Leu Val Ala Gly Asp Ser
145                 150                 155                 160

Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
                165                 170                 175

Lys Ala Ser Pro Asp Leu Val Pro Met Gly Glu Trp Thr Ala Arg Val
            180                 185                 190

Val His Leu Leu Asn Asp Gln His Met Gly Val Val Thr Ala Ala Val
        195                 200                 205

Ser Leu Ile Thr Cys Leu Cys Lys Lys Asn Pro Asp Asp Phe Lys Thr
    210                 215                 220

Cys Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Ser Ser Ala
225                 230                 235                 240

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                245                 250                 255

Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Glu
            260                 265                 270

Asp Ala Ala Val Lys Gly Arg Leu Val Glu Cys Leu Glu Thr Val Leu
        275                 280                 285

Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn
    290                 295                 300

Ala Lys Asn Ala Ile Leu Phe Glu Thr Ile Ser Leu Ile Ile His Tyr
305                 310                 315                 320

Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln
                325                 330                 335
```

```
Phe Leu Gln His Arg Glu Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser
            340                 345                 350

Met Cys Thr Leu Ala Ser Ser Glu Phe Ser His Glu Ala Val Lys Thr
        355                 360                 365

His Ile Asp Thr Val Ile Asn Ala Leu Lys Thr Glu Arg Asp Val Ser
    370                 375                 380

Val Arg Gln Arg Ala Ala Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser
385                 390                 395                 400

Asn Ala Lys Gln Ile Val Ser Glu Met Leu Arg Tyr Leu Glu Thr Ala
                405                 410                 415

Asp Tyr Ala Ile Arg Glu Glu Ile Val Leu Lys Val Ala Ile Leu Ala
            420                 425                 430

Glu Lys Tyr Ala Val Asp Tyr Ser Trp Tyr Val Asp Thr Ile Leu Asn
        435                 440                 445

Leu Ile Arg Ile Ala Gly Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg
    450                 455                 460

Val Leu Gln Ile Val Thr Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala
465                 470                 475                 480

Lys Thr Val Phe Glu Ala Leu Gln Ala Pro Ala Cys His Glu Asn Met
                485                 490                 495

Val Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala
            500                 505                 510

Gly Asp Pro Arg Ser Ser Pro Pro Val Gln Phe Ser Leu Leu His Ser
        515                 520                 525

Lys Phe His Leu Cys Ser Val Ala Thr Arg Ala Leu Leu Leu Ser Thr
    530                 535                 540

Tyr Ile Lys Phe Ile Asn Leu Phe Pro Glu Thr Lys Ala Thr Ile Gln
545                 550                 555                 560
```

```
Gly Val Leu Arg Ala Gly Ser Gln Leu Arg Asn Ala Asp Val Glu Leu
                565                 570                 575

Gln Gln Arg Ala Val Glu Tyr Leu Thr Leu Ser Ser Val Ala Ser Thr
            580                 585                 590

Asp Val Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg
        595                 600                 605

Glu Ser Ser Ile Leu Ala Lys Leu Lys Arg Lys Lys Gly Pro Gly Ala
    610                 615                 620

Gly Ser Ala Leu Asp Asp Gly Arg Arg Asp Pro Ser Ser Asn Asp Ile
625                 630                 635                 640

Asn Gly Gly Met Glu Pro Thr Pro Ser Thr Val Ser Thr Pro Ser Pro
                645                 650                 655

Ser Ala Asp Leu Leu Gly Leu Arg Ala Ala Pro Pro Pro Ala Ala Pro
            660                 665                 670

Pro Ala Ser Ala Gly Ala Gly Asn Leu Leu Val Asp Val Phe Asp Gly
        675                 680                 685

Pro Ala Ala Gln Pro Ser Leu Gly Pro Thr Pro Glu Glu Ala Phe Leu
    690                 695                 700

Ser Pro Gly Pro Glu Asp Ile Gly Pro Pro Ile Pro Glu Ala Asp Glu
705                 710                 715                 720

Leu Leu Asn Lys Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu Asn
                725                 730                 735

Gln Leu Leu Gln Ile Gly Val Lys Ser Glu Phe Arg Gln Asn Leu Gly
            740                 745                 750

Arg Met Tyr Leu Phe Tyr Gly Asn Lys Thr Ser Val Gln Phe Gln Asn
        755                 760                 765

Phe Ser Pro Thr Val Val His Pro Gly Asp Leu Gln Thr Gln Leu Ala
    770                 775                 780
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Val Gln Thr Lys Arg Val Ala Ala Gln Val Asp Gly Gly Ala Gln Val
785                 790                 795                 800

Gln Gln Val Leu Asn Ile Glu Cys Leu Arg Asp Phe Leu Thr Pro Pro
                805                 810                 815

Leu Leu Ser Val Arg Phe Arg Tyr Gly Gly Ala Pro Gln Ala Leu Thr
            820                 825                 830

Leu Lys Leu Pro Val Thr Ile Asn Lys Phe Phe Gln Pro Thr Glu Met
        835                 840                 845

Ala Ala Gln Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Leu Pro Gln
    850                 855                 860

Gln Glu Ala Gln Lys Ile Phe Lys Ala Asn His Pro Met Asp Ala Glu
865                 870                 875                 880

Val Thr Lys Ala Lys Leu Leu Gly Phe Gly Ser Ala Leu Leu Asp Asn
                885                 890                 895

Val Asp Pro Asn Pro Glu Asn Phe Val Gly Ala Gly Ile Ile Gln Thr
            900                 905                 910

Lys Ala Leu Gln Val Gly Cys Leu Leu Arg Leu Glu Pro Asn Ala Gln
        915                 920                 925

Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Pro Val Ser
    930                 935                 940

Arg His Leu Cys Glu Leu Leu Ala Gln Gln Phe
945                 950                 955


<210> 2427
<211> 977
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<220>
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<223> /note="ENSP ID: ENSP00000351926"

<400> 2427

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Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1               5                   10                  15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg
            20                  25                  30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
        35                  40                  45

Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe
    50                  55                  60

Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala Val
65                  70                  75                  80

Asn Leu Leu Ser Ser Asn Lys Tyr Thr Glu Lys Gln Ile Gly Tyr Leu
                85                  90                  95

Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile
            100                 105                 110

Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe Met
        115                 120                 125

Cys Leu Ala Leu His Cys Ile Ala Asn Val Gly Ser Arg Glu Met Gly
    130                 135                 140

Glu Ala Phe Ala Ala Asp Ile Pro Arg Ile Leu Val Ala Gly Asp Ser
145                 150                 155                 160

Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
                165                 170                 175
```

```
Lys Ala Ser Pro Asp Leu Val Pro Met Gly Glu Trp Thr Ala Arg Val
            180                 185                 190

Val His Leu Leu Asn Asp Gln His Met Gly Val Val Thr Ala Ala Val
        195                 200                 205

Ser Leu Ile Thr Cys Leu Cys Lys Lys Asn Pro Asp Asp Phe Lys Thr
    210                 215                 220

Cys Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Ser Ser Ala
225                 230                 235                 240

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                245                 250                 255

Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Glu
            260                 265                 270

Asp Ala Ala Val Lys Gly Arg Leu Val Glu Cys Leu Glu Thr Val Leu
        275                 280                 285

Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn
    290                 295                 300

Ala Lys Asn Ala Ile Leu Phe Glu Thr Ile Ser Leu Ile Ile His Tyr
305                 310                 315                 320

Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln
                325                 330                 335

Phe Leu Gln His Arg Glu Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser
            340                 345                 350

Met Cys Thr Leu Ala Ser Ser Glu Phe Ser His Glu Ala Val Lys Thr
        355                 360                 365

His Ile Asp Thr Val Ile Asn Ala Leu Lys Thr Glu Arg Asp Val Ser
    370                 375                 380

Val Arg Gln Arg Ala Ala Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser
385                 390                 395                 400
```

```
Asn Ala Lys Gln Ile Val Ser Glu Met Leu Arg Tyr Leu Glu Thr Ala
                405                 410                 415

Asp Tyr Ala Ile Arg Glu Glu Ile Val Leu Lys Val Ala Ile Leu Ala
            420                 425                 430

Glu Lys Tyr Ala Val Asp Tyr Ser Trp Tyr Val Asp Thr Ile Leu Asn
        435                 440                 445

Leu Ile Arg Ile Ala Gly Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg
    450                 455                 460

Val Leu Gln Ile Val Thr Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala
465                 470                 475                 480

Lys Thr Val Phe Glu Ala Leu Gln Ala Pro Ala Cys His Glu Asn Met
                485                 490                 495

Val Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala
            500                 505                 510

Gly Asp Pro Arg Ser Ser Pro Pro Val Gln Phe Ser Leu Leu His Ser
        515                 520                 525

Lys Phe His Leu Cys Ser Val Ala Thr Arg Ala Leu Leu Leu Ser Thr
    530                 535                 540

Tyr Ile Lys Phe Ile Asn Leu Phe Pro Glu Thr Lys Ala Thr Ile Gln
545                 550                 555                 560

Gly Val Leu Arg Ala Gly Ser Gln Leu Arg Asn Ala Asp Val Glu Leu
                565                 570                 575

Gln Gln Arg Ala Val Glu Tyr Leu Thr Leu Ser Ser Val Ala Ser Thr
            580                 585                 590

Asp Val Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg
        595                 600                 605

Glu Ser Ser Ile Leu Ala Lys Leu Lys Arg Lys Lys Gly Pro Gly Ala
    610                 615                 620
```

```
Gly Ser Ala Leu Asp Asp Gly Arg Arg Asp Pro Ser Ser Asn Asp Ile
625                 630                 635                 640

Asn Gly Gly Met Glu Pro Thr Pro Ser Thr Val Ser Thr Pro Ser Pro
                645                 650                 655

Ser Ala Asp Leu Leu Gly Leu Arg Ala Ala Pro Pro Pro Ala Ala Pro
            660                 665                 670

Pro Ala Ser Ala Gly Ala Gly Asn Leu Leu Val Asp Val Phe Asp Gly
        675                 680                 685

Pro Ala Ala Gln Pro Ser Leu Gly Pro Thr Pro Glu Glu Ala Phe Leu
    690                 695                 700

Ser Glu Leu Glu Pro Pro Ala Pro Glu Ser Pro Met Ala Leu Leu Ala
705                 710                 715                 720

Asp Pro Ala Pro Ala Ala Asp Pro Gly Pro Glu Asp Ile Gly Pro Pro
                725                 730                 735

Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys Asn Asn
            740                 745                 750

Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys Ser Glu
        755                 760                 765

Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn Lys Thr
    770                 775                 780

Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro Gly Asp
785                 790                 795                 800

Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala Gln Val
                805                 810                 815

Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys Leu Arg
            820                 825                 830

Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr Gly Gly
        835                 840                 845

Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn Lys Phe
```

```
    850                 855                 860

Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg Trp Lys
865                 870                 875                 880

Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys Ala Asn
                885                 890                 895

His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly Phe Gly
            900                 905                 910

Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe Val Gly
        915                 920                 925

Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu Leu Arg
    930                 935                 940

Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr
945                 950                 955                 960

Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala Gln Gln
                965                 970                 975

Phe
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<210> 2428
<211> 57
<212> PRT
<213> Homo sapiens

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<220>
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<222> (1)..(1)
<223> Any amino acid

<400> 2428
Xaa Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1   5   10   15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg
            20   25   30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
        35   40   45

Ala Leu Asp Gly Tyr Lys Glu Pro Arg
    50   55

<210> 2429
<211> 940
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<400> 2429
Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1   5   10   15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg

```
            20                  25                  30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
        35                  40                  45

Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe
    50                  55                  60

Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala Val
65                  70                  75                  80

Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu
                85                  90                  95

Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile
            100                 105                 110

Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe Met
        115                 120                 125

Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser Arg Glu Met Ala
    130                 135                 140

Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp Thr
145                 150                 155                 160

Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
                165                 170                 175

Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg Val
            180                 185                 190

Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala Thr
        195                 200                 205

Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr
    210                 215                 220

Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser Ala
225                 230                 235                 240

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                245                 250                 255
```

```
Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Glu
            260                 265                 270

Asp Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu
        275                 280                 285

Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn
    290                 295                 300

Ala Lys Asn Ala Val Leu Phe Glu Ala Ile Ser Leu Ile Ile His His
305                 310                 315                 320

Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln
                325                 330                 335

Phe Leu Gln His Arg Glu Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser
            340                 345                 350

Met Cys Thr Leu Ala Ser Ser Glu Phe Ser His Glu Ala Val Lys Thr
        355                 360                 365

His Ile Glu Thr Val Ile Asn Ala Leu Lys Thr Glu Arg Asp Val Ser
    370                 375                 380

Val Arg Gln Arg Ala Val Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser
385                 390                 395                 400

Asn Ala Pro Gln Ile Val Ala Glu Met Leu Ser Tyr Leu Glu Thr Ala
                405                 410                 415

Asp Tyr Ser Ile Arg Glu Glu Ile Val Leu Lys Val Ala Ile Leu Ala
            420                 425                 430

Glu Lys Tyr Ala Val Asp Tyr Thr Trp Tyr Val Asp Thr Ile Leu Asn
        435                 440                 445

Leu Ile Arg Ile Ala Gly Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg
    450                 455                 460

Val Ile Gln Ile Val Ile Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala
465                 470                 475                 480
```

```
Lys Thr Val Phe Glu Ala Leu Gln Ala Pro Ala Cys His Glu Asn Leu
                485                 490                 495

Val Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala
            500                 505                 510

Gly Asp Pro Arg Ser Ser Pro Leu Ile Gln Phe His Leu Leu His Ser
        515                 520                 525

Lys Phe His Leu Cys Ser Val Pro Thr Arg Ala Leu Leu Leu Ser Thr
    530                 535                 540

Tyr Ile Lys Phe Val Asn Leu Phe Pro Glu Val Lys Pro Thr Ile Gln
545                 550                 555                 560

Asp Val Leu Arg Ser Asp Ser Gln Leu Arg Asn Ala Asp Val Glu Leu
                565                 570                 575

Gln Gln Arg Ala Val Glu Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr
            580                 585                 590

Asp Ile Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg
        595                 600                 605

Glu Ser Ser Ile Leu Ala Lys Leu Lys Lys Lys Lys Gly Pro Ser Thr
    610                 615                 620

Val Thr Asp Leu Glu Asp Thr Lys Arg Asp Arg Ser Val Asp Val Asn
625                 630                 635                 640

Gly Gly Pro Glu Pro Ala Pro Ala Ser Thr Ser Ala Val Ser Thr Pro
                645                 650                 655

Ser Pro Ser Ala Asp Leu Leu Gly Leu Gly Ala Ala Pro Pro Ala Pro
            660                 665                 670

Ala Gly Pro Pro Pro Ser Ser Gly Gly Ser Gly Leu Leu Val Asp Val
        675                 680                 685

Phe Ser Asp Ser Ala Ser Val Val Ala Pro Leu Ala Pro Gly Ser Glu
    690                 695                 700
```

```
Asp Asn Phe Ala Arg Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu
705                 710                 715                 720

Asn Gln Leu Leu Gln Ile Gly Leu Lys Ser Glu Phe Arg Gln Asn Leu
                725                 730                 735

Gly Arg Met Phe Ile Phe Tyr Gly Asn Lys Thr Ser Thr Gln Phe Leu
            740                 745                 750

Asn Phe Thr Pro Thr Leu Ile Cys Ser Asp Asp Leu Gln Pro Asn Leu
        755                 760                 765

Asn Leu Gln Thr Lys Pro Val Asp Pro Thr Val Glu Gly Gly Ala Gln
    770                 775                 780

Val Gln Gln Val Val Asn Ile Glu Cys Val Ser Asp Phe Thr Glu Ala
785                 790                 795                 800

Pro Val Leu Asn Ile Gln Phe Arg Tyr Gly Gly Thr Phe Gln Asn Val
                805                 810                 815

Ser Val Gln Leu Pro Ile Thr Leu Asn Lys Phe Phe Gln Pro Thr Glu
            820                 825                 830

Met Ala Ser Gln Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Asn Pro
        835                 840                 845

Gln Gln Glu Val Gln Asn Ile Phe Lys Ala Lys His Pro Met Asp Thr
    850                 855                 860

Glu Val Thr Lys Ala Lys Ile Ile Gly Phe Gly Ser Ala Leu Leu Glu
865                 870                 875                 880

Glu Val Asp Pro Asn Pro Ala Asn Phe Val Gly Ala Gly Ile Ile His
                885                 890                 895

Thr Lys Thr Thr Gln Ile Gly Cys Leu Leu Arg Leu Glu Pro Asn Leu
            900                 905                 910

Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Ala Val
        915                 920                 925

Ser Gln Arg Leu Cys Glu Leu Leu Ser Ala Gln Phe
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930 935 940

<210> 2430
<211> 939
<212> PRT
<213> Homo sapiens

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<223> /note="Payload ID: 594; "

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<223> /note="Gene Symbol: AP2A2; "

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<223> /note="Gene Name:
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<223> /note="Uniprot ID: O94973; "

<220>
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<400> 2430
Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1 5 10 15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg
20 25 30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
35 40 45

Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe
50 55 60

Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala Val
65 70 75 80

Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu
85 90 95

Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile
100 105 110

```
Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe Met
        115                 120                 125

Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser Arg Glu Met Ala
    130                 135                 140

Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp Thr
145                 150                 155                 160

Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
                165                 170                 175

Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg Val
            180                 185                 190

Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala Thr
        195                 200                 205

Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr
    210                 215                 220

Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser Ala
225                 230                 235                 240

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                245                 250                 255

Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp
            260                 265                 270

Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn
        275                 280                 285

Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn Ala
    290                 295                 300

Lys Asn Ala Val Leu Phe Glu Ala Ile Ser Leu Ile Ile His His Asp
305                 310                 315                 320

Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln Phe
                325                 330                 335
```

```
Leu Gln His Arg Glu Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser Met
            340                 345                 350

Cys Thr Leu Ala Ser Ser Glu Phe Ser His Glu Ala Val Lys Thr His
        355                 360                 365

Ile Glu Thr Val Ile Asn Ala Leu Lys Thr Glu Arg Asp Val Ser Val
    370                 375                 380

Arg Gln Arg Ala Val Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser Asn
385                 390                 395                 400

Ala Pro Gln Ile Val Ala Glu Met Leu Ser Tyr Leu Glu Thr Ala Asp
                405                 410                 415

Tyr Ser Ile Arg Glu Glu Ile Val Leu Lys Val Ala Ile Leu Ala Glu
            420                 425                 430

Lys Tyr Ala Val Asp Tyr Thr Trp Tyr Val Asp Thr Ile Leu Asn Leu
        435                 440                 445

Ile Arg Ile Ala Gly Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg Val
    450                 455                 460

Ile Gln Ile Val Ile Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala Lys
465                 470                 475                 480

Thr Val Phe Glu Ala Leu Gln Ala Pro Ala Cys His Glu Asn Leu Val
                485                 490                 495

Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala Gly
            500                 505                 510

Asp Pro Arg Ser Ser Pro Leu Ile Gln Phe His Leu Leu His Ser Lys
        515                 520                 525

Phe His Leu Cys Ser Val Pro Thr Arg Ala Leu Leu Leu Ser Thr Tyr
    530                 535                 540

Ile Lys Phe Val Asn Leu Phe Pro Glu Val Lys Pro Thr Ile Gln Asp
545                 550                 555                 560
```

```
Val Leu Arg Ser Asp Ser Gln Leu Arg Asn Ala Asp Val Glu Leu Gln
                565                 570                 575

Gln Arg Ala Val Glu Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr Asp
            580                 585                 590

Ile Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg Glu
        595                 600                 605

Ser Ser Ile Leu Ala Lys Leu Lys Lys Lys Lys Gly Pro Ser Thr Val
    610                 615                 620

Thr Asp Leu Glu Asp Thr Lys Arg Asp Arg Ser Val Asp Val Asn Gly
625                 630                 635                 640

Gly Pro Glu Pro Ala Pro Ala Ser Thr Ser Ala Val Ser Thr Pro Ser
                645                 650                 655

Pro Ser Ala Asp Leu Leu Gly Leu Gly Ala Ala Pro Pro Ala Pro Ala
            660                 665                 670

Gly Pro Pro Pro Ser Ser Gly Gly Ser Gly Leu Leu Val Asp Val Phe
        675                 680                 685

Ser Asp Ser Ala Ser Val Val Ala Pro Leu Ala Pro Gly Ser Glu Asp
    690                 695                 700

Asn Phe Ala Arg Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu Asn
705                 710                 715                 720

Gln Leu Leu Gln Ile Gly Leu Lys Ser Glu Phe Arg Gln Asn Leu Gly
                725                 730                 735

Arg Met Phe Ile Phe Tyr Gly Asn Lys Thr Ser Thr Gln Phe Leu Asn
            740                 745                 750

Phe Thr Pro Thr Leu Ile Cys Ser Asp Asp Leu Gln Pro Asn Leu Asn
        755                 760                 765

Leu Gln Thr Lys Pro Val Asp Pro Thr Val Glu Gly Gly Ala Gln Val
    770                 775                 780

Gln Gln Val Val Asn Ile Glu Cys Val Ser Asp Phe Thr Glu Ala Pro
```

785 790 795 800

Val Leu Asn Ile Gln Phe Arg Tyr Gly Gly Thr Phe Gln Asn Val Ser
805 810 815

Val Gln Leu Pro Ile Thr Leu Asn Lys Phe Phe Gln Pro Thr Glu Met
820 825 830

Ala Ser Gln Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Asn Pro Gln
835 840 845

Gln Glu Val Gln Asn Ile Phe Lys Ala Lys His Pro Met Asp Thr Glu
850 855 860

Val Thr Lys Ala Lys Ile Ile Gly Phe Gly Ser Ala Leu Leu Glu Glu
865 870 875 880

Val Asp Pro Asn Pro Ala Asn Phe Val Gly Ala Gly Ile Ile His Thr
885 890 895

Lys Thr Thr Gln Ile Gly Cys Leu Leu Arg Leu Glu Pro Asn Leu Gln
900 905 910

Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Ala Val Ser
915 920 925

Gln Arg Leu Cys Glu Leu Leu Ser Ala Gln Phe
930 935

<210> 2431
<211> 656
<212> PRT
<213> Homo sapiens

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Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1   5   10   15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg
            20   25   30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
        35   40   45

Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe
    50   55   60

Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala Val
65   70   75   80

Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu
                85   90   95

Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile
            100   105   110

Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe Met
        115   120   125

Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser Arg Glu Met Ala
    130   135   140

Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp Thr
145   150   155   160

Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
                165   170   175

Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg Val
            180   185   190

```
Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala Thr
        195                 200                 205

Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr
    210                 215                 220

Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser Ala
225                 230                 235                 240

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                245                 250                 255

Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Glu
            260                 265                 270

Asp Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu
        275                 280                 285

Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn
    290                 295                 300

Ala Lys Asn Ala Val Leu Phe Glu Ala Ile Ser Leu Ile Ile His His
305                 310                 315                 320

Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln
                325                 330                 335

Phe Leu Gln His Arg Glu Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser
            340                 345                 350

Met Cys Thr Leu Ala Ser Ser Glu Phe Ser His Glu Ala Val Lys Thr
        355                 360                 365

His Ile Glu Thr Val Ile Asn Ala Leu Lys Thr Glu Arg Asp Val Ser
    370                 375                 380

Val Arg Gln Arg Ala Val Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser
385                 390                 395                 400

Asn Ala Pro Gln Ile Val Ala Glu Met Leu Ser Tyr Leu Glu Thr Ala
                405                 410                 415
```

```
Asp Tyr Ser Ile Arg Glu Glu Ile Val Leu Lys Val Ala Ile Leu Ala
            420                 425                 430

Glu Lys Tyr Ala Val Asp Tyr Thr Trp Tyr Val Asp Thr Ile Leu Asn
        435                 440                 445

Leu Ile Arg Ile Ala Gly Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg
    450                 455                 460

Val Ile Gln Ile Val Ile Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala
465                 470                 475                 480

Lys Thr Val Phe Glu Ala Leu Gln Ala Pro Ala Cys His Glu Asn Leu
                485                 490                 495

Val Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala
            500                 505                 510

Gly Asp Pro Arg Ser Ser Pro Leu Ile Gln Phe His Leu Leu His Ser
        515                 520                 525

Lys Phe His Leu Cys Ser Val Pro Thr Arg Ala Leu Leu Leu Ser Thr
    530                 535                 540

Tyr Ile Lys Phe Val Asn Leu Phe Pro Glu Val Lys Pro Thr Ile Gln
545                 550                 555                 560

Asp Val Leu Arg Ser Asp Ser Gln Leu Arg Asn Ala Asp Val Glu Leu
                565                 570                 575

Gln Gln Arg Ala Val Glu Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr
            580                 585                 590

Asp Ile Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg
        595                 600                 605

Glu Ser Ser Ile Leu Ala Lys Leu Lys Lys Lys Lys Gly Pro Ser Thr
    610                 615                 620

Val Thr Asp Leu Glu Asp Thr Lys Arg Asp Arg Ser Val Asp Val Asn
625                 630                 635                 640

Gly Gly Pro Glu Pro Ala Pro Ala Ser Thr Ser Ala Val Val Cys Leu
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645 650 655

<210> 2432
<211> 184
<212> PRT
<213> Homo sapiens

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subunit; "

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Glu Phe Phe Leu Pro Arg Leu Val Val Thr Ala Ser Gly Thr Pro Trp
1 5 10 15

Phe Ser Ser Gln Cys Phe Pro Ser Gly Ser Ser Glu Gly Lys Ser Lys
20 25 30

Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser
35 40 45

Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr
50 55 60

Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His Asp Ile Asp Phe
65 70 75 80

Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu
85 90 95

Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser
100 105 110

Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser
115 120 125

```
Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val
    130                 135                 140

Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val
145                 150                 155                 160

Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln Ser Ala Ala Leu
                165                 170                 175

Cys Leu Leu Arg Leu Tyr Arg Thr
            180


<210> 2433
<211> 90
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 594; "

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<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434432"

<400> 2433
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1               5                   10                  15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
            20                  25                  30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
        35                  40                  45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser
    50                  55                  60
```

```
Arg Glu Met Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val
65                  70                  75                  80


Ala Gly Asp Thr Met Asp Ser Val Lys Gln
                85                  90


<210> 2434
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<220>
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<220>
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<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000434553"

<400> 2434
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1               5                   10                  15


Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
            20                  25                  30


Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
        35                  40                  45


Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala
    50                  55                  60


<210> 2435
<211> 138
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AP2A2; "

<220>
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subunit; "

<220>
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<223> /note="ENSP ID: ENSP00000434563"

<400> 2435
Met Leu Val Gln Phe Phe Gln Arg Thr Leu Asp Ser Leu Leu Leu Leu
1 5 10 15

Gly Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
20 25 30

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
35 40 45

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
50 55 60

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
65 70 75 80

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
85 90 95

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
100 105 110

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
115 120 125

Ile Ala Ser Val Gly Ser Arg Glu Met Ala
130 135

<210> 2436
<211> 185
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435756"

<400> 2436
Val Arg Val Trp Pro Arg Arg Ile Glu Glu Ile Ala Cys Lys Ser Lys
1 5 10 15

Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser
20 25 30

Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr
35 40 45

Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His Asp Ile Asp Phe
50 55 60

Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu
65 70 75 80

Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser
85 90 95

Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser
100 105 110

Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val
115 120 125

Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val
130 135 140

Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln Ser Ala Ala Leu
145 150 155 160

```
Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu Val Pro Met Gly
                165                 170                 175

Asp Trp Thr Ser Arg Val Val His Leu
            180                 185


<210> 2437
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000435863"

<400> 2437
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1               5                   10                  15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
            20                  25                  30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
        35                  40                  45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val
    50                  55                  60


<210> 2438
<211> 378
<212> PRT
<213> Homo sapiens

<220>
<221> source
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<223> /note="Payload ID: 594; "

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<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
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<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000436059"

<400> 2438

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Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val Phe
1               5                  10                  15

Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys Arg
            20                  25                  30

Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys
        35                  40                  45

Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe
    50                  55                  60

Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala Val
65                  70                  75                  80

Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu
                85                  90                  95

Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile
            100                 105                 110

Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe Met
        115                 120                 125

Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser Arg Glu Met Ala
    130                 135                 140

Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp Thr
145                 150                 155                 160
```

```
Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
                165                 170                 175

Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg Val
            180                 185                 190

Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala Thr
        195                 200                 205

Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr
    210                 215                 220

Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser Ala
225                 230                 235                 240

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                245                 250                 255

Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp
            260                 265                 270

Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn
        275                 280                 285

Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn Ala
    290                 295                 300

Lys Asn Ala Val Leu Phe Glu Ala Ile Ser Leu Ile Ile His His Asp
305                 310                 315                 320

Arg Cys Val Gly Cys Leu Cys Thr Gly Ser Arg Cys Ala Gln Val Arg
                325                 330                 335

Lys Pro Phe Leu Arg Asp Tyr Val Asn Cys Ser Gln Arg Ser Phe Ser
            340                 345                 350

Pro Glu Asp Gly Arg Pro Gly Ser Cys Val Leu Cys Cys Leu Arg Leu
        355                 360                 365

Cys Arg Leu Ser Ser Trp Pro Ser Cys Arg
    370                 375
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<210> 2439

<211> 125
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
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<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000437228"

<400> 2439

Met	Asp	Ser	Val	Lys	Gln	Ser	Ala	Ala	Leu	Cys	Leu	Leu	Arg	Leu	Tyr
1				5				10					15		
Arg	Thr	Ser	Pro	Asp	Leu	Val	Pro	Met	Gly	Asp	Trp	Thr	Ser	Arg	Val
			20					25				30			
Val	His	Leu	Leu	Asn	Asp	Gln	His	Leu	Gly	Val	Val	Thr	Ala	Ala	Thr
		35					40					45			
Ser	Leu	Ile	Thr	Thr	Leu	Ala	Gln	Lys	Asn	Pro	Glu	Glu	Phe	Lys	Thr
	50					55					60				
Ser	Val	Ser	Leu	Ala	Val	Ser	Arg	Leu	Ser	Arg	Ile	Val	Thr	Ser	Ala
65					70					75					80
Ser	Thr	Asp	Leu	Gln	Asp	Tyr	Thr	Tyr	Tyr	Phe	Val	Pro	Ala	Pro	Trp
				85					90					95	
Leu	Ser	Val	Lys	Leu	Leu	Arg	Leu	Leu	Gln	Cys	Tyr	Pro	Pro	Pro	Asp
			100					105					110		
Pro	Ala	Val	Arg	Gly	Arg	Leu	Thr	Glu	Cys	Leu	Glu	Thr			
		115					120					125			

<210> 2440
<211> 356

<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 594; "

<220>
<221> source
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<220>
<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485693"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2440
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1 5 10 15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
20 25 30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
35 40 45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
50 55 60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65 70 75 80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
85 90 95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
100 105 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu

```
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145                 150                 155                 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp
                165                 170                 175

Gln His Leu Gly Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu
            180                 185                 190

Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val
        195                 200                 205

Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp
    210                 215                 220

Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu
225                 230                 235                 240

Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp Pro Ala Val Arg Gly Arg
                245                 250                 255

Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro Pro
            260                 265                 270

Lys Ser Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Val Leu Phe
        275                 280                 285

Glu Ala Ile Ser Leu Ile Ile His His Asp Arg Cys Val Gly Cys Leu
    290                 295                 300

Cys Thr Gly Ser Arg Cys Ala Gln Val Arg Lys Pro Phe Leu Arg Asp
305                 310                 315                 320

Tyr Val Asn Cys Ser Gln Arg Ser Phe Ser Pro Glu Asp Gly Arg Pro
                325                 330                 335

Gly Ser Cys Val Leu Cys Cys Leu Arg Leu Cys Arg Leu Ser Ser Trp
            340                 345                 350
```

Leu Ser Cys Arg
        355

<210> 2441
<211> 90
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485814"

<400> 2441
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1   5   10   15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
            20   25   30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
        35   40   45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser
    50   55   60

Arg Glu Met Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val
65   70   75   80

Ala Gly Asp Thr Met Asp Ser Val Lys Gln
                85   90

<210> 2442
<211> 90
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
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<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485960"

<400> 2442
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1 5 10 15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
20 25 30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
35 40 45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser
50 55 60

Arg Glu Met Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val
65 70 75 80

Ala Gly Asp Thr Met Asp Ser Val Lys Gln
85 90

<210> 2443
<211> 634
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000485977"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2443
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1 5 10 15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
20 25 30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
35 40 45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
50 55 60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65 70 75 80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
85 90 95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
100 105 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
115 120 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
130 135 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145 150 155 160

```
Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp
                165                 170                 175

Gln His Leu Gly Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu
            180                 185                 190

Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val
        195                 200                 205

Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp
    210                 215                 220

Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu
225                 230                 235                 240

Arg Leu Leu Gln Cys Tyr Pro Pro Pro Glu Asp Pro Ala Val Arg Gly
                245                 250                 255

Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro
            260                 265                 270

Pro Lys Ser Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Val Leu
        275                 280                 285

Phe Glu Ala Ile Ser Leu Ile Ile His His Asp Ser Glu Pro Asn Leu
    290                 295                 300

Leu Val Arg Ala Cys Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu
305                 310                 315                 320

Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser
                325                 330                 335

Ser Glu Phe Ser His Glu Ala Val Lys Thr His Ile Glu Thr Val Ile
            340                 345                 350

Asn Ala Leu Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Val
        355                 360                 365

Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser Asn Ala Pro Gln Ile Val
    370                 375                 380
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```
Ala Glu Met Leu Ser Tyr Leu Glu Thr Ala Asp Tyr Ser Ile Arg Glu
385                 390                 395                 400

Glu Ile Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp
                405                 410                 415

Tyr Thr Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly
            420                 425                 430

Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg Val Ile Gln Ile Val Ile
        435                 440                 445

Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala
    450                 455                 460

Leu Gln Ala Pro Ala Cys His Glu Asn Leu Val Lys Val Gly Gly Tyr
465                 470                 475                 480

Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser
                485                 490                 495

Pro Leu Ile Gln Phe His Leu Leu His Ser Lys Phe His Leu Cys Ser
            500                 505                 510

Val Pro Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Val Asn
        515                 520                 525

Leu Phe Pro Glu Val Lys Pro Thr Ile Gln Asp Val Leu Arg Ser Asp
    530                 535                 540

Ser Gln Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu
545                 550                 555                 560

Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr Asp Ile Leu Ala Thr Val
                565                 570                 575

Leu Glu Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala
            580                 585                 590

Lys Leu Lys Lys Lys Lys Gly Pro Ser Thr Val Thr Asp Leu Glu Asp
        595                 600                 605

Thr Lys Arg Asp Arg Ser Val Asp Val Asn Gly Gly Pro Glu Pro Ala
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610 615 620

Pro Ala Ser Thr Ser Ala Val Val Cys Leu
625 630

<210> 2444
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486035"

<400> 2444
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1 5 10 15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
20 25 30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
35 40 45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala
50 55 60

<210> 2445
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>

<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486155"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2445

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Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1               5                  10                  15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
            20                  25                  30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
        35                  40                  45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
    50                  55                  60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65                  70                  75                  80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
                85                  90                  95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
            100                 105                 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr
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145 150 155

<210> 2446
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486169"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2446
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1 5 10 15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
20 25 30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
35 40 45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
50 55 60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65 70 75 80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
85 90 95

```
Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
            100                 105                 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145                 150                 155                 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu
                165                 170


<210> 2447
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, alpha 2
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486204"

<400> 2447
Met Leu Val Gln Phe Phe Gln Arg Thr Leu Asp Ser Leu Leu Leu Leu
1               5                   10                  15

Gly Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
            20                  25                  30

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
        35                  40                  45

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
```

```
    50                  55                  60

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
65                  70                  75                  80

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
                85                  90                  95

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
            100                 105                 110

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
        115                 120                 125

Ile Ala Ser Val Gly Ser Arg Glu Met Ala
    130                 135


<210> 2448
<211> 356
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
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<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, alpha 2
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486729"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2448
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1               5                   10                  15
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Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
            20                  25                  30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
        35                  40                  45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
    50                  55                  60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65                  70                  75                  80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
                85                  90                  95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
            100                 105                 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145                 150                 155                 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp
                165                 170                 175

Gln His Leu Gly Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu
            180                 185                 190

Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val
        195                 200                 205

Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp
    210                 215                 220

Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu
225                 230                 235                 240

Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp Pro Ala Val Arg Gly Arg
```

```
                245                 250                 255

Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro Pro
            260                 265                 270

Lys Ser Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Val Leu Phe
        275                 280                 285

Glu Ala Ile Ser Leu Ile Ile His His Asp Arg Cys Val Gly Cys Leu
    290                 295                 300

Cys Thr Gly Ser Arg Cys Ala Gln Val Arg Lys Pro Phe Leu Arg Asp
305                 310                 315                 320

Tyr Val Asn Cys Ser Gln Arg Ser Phe Ser Pro Glu Asp Gly Arg Pro
                325                 330                 335

Gly Ser Cys Val Leu Cys Cys Leu Arg Leu Cys Arg Leu Ser Ser Trp
            340                 345                 350

Pro Ser Cys Arg
        355


<210> 2449
<211> 173
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
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<220>
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486890"


<220>
<221> MOD_RES
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<222> (1)..(1)
<223> Any amino acid

<400> 2449
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1 5 10 15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
20 25 30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
35 40 45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
50 55 60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65 70 75 80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
85 90 95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
100 105 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
115 120 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
130 135 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145 150 155 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu
165 170

<210> 2450
<211> 138
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486895"

<400> 2450
Met Leu Val Gln Phe Phe Gln Arg Thr Leu Asp Ser Leu Leu Leu Leu
1 5 10 15

Gly Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
20 25 30

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
35 40 45

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
50 55 60

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
65 70 75 80

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
85 90 95

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
100 105 110

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
115 120 125

Ile Ala Ser Val Gly Ser Arg Glu Met Ala
130 135

<210> 2451
<211> 62
<212> PRT
<213> Homo sapiens

<220>

<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
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<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486964"

<400> 2451
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1 5 10 15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
20 25 30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
35 40 45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val
50 55 60

<210> 2452
<211> 125
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000486996"

<400> 2452
Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr
1   5   10   15

Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg Val
            20   25   30

Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala Thr
        35   40   45

Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr
    50   55   60

Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser Ala
65   70   75   80

Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp
                85   90   95

Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp
            100   105   110

Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr
        115   120   125

<210> 2453
<211> 140
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, alpha 2
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487022"

<400> 2453

```
Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met
1               5                   10                  15

Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg
            20                  25                  30

Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg Val Val
        35                  40                  45

His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala Thr Ser
    50                  55                  60

Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser
65                  70                  75                  80

Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser
                85                  90                  95

Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu
            100                 105                 110

Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp Pro
        115                 120                 125

Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr
    130                 135                 140


<210> 2454
<211> 917
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>
<221> source
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<223> /note="ENSP ID: ENSP00000487149"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2454

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Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1               5                  10                  15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
            20                  25                  30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
        35                  40                  45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
    50                  55                  60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65                  70                  75                  80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
                85                  90                  95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
            100                 105                 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145                 150                 155                 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp
                165                 170                 175

Gln His Leu Gly Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu
            180                 185                 190
```

```
Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val
        195                 200                 205

Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp
    210                 215                 220

Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu
225                 230                 235                 240

Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp Pro Ala Val Arg Gly Arg
                245                 250                 255

Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro Pro
            260                 265                 270

Lys Ser Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Val Leu Phe
        275                 280                 285

Glu Ala Ile Ser Leu Ile Ile His His Asp Ser Glu Pro Asn Leu Leu
    290                 295                 300

Val Arg Ala Cys Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu Thr
305                 310                 315                 320

Asn Leu Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser
                325                 330                 335

Glu Phe Ser His Glu Ala Val Lys Thr His Ile Glu Thr Val Ile Asn
            340                 345                 350

Ala Leu Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Val Asp
        355                 360                 365

Leu Leu Tyr Ala Met Cys Asp Arg Ser Asn Ala Pro Gln Ile Val Ala
    370                 375                 380

Glu Met Leu Ser Tyr Leu Glu Thr Ala Asp Tyr Ser Ile Arg Glu Glu
385                 390                 395                 400

Ile Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr
                405                 410                 415

Thr Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp
```

```
            420                 425                 430

Tyr Val Ser Glu Glu Val Trp Tyr Arg Val Ile Gln Ile Val Ile Asn
        435                 440                 445

Arg Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu
    450                 455                 460

Gln Ala Pro Ala Cys His Glu Asn Leu Val Lys Val Gly Gly Tyr Ile
465                 470                 475                 480

Leu Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro
                485                 490                 495

Leu Ile Gln Phe His Leu Leu His Ser Lys Phe His Leu Cys Ser Val
            500                 505                 510

Pro Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Val Asn Leu
        515                 520                 525

Phe Pro Glu Val Lys Pro Thr Ile Gln Asp Val Leu Arg Ser Asp Ser
    530                 535                 540

Gln Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr
545                 550                 555                 560

Leu Arg Leu Ser Thr Val Ala Ser Thr Asp Ile Leu Ala Thr Val Leu
                565                 570                 575

Glu Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys
            580                 585                 590

Leu Lys Lys Lys Lys Gly Pro Ser Thr Val Thr Asp Leu Glu Asp Thr
        595                 600                 605

Lys Arg Asp Arg Ser Val Asp Val Asn Gly Gly Pro Glu Pro Ala Pro
    610                 615                 620

Ala Ser Thr Ser Ala Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu
625                 630                 635                 640

Gly Leu Gly Ala Ala Pro Pro Ala Pro Ala Gly Pro Pro Pro Ser Ser
                645                 650                 655
```

Gly Gly Ser Gly Leu Leu Val Asp Val Phe Ser Asp Ser Ala Ser Val
660 665 670

Val Ala Pro Leu Ala Pro Gly Ser Glu Asp Asn Phe Ala Arg Phe Val
675 680 685

Cys Lys Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly
690 695 700

Leu Lys Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Phe Ile Phe Tyr
705 710 715 720

Gly Asn Lys Thr Ser Thr Gln Phe Leu Asn Phe Thr Pro Thr Leu Ile
725 730 735

Cys Ser Asp Asp Leu Gln Pro Asn Leu Asn Leu Gln Thr Lys Pro Val
740 745 750

Asp Pro Thr Val Glu Gly Gly Ala Gln Val Gln Gln Val Val Asn Ile
755 760 765

Glu Cys Val Ser Asp Phe Thr Glu Ala Pro Val Leu Asn Ile Gln Phe
770 775 780

Arg Tyr Gly Gly Thr Phe Gln Asn Val Ser Val Gln Leu Pro Ile Thr
785 790 795 800

Leu Asn Lys Phe Phe Gln Pro Thr Glu Met Ala Ser Gln Asp Phe Phe
805 810 815

Gln Arg Trp Lys Gln Leu Ser Asn Pro Gln Gln Glu Val Gln Asn Ile
820 825 830

Phe Lys Ala Lys His Pro Met Asp Thr Glu Val Thr Lys Ala Lys Ile
835 840 845

Ile Gly Phe Gly Ser Ala Leu Leu Glu Glu Val Asp Pro Asn Pro Ala
850 855 860

Asn Phe Val Gly Ala Gly Ile Ile His Thr Lys Thr Thr Gln Ile Gly
865 870 875 880

Cys Leu Leu Arg Leu Glu Pro Asn Leu Gln Ala Gln Met Tyr Arg Leu
885 890 895

Thr Leu Arg Thr Ser Lys Glu Ala Val Ser Gln Arg Leu Cys Glu Leu
900 905 910

Leu Ser Ala Gln Phe
915

<210> 2455
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487205"

<400> 2455
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1 5 10 15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
20 25 30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
35 40 45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val
50 55 60

<210> 2456
<211> 156
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, alpha 2
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487264"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2456
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1 5 10 15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
20 25 30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
35 40 45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
50 55 60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65 70 75 80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
85 90 95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
100 105 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
115 120 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130   135   140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr
145   150   155

<210> 2457
<211> 634
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
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<220>
<221> source
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487282"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2457
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1   5   10   15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
            20   25   30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
        35   40   45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
    50   55   60

Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65   70   75   80

```
Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
                85                  90                  95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
            100                 105                 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145                 150                 155                 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp
                165                 170                 175

Gln His Leu Gly Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu
            180                 185                 190

Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val
        195                 200                 205

Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp
    210                 215                 220

Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu
225                 230                 235                 240

Arg Leu Leu Gln Cys Tyr Pro Pro Pro Glu Asp Pro Ala Val Arg Gly
                245                 250                 255

Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro
            260                 265                 270

Pro Lys Ser Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Val Leu
        275                 280                 285

Phe Glu Ala Ile Ser Leu Ile Ile His His Asp Ser Glu Pro Asn Leu
    290                 295                 300
```

```
Leu Val Arg Ala Cys Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu
305                 310                 315                 320

Thr Asn Leu Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser
                325                 330                 335

Ser Glu Phe Ser His Glu Ala Val Lys Thr His Ile Glu Thr Val Ile
            340                 345                 350

Asn Ala Leu Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Val
        355                 360                 365

Asp Leu Leu Tyr Ala Met Cys Asp Arg Ser Asn Ala Pro Gln Ile Val
    370                 375                 380

Ala Glu Met Leu Ser Tyr Leu Glu Thr Ala Asp Tyr Ser Ile Arg Glu
385                 390                 395                 400

Glu Ile Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp
                405                 410                 415

Tyr Thr Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly
            420                 425                 430

Asp Tyr Val Ser Glu Glu Val Trp Tyr Arg Val Ile Gln Ile Val Ile
        435                 440                 445

Asn Arg Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala
    450                 455                 460

Leu Gln Ala Pro Ala Cys His Glu Asn Leu Val Lys Val Gly Gly Tyr
465                 470                 475                 480

Ile Leu Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser
                485                 490                 495

Pro Leu Ile Gln Phe His Leu Leu His Ser Lys Phe His Leu Cys Ser
            500                 505                 510

Val Pro Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Val Asn
        515                 520                 525
```

```
Leu Phe Pro Glu Val Lys Pro Thr Ile Gln Asp Val Leu Arg Ser Asp
    530                 535                 540

Ser Gln Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu
545                 550                 555                 560

Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr Asp Ile Leu Ala Thr Val
                565                 570                 575

Leu Glu Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala
            580                 585                 590

Lys Leu Lys Lys Lys Lys Gly Pro Ser Thr Val Thr Asp Leu Glu Asp
        595                 600                 605

Thr Lys Arg Asp Arg Ser Val Asp Val Asn Gly Gly Pro Glu Pro Ala
    610                 615                 620

Pro Ala Ser Thr Ser Ala Val Val Cys Leu
625                 630


<210> 2458
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, alpha 2
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487352"

<400> 2458
Met Glu Ala Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln
1               5                   10                  15

Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu
```

```
            20                  25                  30

Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn
        35                  40                  45

Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala
    50                  55                  60


<210> 2459
<211> 917
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 594; "

<220>
<221> source
<223> /note="Gene Symbol: AP2A2; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, alpha 2
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487425"


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 2459
Xaa Lys Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala
1               5                   10                  15

Asn Ile Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser
            20                  25                  30

Lys Lys Lys Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His
        35                  40                  45

Asp Ile Asp Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn
    50                  55                  60
```

```
Arg Tyr Thr Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val
65                  70                  75                  80

Asn Ser Asn Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn
                85                  90                  95

Asp Leu Ala Ser Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys
            100                 105                 110

Ile Ala Ser Val Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu
        115                 120                 125

Ile Pro Lys Val Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln
    130                 135                 140

Ser Ala Ala Leu Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu
145                 150                 155                 160

Val Pro Met Gly Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp
                165                 170                 175

Gln His Leu Gly Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu
            180                 185                 190

Ala Gln Lys Asn Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val
        195                 200                 205

Ser Arg Leu Ser Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp
    210                 215                 220

Tyr Thr Tyr Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu
225                 230                 235                 240

Arg Leu Leu Gln Cys Tyr Pro Pro Pro Asp Pro Ala Val Arg Gly Arg
                245                 250                 255

Leu Thr Glu Cys Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro Pro
            260                 265                 270

Lys Ser Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Val Leu Phe
        275                 280                 285

Glu Ala Ile Ser Leu Ile Ile His His Asp Ser Glu Pro Asn Leu Leu
```

290 295 300

Val Arg Ala Cys Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu Thr
305 310 315 320

Asn Leu Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser
325 330 335

Glu Phe Ser His Glu Ala Val Lys Thr His Ile Glu Thr Val Ile Asn
340 345 350

Ala Leu Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Val Asp
355 360 365

Leu Leu Tyr Ala Met Cys Asp Arg Ser Asn Ala Pro Gln Ile Val Ala
370 375 380

Glu Met Leu Ser Tyr Leu Glu Thr Ala Asp Tyr Ser Ile Arg Glu Glu
385 390 395 400

Ile Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr
405 410 415

Thr Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp
420 425 430

Tyr Val Ser Glu Glu Val Trp Tyr Arg Val Ile Gln Ile Val Ile Asn
435 440 445

Arg Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu
450 455 460

Gln Ala Pro Ala Cys His Glu Asn Leu Val Lys Val Gly Gly Tyr Ile
465 470 475 480

Leu Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro
485 490 495

Leu Ile Gln Phe His Leu Leu His Ser Lys Phe His Leu Cys Ser Val
500 505 510

Pro Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Val Asn Leu
515 520 525

```
Phe Pro Glu Val Lys Pro Thr Ile Gln Asp Val Leu Arg Ser Asp Ser
    530                 535                 540

Gln Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr
545                 550                 555                 560

Leu Arg Leu Ser Thr Val Ala Ser Thr Asp Ile Leu Ala Thr Val Leu
                565                 570                 575

Glu Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys
            580                 585                 590

Leu Lys Lys Lys Lys Gly Pro Ser Thr Val Thr Asp Leu Glu Asp Thr
        595                 600                 605

Lys Arg Asp Arg Ser Val Asp Val Asn Gly Gly Pro Glu Pro Ala Pro
    610                 615                 620

Ala Ser Thr Ser Ala Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu
625                 630                 635                 640

Gly Leu Gly Ala Ala Pro Pro Ala Pro Ala Gly Pro Pro Pro Ser Ser
                645                 650                 655

Gly Gly Ser Gly Leu Leu Val Asp Val Phe Ser Asp Ser Ala Ser Val
            660                 665                 670

Val Ala Pro Leu Ala Pro Gly Ser Glu Asp Asn Phe Ala Arg Phe Val
        675                 680                 685

Cys Lys Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly
    690                 695                 700

Leu Lys Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Phe Ile Phe Tyr
705                 710                 715                 720

Gly Asn Lys Thr Ser Thr Gln Phe Leu Asn Phe Thr Pro Thr Leu Ile
                725                 730                 735

Cys Ser Asp Asp Leu Gln Pro Asn Leu Asn Leu Gln Thr Lys Pro Val
            740                 745                 750
```

```
Asp Pro Thr Val Glu Gly Gly Ala Gln Val Gln Gln Val Val Asn Ile
        755                 760                 765

Glu Cys Val Ser Asp Phe Thr Glu Ala Pro Val Leu Asn Ile Gln Phe
    770                 775                 780

Arg Tyr Gly Gly Thr Phe Gln Asn Val Ser Val Gln Leu Pro Ile Thr
785                 790                 795                 800

Leu Asn Lys Phe Phe Gln Pro Thr Glu Met Ala Ser Gln Asp Phe Phe
                805                 810                 815

Gln Arg Trp Lys Gln Leu Ser Asn Pro Gln Gln Glu Val Gln Asn Ile
            820                 825                 830

Phe Lys Ala Lys His Pro Met Asp Thr Glu Val Thr Lys Ala Lys Ile
        835                 840                 845

Ile Gly Phe Gly Ser Ala Leu Leu Glu Glu Val Asp Pro Asn Pro Ala
    850                 855                 860

Asn Phe Val Gly Ala Gly Ile Ile His Thr Lys Thr Thr Gln Ile Gly
865                 870                 875                 880

Cys Leu Leu Arg Leu Glu Pro Asn Leu Gln Ala Gln Met Tyr Arg Leu
                885                 890                 895

Thr Leu Arg Thr Ser Lys Glu Ala Val Ser Gln Arg Leu Cys Glu Leu
            900                 905                 910

Leu Ser Ala Gln Phe
        915


<210> 2460
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "
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<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000464966"

<400> 2460

```
Ser Glu Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val
1               5                  10                  15

Asp Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys
            20                  25                  30

Val Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile
        35                  40                  45

Gln Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg
    50                  55                  60

Asp Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr
65                  70                  75                  80

Leu Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala
                85                  90                  95

Met Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp
            100                 105                 110

Glu Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln
        115                 120                 125

Val Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys
    130                 135                 140

Pro Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr
145                 150                 155                 160

Gln Leu Lys Lys
```

<210> 2461

<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465357"

<400> 2461
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65 70 75 80

<210> 2462
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>

<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000465848"

<400> 2462
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Arg
35 40 45

Cys Cys Ser Ser Glu Val Asn Phe Cys Tyr Phe Ser Phe Val Cys
50 55 60

<210> 2463
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466580"

<400> 2463
Asp Leu Ile Glu Pro Thr Leu Leu Asp Glu Leu Ile Cys His Ile Gly
1 5 10 15

Ser Leu Ala Ser Val Tyr His Lys Pro Pro Asn Ala Phe Val Glu Gly
20 25 30

```
Ser His Gly Ile His Arg Lys His Leu Pro Ile His His Gly Ser Thr
        35                  40                  45

Asp Ala Gly Asp Ser Pro Val Gly Thr Thr Thr Ala Thr Asn Leu Glu
    50                  55                  60

Gln Pro Gln Val Ile Pro Ser Gln Gly Asp Leu Leu Gly Asp Leu Leu
65                  70                  75                  80

Asn Leu Asp Leu Gly Pro Pro Val Asn Val Pro Gln Val Ser Ser Met
                85                  90                  95

Gln Met Gly Ala Val Asp Leu Leu Gly Gly Gly Leu Asp Ser Leu Pro
            100                 105                 110

Gln Lys Leu Phe Thr Val Gln Phe Ser Ser Ala Tyr Ser Glu Ile Glu
        115                 120                 125

Arg Tyr Pro Arg Asn Gln Asp Glu Lys Lys Leu Lys Pro Leu Phe Leu
    130                 135                 140

Leu Trp Ile Arg Met Trp Leu Asn Ile Tyr Ser Leu Arg Glu Ser Arg
145                 150                 155                 160

Phe Leu Phe Arg Glu His His Lys Glu Asp Leu Asn Leu Pro Val Trp
                165                 170                 175

Lys Lys Met Ser Phe
            180


<210> 2464
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
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adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000466812"

<400> 2464
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1   5   10   15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20   25   30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35   40   45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50   55   60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65   70   75   80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
                85   90   95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100   105   110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115   120   125

Cys Leu Lys Asp
    130

<210> 2465
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000467382"

<400> 2465
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Arg
35 40 45

Cys Cys Ser Ser Glu Val Asn Phe Cys Tyr Phe Ser Phe Val Cys
50 55 60

<210> 2466
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468183"

<400> 2466
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

```
Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile
145                 150
```

<210> 2467
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000468813"

<400> 2467
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1   5   10   15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20   25   30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Arg
        35   40   45

Cys Cys Ser Ser Glu Val Asn Phe Cys Tyr Phe Ser Phe Val Cys
    50   55   60

<210> 2468
<211> 677
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, beta 1
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478115"

<400> 2468
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1   5   10   15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20   25   30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35   40   45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50   55   60

```
Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
            180                 185                 190

Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
```

```
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525
```

```
Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
            580                 585                 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
        595                 600                 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
    610                 615                 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625                 630                 635                 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
                645                 650                 655

Gly Gly Gly Leu Asp Ser Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile
            660                 665                 670

Gly Gly Ser Pro Ala
        675


<210> 2469
<211> 663
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
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<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000478471"

<400> 2469

```
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1               5                  10                  15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20                  25                  30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
            180                 185                 190
```

```
Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
```

```
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
            580                 585                 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
        595                 600                 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
    610                 615                 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625                 630                 635                 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
                645                 650                 655
```

Gly Gly Gly Leu Asp Ser Leu
660

<210> 2470
<211> 677
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000479691"

<400> 2470
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65 70 75 80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
85 90 95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
100 105 110

```
Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
            180                 185                 190

Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335
```

```
Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
```

565 570 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
580 585 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
595 600 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
610 615 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625 630 635 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
645 650 655

Gly Gly Gly Leu Asp Ser Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile
660 665 670

Gly Gly Ser Pro Ala
675

<210> 2471
<211> 49
<212> PRT
<213> Homo sapiens

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<220>
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subunit; "

<220>
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<223> /note="ENSP ID: ENSP00000481246"

<400> 2471
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20   25   30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35   40   45

Thr

<210> 2472
<211> 639
<212> PRT
<213> Homo sapiens

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<400> 2472
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1   5   10   15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20   25   30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35   40   45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50   55   60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65   70   75   80

```
Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Glu Asp
                85                  90                  95

Pro Tyr Val Arg Lys Thr Ala Ala Val Cys Val Ala Lys Leu His Asp
            100                 105                 110

Ile Asn Ala Gln Met Val Glu Asp Gln Gly Phe Leu Asp Ser Leu Arg
        115                 120                 125

Asp Leu Ile Ala Asp Ser Asn Pro Met Val Val Ala Asn Ala Val Ala
    130                 135                 140

Ala Leu Ser Glu Ile Ser Glu Ser His Pro Asn Ser Asn Leu Leu Asp
145                 150                 155                 160

Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu Thr Ala Leu Asn Glu Cys
                165                 170                 175

Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp Cys Leu Ser Asn Tyr Asn
            180                 185                 190

Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile Cys Glu Arg Val Thr Pro
        195                 200                 205

Arg Leu Ser His Ala Asn Ser Ala Val Val Leu Ser Ala Val Lys Val
    210                 215                 220

Leu Met Lys Phe Leu Glu Leu Leu Pro Lys Asp Ser Asp Tyr Tyr Asn
225                 230                 235                 240

Met Leu Leu Lys Lys Leu Ala Pro Pro Leu Val Thr Leu Leu Ser Gly
                245                 250                 255

Glu Pro Glu Val Gln Tyr Val Ala Leu Arg Asn Ile Asn Leu Ile Val
            260                 265                 270

Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu Ile Lys Val Phe Phe Val
        275                 280                 285

Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu Glu Lys Leu Asp Ile Met
    290                 295                 300
```

```
Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala Gln Val Leu Ala Glu Leu
305                 310                 315                 320

Lys Glu Tyr Ala Thr Glu Val Asp Val Asp Phe Val Arg Lys Ala Val
                325                 330                 335

Arg Ala Ile Gly Arg Cys Ala Ile Lys Val Glu Gln Ser Ala Glu Arg
            340                 345                 350

Cys Val Ser Thr Leu Leu Asp Leu Ile Gln Thr Lys Val Asn Tyr Val
        355                 360                 365

Val Gln Glu Ala Ile Val Val Ile Arg Asp Ile Phe Arg Lys Tyr Pro
    370                 375                 380

Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu Cys Glu Asn Leu Asp Ser
385                 390                 395                 400

Leu Asp Glu Pro Asp Ala Arg Ala Ala Met Ile Trp Ile Val Gly Glu
                405                 410                 415

Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu Leu Leu Glu Ser Phe Leu
            420                 425                 430

Glu Gly Phe His Asp Glu Ser Thr Gln Val Gln Leu Thr Leu Leu Thr
        435                 440                 445

Ala Ile Val Lys Leu Phe Leu Lys Lys Pro Ser Glu Thr Gln Glu Leu
    450                 455                 460

Val Gln Gln Val Leu Ser Leu Ala Thr Gln Asp Ser Asp Asn Pro Asp
465                 470                 475                 480

Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg Leu Leu Ser Thr Asp Pro
                485                 490                 495

Val Thr Ala Lys Glu Val Val Leu Ser Glu Lys Pro Leu Ile Ser Glu
            500                 505                 510

Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu Asp Glu Leu Ile Cys His
        515                 520                 525

Ile Gly Ser Leu Ala Ser Val Tyr His Lys Pro Pro Asn Ala Phe Val
```

```
    530                 535                 540

Glu Gly Ser His Gly Ile His Arg Lys His Leu Pro Ile His His Gly
545                 550                 555                 560

Ser Thr Asp Ala Gly Asp Ser Pro Val Gly Thr Thr Thr Ala Thr Asn
                565                 570                 575

Leu Glu Gln Pro Gln Val Ile Pro Ser Gln Gly Asp Leu Leu Gly Asp
            580                 585                 590

Leu Leu Asn Leu Asp Leu Gly Pro Pro Val Asn Val Pro Gln Val Ser
        595                 600                 605

Ser Met Gln Met Gly Ala Val Asp Leu Leu Gly Gly Gly Leu Asp Ser
    610                 615                 620

Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile Gly Gly Ser Pro Ala
625                 630                 635


<210> 2473
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<212> PRT
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<223> /note="Uniprot ID:  P63010; "

<220>
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<400> 2473
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1               5                   10                  15
```

```
Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20                  25                  30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
            180                 185                 190

Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240
```

```
Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460
```

```
Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
            580                 585                 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
        595                 600                 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
    610                 615                 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625                 630                 635                 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
                645                 650                 655

Gly Gly Gly Leu Asp Ser Leu Val Gly Gln Ser Phe Ile Pro Ser Ser
            660                 665                 670

Val Pro Ala Thr Phe Ala Pro Ser Pro Thr Pro Ala Val Val Ser Ser
        675                 680                 685

Gly Leu Asn Asp Leu Phe Glu Leu Ser Thr Gly Ile Gly Met Ala Pro
```

690 695 700

Gly Gly Tyr Val Ala Pro Lys Ala Val Trp Leu Pro Ala Val Lys Ala
705 710 715 720

Lys Gly Leu Glu Ile Ser Gly Thr Phe Thr His Arg Gln Gly His Ile
725 730 735

Tyr Met Glu Met Asn Phe Thr Asn Lys Ala Leu Gln His Met Thr Asp
740 745 750

Phe Ala Ile Gln Phe Asn Lys Asn Ser Phe Gly Val Ile Pro Ser Thr
755 760 765

Pro Leu Ala Ile His Thr Pro Leu Met Pro Asn Gln Ser Ile Asp Val
770 775 780

Ser Leu Pro Leu Asn Thr Leu Gly Pro Val Met Lys Met Glu Pro Leu
785 790 795 800

Asn Asn Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe Tyr Phe
805 810 815

Ser Cys Leu Ile Pro Leu Asn Val Leu Phe Val Glu Asp Gly Lys Met
820 825 830

Glu Arg Gln Val Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn Glu Asn
835 840 845

Glu Leu Gln Phe Gln Ile Lys Glu Cys His Leu Asn Ala Asp Thr Val
850 855 860

Ser Ser Lys Leu Gln Asn Asn Asn Val Tyr Thr Ile Ala Lys Arg Asn
865 870 875 880

Val Glu Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr Asn Gly
885 890 895

Ile Trp Ile Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro Asn Tyr
900 905 910

Thr Leu Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln Tyr Ile Tyr
915 920 925

Gln Val Tyr Asp Ser Ile Leu Lys Asn
930 935

<210> 2474
<211> 677
<212> PRT
<213> Homo sapiens

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<400> 2474
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65 70 75 80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
85 90 95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
100 105 110

```
Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
            180                 185                 190

Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335
```

```
Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
```

```
                565                 570                 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
            580                 585                 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
        595                 600                 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
    610                 615                 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625                 630                 635                 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
                645                 650                 655

Gly Gly Gly Leu Asp Ser Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile
            660                 665                 670

Gly Gly Ser Pro Ala
        675


<210> 2475
<211> 951
<212> PRT
<213> Homo sapiens

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Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65 70 75 80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
85 90 95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
100 105 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
115 120 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
130 135 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145 150 155 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
165 170 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
180 185 190

Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
195 200 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
210 215 220

```
Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285

Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445
```

```
Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
            580                 585                 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
        595                 600                 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
    610                 615                 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625                 630                 635                 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
                645                 650                 655

Gly Gly Gly Leu Asp Ser Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile
            660                 665                 670

Gly Gly Ser Pro Ala Val Gly Gln Ser Phe Ile Pro Ser Ser Val Pro
```

675 680 685

Ala Thr Phe Ala Pro Ser Pro Thr Pro Ala Val Val Ser Ser Gly Leu
690 695 700

Asn Asp Leu Phe Glu Leu Ser Thr Gly Ile Gly Met Ala Pro Gly Gly
705 710 715 720

Tyr Val Ala Pro Lys Ala Val Trp Leu Pro Ala Val Lys Ala Lys Gly
725 730 735

Leu Glu Ile Ser Gly Thr Phe Thr His Arg Gln Gly His Ile Tyr Met
740 745 750

Glu Met Asn Phe Thr Asn Lys Ala Leu Gln His Met Thr Asp Phe Ala
755 760 765

Ile Gln Phe Asn Lys Asn Ser Phe Gly Val Ile Pro Ser Thr Pro Leu
770 775 780

Ala Ile His Thr Pro Leu Met Pro Asn Gln Ser Ile Asp Val Ser Leu
785 790 795 800

Pro Leu Asn Thr Leu Gly Pro Val Met Lys Met Glu Pro Leu Asn Asn
805 810 815

Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe Tyr Phe Ser Cys
820 825 830

Leu Ile Pro Leu Asn Val Leu Phe Val Glu Asp Gly Lys Met Glu Arg
835 840 845

Gln Val Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn Glu Asn Glu Leu
850 855 860

Gln Phe Gln Ile Lys Glu Cys His Leu Asn Ala Asp Thr Val Ser Ser
865 870 875 880

Lys Leu Gln Asn Asn Asn Val Tyr Thr Ile Ala Lys Arg Asn Val Glu
885 890 895

Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr Asn Gly Ile Trp
900 905 910

Ile Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro Asn Tyr Thr Leu
915 920 925

Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln Tyr Ile Tyr Gln Val
930 935 940

Tyr Asp Ser Ile Leu Lys Asn
945 950

<210> 2476
<211> 951
<212> PRT
<213> Homo sapiens

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<223> /note="Uniprot ID: P63010; "

<220>
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Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1 5 10 15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
20 25 30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
35 40 45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
50 55 60

```
Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Cys Glu
                85                  90                  95

Asp Pro Asn Pro Leu Ile Arg Ala Leu Ala Val Arg Thr Met Gly Cys
            100                 105                 110

Ile Arg Val Asp Lys Ile Thr Glu Tyr Leu Cys Glu Pro Leu Arg Lys
        115                 120                 125

Cys Leu Lys Asp Glu Asp Pro Tyr Val Arg Lys Thr Ala Ala Val Cys
    130                 135                 140

Val Ala Lys Leu His Asp Ile Asn Ala Gln Met Val Glu Asp Gln Gly
145                 150                 155                 160

Phe Leu Asp Ser Leu Arg Asp Leu Ile Ala Asp Ser Asn Pro Met Val
                165                 170                 175

Val Ala Asn Ala Val Ala Ala Leu Ser Glu Ile Ser Glu Ser His Pro
            180                 185                 190

Asn Ser Asn Leu Leu Asp Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu
        195                 200                 205

Thr Ala Leu Asn Glu Cys Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp
    210                 215                 220

Cys Leu Ser Asn Tyr Asn Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile
225                 230                 235                 240

Cys Glu Arg Val Thr Pro Arg Leu Ser His Ala Asn Ser Ala Val Val
                245                 250                 255

Leu Ser Ala Val Lys Val Leu Met Lys Phe Leu Glu Leu Leu Pro Lys
            260                 265                 270

Asp Ser Asp Tyr Tyr Asn Met Leu Leu Lys Lys Leu Ala Pro Pro Leu
        275                 280                 285
```

```
Val Thr Leu Leu Ser Gly Glu Pro Glu Val Gln Tyr Val Ala Leu Arg
    290                 295                 300

Asn Ile Asn Leu Ile Val Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu
305                 310                 315                 320

Ile Lys Val Phe Phe Val Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu
                325                 330                 335

Glu Lys Leu Asp Ile Met Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala
            340                 345                 350

Gln Val Leu Ala Glu Leu Lys Glu Tyr Ala Thr Glu Val Asp Val Asp
        355                 360                 365

Phe Val Arg Lys Ala Val Arg Ala Ile Gly Arg Cys Ala Ile Lys Val
    370                 375                 380

Glu Gln Ser Ala Glu Arg Cys Val Ser Thr Leu Leu Asp Leu Ile Gln
385                 390                 395                 400

Thr Lys Val Asn Tyr Val Val Gln Glu Ala Ile Val Val Ile Arg Asp
                405                 410                 415

Ile Phe Arg Lys Tyr Pro Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu
            420                 425                 430

Cys Glu Asn Leu Asp Ser Leu Asp Glu Pro Asp Ala Arg Ala Ala Met
        435                 440                 445

Ile Trp Ile Val Gly Glu Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu
    450                 455                 460

Leu Leu Glu Ser Phe Leu Glu Gly Phe His Asp Glu Ser Thr Gln Val
465                 470                 475                 480

Gln Leu Thr Leu Leu Thr Ala Ile Val Lys Leu Phe Leu Lys Lys Pro
                485                 490                 495

Ser Glu Thr Gln Glu Leu Val Gln Gln Val Leu Ser Leu Ala Thr Gln
            500                 505                 510

Asp Ser Asp Asn Pro Asp Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg
```

```
        515                 520                 525

Leu Leu Ser Thr Asp Pro Val Thr Ala Lys Glu Val Val Leu Ser Glu
    530                 535                 540

Lys Pro Leu Ile Ser Glu Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu
545                 550                 555                 560

Asp Glu Leu Ile Cys His Ile Gly Ser Leu Ala Ser Val Tyr His Lys
                565                 570                 575

Pro Pro Asn Ala Phe Val Glu Gly Ser His Gly Ile His Arg Lys His
            580                 585                 590

Leu Pro Ile His His Gly Ser Thr Asp Ala Gly Asp Ser Pro Val Gly
        595                 600                 605

Thr Thr Thr Ala Thr Asn Leu Glu Gln Pro Gln Val Ile Pro Ser Gln
    610                 615                 620

Gly Asp Leu Leu Gly Asp Leu Leu Asn Leu Asp Leu Gly Pro Pro Val
625                 630                 635                 640

Asn Val Pro Gln Val Ser Ser Met Gln Met Gly Ala Val Asp Leu Leu
                645                 650                 655

Gly Gly Gly Leu Asp Ser Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile
            660                 665                 670

Gly Gly Ser Pro Ala Val Gly Gln Ser Phe Ile Pro Ser Ser Val Pro
        675                 680                 685

Ala Thr Phe Ala Pro Ser Pro Thr Pro Ala Val Val Ser Ser Gly Leu
    690                 695                 700

Asn Asp Leu Phe Glu Leu Ser Thr Gly Ile Gly Met Ala Pro Gly Gly
705                 710                 715                 720

Tyr Val Ala Pro Lys Ala Val Trp Leu Pro Ala Val Lys Ala Lys Gly
                725                 730                 735

Leu Glu Ile Ser Gly Thr Phe Thr His Arg Gln Gly His Ile Tyr Met
            740                 745                 750
```

```
Glu Met Asn Phe Thr Asn Lys Ala Leu Gln His Met Thr Asp Phe Ala
        755                 760                 765

Ile Gln Phe Asn Lys Asn Ser Phe Gly Val Ile Pro Ser Thr Pro Leu
    770                 775                 780

Ala Ile His Thr Pro Leu Met Pro Asn Gln Ser Ile Asp Val Ser Leu
785                 790                 795                 800

Pro Leu Asn Thr Leu Gly Pro Val Met Lys Met Glu Pro Leu Asn Asn
                805                 810                 815

Leu Gln Val Ala Val Lys Asn Asn Ile Asp Val Phe Tyr Phe Ser Cys
            820                 825                 830

Leu Ile Pro Leu Asn Val Leu Phe Val Glu Asp Gly Lys Met Glu Arg
        835                 840                 845

Gln Val Phe Leu Ala Thr Trp Lys Asp Ile Pro Asn Glu Asn Glu Leu
    850                 855                 860

Gln Phe Gln Ile Lys Glu Cys His Leu Asn Ala Asp Thr Val Ser Ser
865                 870                 875                 880

Lys Leu Gln Asn Asn Asn Val Tyr Thr Ile Ala Lys Arg Asn Val Glu
                885                 890                 895

Gly Gln Asp Met Leu Tyr Gln Ser Leu Lys Leu Thr Asn Gly Ile Trp
            900                 905                 910

Ile Leu Ala Glu Leu Arg Ile Gln Pro Gly Asn Pro Asn Tyr Thr Leu
        915                 920                 925

Ser Leu Lys Cys Arg Ala Pro Glu Val Ser Gln Tyr Ile Tyr Gln Val
    930                 935                 940

Tyr Asp Ser Ile Leu Lys Asn
945                 950
```

<210> 2477
<211> 913
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000484708"

<400> 2477

```
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1               5                  10                  15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20                  25                  30

Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Ser
        35                  40                  45

Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn Leu Glu
    50                  55                  60

Leu Lys Lys Leu Val Tyr Leu Tyr Leu Met Asn Tyr Ala Lys Ser Gln
65                  70                  75                  80

Pro Asp Met Ala Ile Met Ala Val Asn Ser Phe Val Lys Asp Glu Asp
                85                  90                  95

Pro Tyr Val Arg Lys Thr Ala Ala Val Cys Val Ala Lys Leu His Asp
            100                 105                 110

Ile Asn Ala Gln Met Val Glu Asp Gln Gly Phe Leu Asp Ser Leu Arg
        115                 120                 125

Asp Leu Ile Ala Asp Ser Asn Pro Met Val Val Ala Asn Ala Val Ala
    130                 135                 140
```

```
Ala Leu Ser Glu Ile Ser Glu Ser His Pro Asn Ser Asn Leu Leu Asp
145                 150                 155                 160

Leu Asn Pro Gln Asn Ile Asn Lys Leu Leu Thr Ala Leu Asn Glu Cys
                165                 170                 175

Thr Glu Trp Gly Gln Ile Phe Ile Leu Asp Cys Leu Ser Asn Tyr Asn
            180                 185                 190

Pro Lys Asp Asp Arg Glu Ala Gln Ser Ile Cys Glu Arg Val Thr Pro
        195                 200                 205

Arg Leu Ser His Ala Asn Ser Ala Val Val Leu Ser Ala Val Lys Val
    210                 215                 220

Leu Met Lys Phe Leu Glu Leu Leu Pro Lys Asp Ser Asp Tyr Tyr Asn
225                 230                 235                 240

Met Leu Leu Lys Lys Leu Ala Pro Pro Leu Val Thr Leu Leu Ser Gly
                245                 250                 255

Glu Pro Glu Val Gln Tyr Val Ala Leu Arg Asn Ile Asn Leu Ile Val
            260                 265                 270

Gln Lys Arg Pro Glu Ile Leu Lys Gln Glu Ile Lys Val Phe Phe Val
        275                 280                 285

Lys Tyr Asn Asp Pro Ile Tyr Val Lys Leu Glu Lys Leu Asp Ile Met
    290                 295                 300

Ile Arg Leu Ala Ser Gln Ala Asn Ile Ala Gln Val Leu Ala Glu Leu
305                 310                 315                 320

Lys Glu Tyr Ala Thr Glu Val Asp Val Asp Phe Val Arg Lys Ala Val
                325                 330                 335

Arg Ala Ile Gly Arg Cys Ala Ile Lys Val Glu Gln Ser Ala Glu Arg
            340                 345                 350

Cys Val Ser Thr Leu Leu Asp Leu Ile Gln Thr Lys Val Asn Tyr Val
        355                 360                 365

Val Gln Glu Ala Ile Val Val Ile Arg Asp Ile Phe Arg Lys Tyr Pro
```

370 375 380

Asn Lys Tyr Glu Ser Ile Ile Ala Thr Leu Cys Glu Asn Leu Asp Ser
385 390 395 400

Leu Asp Glu Pro Asp Ala Arg Ala Ala Met Ile Trp Ile Val Gly Glu
405 410 415

Tyr Ala Glu Arg Ile Asp Asn Ala Asp Glu Leu Leu Glu Ser Phe Leu
420 425 430

Glu Gly Phe His Asp Glu Ser Thr Gln Val Gln Leu Thr Leu Leu Thr
435 440 445

Ala Ile Val Lys Leu Phe Leu Lys Lys Pro Ser Glu Thr Gln Glu Leu
450 455 460

Val Gln Gln Val Leu Ser Leu Ala Thr Gln Asp Ser Asp Asn Pro Asp
465 470 475 480

Leu Arg Asp Arg Gly Tyr Ile Tyr Trp Arg Leu Leu Ser Thr Asp Pro
485 490 495

Val Thr Ala Lys Glu Val Val Leu Ser Glu Lys Pro Leu Ile Ser Glu
500 505 510

Glu Thr Asp Leu Ile Glu Pro Thr Leu Leu Asp Glu Leu Ile Cys His
515 520 525

Ile Gly Ser Leu Ala Ser Val Tyr His Lys Pro Pro Asn Ala Phe Val
530 535 540

Glu Gly Ser His Gly Ile His Arg Lys His Leu Pro Ile His His Gly
545 550 555 560

Ser Thr Asp Ala Gly Asp Ser Pro Val Gly Thr Thr Thr Ala Thr Asn
565 570 575

Leu Glu Gln Pro Gln Val Ile Pro Ser Gln Gly Asp Leu Leu Gly Asp
580 585 590

Leu Leu Asn Leu Asp Leu Gly Pro Pro Val Asn Val Pro Gln Val Ser
595 600 605

Ser Met Gln Met Gly Ala Val Asp Leu Leu Gly Gly Gly Leu Asp Ser
610 615 620

Leu Leu Gly Ser Asp Leu Gly Gly Gly Ile Gly Gly Ser Pro Ala Val
625 630 635 640

Gly Gln Ser Phe Ile Pro Ser Ser Val Pro Ala Thr Phe Ala Pro Ser
645 650 655

Pro Thr Pro Ala Val Val Ser Ser Gly Leu Asn Asp Leu Phe Glu Leu
660 665 670

Ser Thr Gly Ile Gly Met Ala Pro Gly Gly Tyr Val Ala Pro Lys Ala
675 680 685

Val Trp Leu Pro Ala Val Lys Ala Lys Gly Leu Glu Ile Ser Gly Thr
690 695 700

Phe Thr His Arg Gln Gly His Ile Tyr Met Glu Met Asn Phe Thr Asn
705 710 715 720

Lys Ala Leu Gln His Met Thr Asp Phe Ala Ile Gln Phe Asn Lys Asn
725 730 735

Ser Phe Gly Val Ile Pro Ser Thr Pro Leu Ala Ile His Thr Pro Leu
740 745 750

Met Pro Asn Gln Ser Ile Asp Val Ser Leu Pro Leu Asn Thr Leu Gly
755 760 765

Pro Val Met Lys Met Glu Pro Leu Asn Asn Leu Gln Val Ala Val Lys
770 775 780

Asn Asn Ile Asp Val Phe Tyr Phe Ser Cys Leu Ile Pro Leu Asn Val
785 790 795 800

Leu Phe Val Glu Asp Gly Lys Met Glu Arg Gln Val Phe Leu Ala Thr
805 810 815

Trp Lys Asp Ile Pro Asn Glu Asn Glu Leu Gln Phe Gln Ile Lys Glu
820 825 830

```
Cys His Leu Asn Ala Asp Thr Val Ser Ser Lys Leu Gln Asn Asn Asn
        835                 840                 845

Val Tyr Thr Ile Ala Lys Arg Asn Val Glu Gly Gln Asp Met Leu Tyr
    850                 855                 860

Gln Ser Leu Lys Leu Thr Asn Gly Ile Trp Ile Leu Ala Glu Leu Arg
865                 870                 875                 880

Ile Gln Pro Gly Asn Pro Asn Tyr Thr Leu Ser Leu Lys Cys Arg Ala
                885                 890                 895

Pro Glu Val Ser Gln Tyr Ile Tyr Gln Val Tyr Asp Ser Ile Leu Lys
            900                 905                 910

Asn
```

<210> 2478
<211> 63
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 595; "

<220>
<221> source
<223> /note="Gene Symbol: AP2B1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, beta 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000487324"

<400> 2478

```
Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu Ile Phe
1               5                   10                  15

Glu Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg Lys Glu
            20                  25                  30
```

```
Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp Val Arg
        35                  40                  45


Cys Cys Ser Ser Glu Val Asn Phe Cys Tyr Phe Ser Phe Val Cys
    50                  55                  60


<210> 2479
<211> 435
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 596; "

<220>
<221> source
<223> /note="Gene Symbol: AP2M1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, mu 1
      subunit; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96CW1; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000292807"

<400> 2479
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1               5                  10                  15


Ser Arg Val Tyr Arg Asp Asp Ile Gly Arg Asn Ala Val Asp Ala Phe
            20                  25                  30


Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
        35                  40                  45


Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
    50                  55                  60


Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65                  70                  75                  80


Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
```

```
                85                  90                  95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
            100                 105                 110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
        115                 120                 125

Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln His Gln Thr
    130                 135                 140

Lys Glu Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly
145                 150                 155                 160

Trp Arg Arg Glu Gly Ile Lys Tyr Arg Arg Asn Glu Leu Phe Leu Asp
                165                 170                 175

Val Leu Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu
            180                 185                 190

Ser Ala His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly
        195                 200                 205

Met Pro Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys
    210                 215                 220

Gln Gly Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser
225                 230                 235                 240

Ile Ala Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys
                245                 250                 255

Phe Asp Ser Glu Arg Ser Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe
            260                 265                 270

Glu Leu Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg
        275                 280                 285

Val Ile Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys
    290                 295                 300

Val Val Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile
305                 310                 315                 320
```

```
Glu Val Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile
                325                 330                 335

Cys Met Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val
            340                 345                 350

Trp Lys Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala
        355                 360                 365

Glu Ile Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro
    370                 375                 380

Pro Ile Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys
385                 390                 395                 400

Val Arg Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His
                405                 410                 415

Asp Val Ile Lys Trp Val Arg Tyr Ile Gly Arg Ser Gly Ile Tyr Glu
            420                 425                 430

Thr Arg Cys
        435


<210> 2480
<211> 433
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 596; "

<220>
<221> source
<223> /note="Gene Symbol: AP2M1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, mu 1
      subunit; "

<220>
<221> source
<223> /note="Uniprot ID:  Q96CW1; "
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000371894"

<400> 2480
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1   5   10   15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Arg Asn Ala Val Asp Ala Phe
            20   25   30

Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
        35   40   45

Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
    50   55   60

Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65   70   75   80

Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
                85   90   95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
            100   105   110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
        115   120   125

Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln Thr Lys Glu
    130   135   140

Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly Trp Arg
145   150   155   160

Arg Glu Gly Ile Lys Tyr Arg Arg Asn Glu Leu Phe Leu Asp Val Leu
                165   170   175

Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu Ser Ala
            180   185   190

His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly Met Pro
        195   200   205

```
Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys Gln Gly
    210                 215                 220

Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser Ile Ala
225                 230                 235                 240

Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys Phe Asp
                245                 250                 255

Ser Glu Arg Ser Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe Glu Leu
            260                 265                 270

Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg Val Ile
        275                 280                 285

Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys Val Val
    290                 295                 300

Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile Glu Val
305                 310                 315                 320

Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile Cys Met
                325                 330                 335

Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val Trp Lys
            340                 345                 350

Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala Glu Ile
        355                 360                 365

Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro Pro Ile
    370                 375                 380

Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys Val Arg
385                 390                 395                 400

Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His Asp Val
                405                 410                 415

Ile Lys Trp Val Arg Tyr Ile Gly Arg Ser Gly Ile Tyr Glu Thr Arg
            420                 425                 430

Cys
```

<210> 2481
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 596; "

<220>
<221> source
<223> /note="Gene Symbol: AP2M1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, mu 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000395438"

<400> 2481
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1 5 10 15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Arg Asn Ala Val Asp Ala Phe
20 25 30

Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
35 40 45

Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
50 55 60

Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65 70 75 80

Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
85 90 95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
100 105 110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
115 120 125

```
Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln His Gln Thr
    130                 135                 140

Lys Glu Glu Gln Ser Gln Ile Thr Ser Gln Gly Lys Gly Thr Ala Asp
145                 150                 155                 160

Glu Thr Ser Lys Ser Gly Lys Gln Ser Ile Ala Ile Asp Asp Cys Thr
                165                 170                 175

Phe His Gln Cys Val Arg Leu Ser Lys Phe Asp Ser Glu Arg Ser Ile
            180                 185                 190

Ser Phe Ile Pro Pro Asp Gly Glu Phe Glu Leu Met Arg Tyr Arg Thr
        195                 200                 205

Thr Lys Asp Ile Ile Leu Pro Phe Arg Val Ile Pro Leu Val Arg Glu
    210                 215                 220

Val Gly Arg Thr Lys Leu Glu Val Lys Val Val Ile Lys Ser Asn Phe
225                 230                 235                 240

Lys Pro Ser Leu Leu Ala Gln Lys Ile Glu Val Arg
                245                 250


<210> 2482
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 596; "

<220>
<221> source
<223> /note="Gene Symbol: AP2M1; "

<220>
<221> source
<223> /note="Gene Name:
      adaptor-related prt complex 2, mu 1
      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000402051"
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<400> 2482
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1   5   10   15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Ser Arg Gln Ala Ala Asp Ser
            20   25   30

Ala Val Phe Ser Ser Ser Gly Pro Phe Pro Gly Glu Trp Leu Glu Ala
        35   40   45

Arg Asn Ala Val Asp Ala Phe Arg Val Asn Val Ile His Ala Arg Gln
    50   55   60

Gln Val Arg Ser Pro Val Thr Asn Ile Ala Arg Thr Ser Phe Phe His
65   70   75   80

Val Lys Arg Ser Asn Ile Trp Leu Ala Ala Val Thr Lys Gln Asn Val
                85   90   95

Asn Ala Ala Met Val Phe Glu Phe Leu Tyr Lys Met Cys Asp Val Met
            100   105   110

Ala Ala Tyr Phe Gly Lys Ile Ser Glu Glu Asn Ile Lys Asn Asn Phe
        115   120   125

Val Leu Ile Tyr Glu Leu Leu Asp
    130   135

<210> 2483
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 596; "

<220>
<221> source
<223> /note="Gene Symbol: AP2M1; "

<220>
<221> source
<223> /note="Gene Name:
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      subunit; "

<220>

<221> source
<223> /note="ENSP ID: ENSP00000402592"

<400> 2483
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1   5   10   15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Asn Arg Arg Asn Ala Val Asp
            20   25   30

Ala Phe Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro
        35   40   45

Val Thr Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn
    50   55   60

Ile Trp Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val
65   70   75   80

Phe Glu Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly
                85   90   95

Lys Ile Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu
            100   105   110

Leu Leu Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr
        115   120   125

Gly Ala Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln His
    130   135   140

Gln Thr Lys Glu Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln
145   150   155   160

<210> 2484
<211> 460
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Payload ID: 596; "

<220>
<221> source
<223> /note="Gene Symbol: AP2M1; "

<220>
<221> source
<223> /note="Gene Name:
adaptor-related prt complex 2, mu 1
subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000403362"

<400> 2484
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1 5 10 15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Ser Arg Gln Ala Ala Asp Ser
20 25 30

Ala Val Phe Ser Ser Ser Gly Pro Phe Pro Gly Glu Trp Leu Glu Ala
35 40 45

Asn Arg Arg Asn Ala Val Asp Ala Phe Arg Val Asn Val Ile His Ala
50 55 60

Arg Gln Gln Val Arg Ser Pro Val Thr Asn Ile Ala Arg Thr Ser Phe
65 70 75 80

Phe His Val Lys Arg Ser Asn Ile Trp Leu Ala Ala Val Thr Lys Gln
85 90 95

Asn Val Asn Ala Ala Met Val Phe Glu Phe Leu Tyr Lys Met Cys Asp
100 105 110

Val Met Ala Ala Tyr Phe Gly Lys Ile Ser Glu Glu Asn Ile Lys Asn
115 120 125

Asn Phe Val Leu Ile Tyr Glu Leu Leu Asp Glu Ile Leu Asp Phe Gly
130 135 140

Tyr Pro Gln Asn Ser Glu Thr Gly Ala Leu Lys Thr Phe Ile Thr Gln
145 150 155 160

Gln Gly Ile Lys Ser Gln His Gln Thr Lys Glu Glu Gln Ser Gln Ile
165 170 175

Thr Ser Gln Val Thr Gly Gln Ile Gly Trp Arg Arg Glu Gly Ile Lys
180 185 190

```
Tyr Arg Arg Asn Glu Leu Phe Leu Asp Val Leu Glu Ser Val Asn Leu
        195                 200                 205

Leu Met Ser Pro Gln Gly Gln Val Leu Ser Ala His Val Ser Gly Arg
    210                 215                 220

Val Val Met Lys Ser Tyr Leu Ser Gly Met Pro Glu Cys Lys Phe Gly
225                 230                 235                 240

Met Asn Asp Lys Ile Val Ile Glu Lys Gln Gly Lys Gly Thr Ala Asp
                245                 250                 255

Glu Thr Ser Lys Ser Gly Lys Gln Ser Ile Ala Ile Asp Asp Cys Thr
            260                 265                 270

Phe His Gln Cys Val Arg Leu Ser Lys Phe Asp Ser Glu Arg Ser Ile
        275                 280                 285

Ser Phe Ile Pro Pro Asp Gly Glu Phe Glu Leu Met Arg Tyr Arg Thr
    290                 295                 300

Thr Lys Asp Ile Ile Leu Pro Phe Arg Val Ile Pro Leu Val Arg Glu
305                 310                 315                 320

Val Gly Arg Thr Lys Leu Glu Val Lys Val Val Ile Lys Ser Asn Phe
                325                 330                 335

Lys Pro Ser Leu Leu Ala Gln Lys Ile Glu Val Arg Ile Pro Thr Pro
            340                 345                 350

Leu Asn Thr Ser Gly Val Gln Val Ile Cys Met Lys Gly Lys Ala Lys
        355                 360                 365

Tyr Lys Ala Ser Glu Asn Ala Ile Val Trp Lys Ile Lys Arg Met Ala
    370                 375                 380

Gly Met Lys Glu Ser Gln Ile Ser Ala Glu Ile Glu Leu Leu Pro Thr
385                 390                 395                 400

Asn Asp Lys Lys Lys Trp Ala Arg Pro Pro Ile Ser Met Asn Phe Glu
                405                 410                 415
```

```
Val Pro Phe Ala Pro Ser Gly Leu Lys Val Arg Tyr Leu Lys Val Phe
            420                 425                 430

Glu Pro Lys Leu Asn Tyr Ser Asp His Asp Val Ile Lys Trp Val Arg
        435                 440                 445

Tyr Ile Gly Arg Ser Gly Ile Tyr Glu Thr Arg Cys
    450                 455                 460


<210> 2485
<211> 113
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000404031"

<400> 2485
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1               5                   10                  15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Arg Asn Ala Val Asp Ala Phe
            20                  25                  30

Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
        35                  40                  45

Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
    50                  55                  60

Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65                  70                  75                  80
```

```
Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
                85                  90                  95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
            100                 105                 110

Asp



<210> 2486
<211> 195
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<400> 2486
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1               5                  10                  15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Arg Asn Ala Val Asp Ala Phe
            20                  25                  30

Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
        35                  40                  45

Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
    50                  55                  60

Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65                  70                  75                  80

Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
```

85 90 95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
100 105 110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
115 120 125

Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln His Gln Val
130 135 140

Ser Ser Ser Leu Ser Phe His Pro Cys Ser Phe Ala Leu Phe Leu Gln
145 150 155 160

Ala Leu Pro Phe Gly Ala Tyr Arg Gly Lys Trp Ile Thr Asp Lys Arg
165 170 175

Arg Ala Val Thr Asp His Gln Pro Gly Asn Trp Ala Asp Trp Leu Ala
180 185 190

Ala Arg Gly
195

<210> 2487
<211> 433
<212> PRT
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<220>
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<400> 2487
Met Ile Gly Gly Leu Phe Ile Tyr Asn His Lys Gly Glu Val Leu Ile
1 5 10 15

Ser Arg Val Tyr Arg Asp Asp Ile Gly Arg Asn Ala Val Asp Ala Phe
20 25 30

Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
35 40 45

Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
50 55 60

Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65 70 75 80

Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
85 90 95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
100 105 110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
115 120 125

Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln Thr Lys Glu
130 135 140

Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly Trp Arg
145 150 155 160

Arg Glu Gly Ile Lys Tyr Arg Arg Asn Glu Leu Phe Leu Asp Val Leu
165 170 175

Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu Ser Ala
180 185 190

His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly Met Pro
195 200 205

Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys Gln Gly
210 215 220

```
Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser Ile Ala
225                 230                 235                 240

Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys Phe Asp
                245                 250                 255

Ser Glu Arg Ser Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe Glu Leu
            260                 265                 270

Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg Val Ile
        275                 280                 285

Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys Val Val
    290                 295                 300

Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile Glu Val
305                 310                 315                 320

Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile Cys Met
                325                 330                 335

Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val Trp Lys
            340                 345                 350

Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala Glu Ile
        355                 360                 365

Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro Pro Ile
    370                 375                 380

Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys Val Arg
385                 390                 395                 400

Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His Asp Val
                405                 410                 415

Ile Lys Trp Val Arg Tyr Ile Gly Arg Ser Gly Ile Tyr Glu Thr Arg
            420                 425                 430

Cys
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<210> 2488
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 596; "

<220>
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<223> /note="Gene Symbol: AP2M1; "

<220>
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<223> /note="Gene Name:
adaptor-related prt complex 2, mu 1
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<220>
<221> source
<223> /note="ENSP ID: ENSP00000416688"

<400> 2488
Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile Glu Val Arg Ile Pro Thr
1 5 10 15

Pro Leu Asn Thr Ser Gly Val Gln Val Ile Cys Met Lys Gly Lys Ala
20 25 30

Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val Trp Lys Ile Lys Arg Met
35 40 45

Ala Gly Met Lys Glu Ser Gln Ile Ser Ala Glu Ile Glu Leu Leu Pro
50 55 60

Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro Pro Ile Ser Met Asn Phe
65 70 75 80

Glu Val Trp Gln Arg Arg Gly Leu Glu Ser Cys Gln Gly Met Leu Glu
85 90 95

Asp Leu Leu Glu Ile Ile Pro Ile Asn Cys Cys Thr Leu Glu Val Arg
100 105 110

Lys Leu Arg Pro Arg Lys Lys Asn Trp Leu
115 120

<210> 2489

<211> 434
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: AP2M1; "

<220>
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subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000481563"

<400> 2489

Met	Ile	Gly	Gly	Leu	Phe	Ile	Tyr	Asn	His	Lys	Gly	Glu	Val	Leu	Ile
1				5				10						15	
Ser	Arg	Val	Tyr	Arg	Asp	Asp	Ile	Gly	Arg	Asn	Ala	Val	Asp	Ala	Phe
			20					25					30		
Arg	Val	Asn	Val	Ile	His	Ala	Arg	Gln	Gln	Val	Arg	Ser	Pro	Val	Thr
		35					40					45			
Asn	Ile	Ala	Arg	Thr	Ser	Phe	Phe	His	Val	Lys	Arg	Ser	Asn	Ile	Trp
	50					55					60				
Leu	Ala	Ala	Val	Thr	Lys	Gln	Asn	Val	Asn	Ala	Ala	Met	Val	Phe	Glu
65					70					75					80
Phe	Leu	Tyr	Lys	Met	Cys	Asp	Val	Met	Ala	Ala	Tyr	Phe	Gly	Lys	Ile
				85					90					95	
Ser	Glu	Glu	Asn	Ile	Lys	Asn	Asn	Phe	Val	Leu	Ile	Tyr	Glu	Leu	Leu
			100					105					110		
Asp	Glu	Ile	Leu	Asp	Phe	Gly	Tyr	Pro	Gln	Asn	Ser	Glu	Thr	Gly	Ala
		115					120					125			
Leu	Lys	Thr	Phe	Ile	Thr	Gln	Gln	Gly	Ile	Lys	Ser	Gln	His	Thr	Lys
	130					135					140				

```
Glu Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly Trp
145                 150                 155                 160

Arg Arg Glu Gly Ile Lys Tyr Arg Arg Asn Glu Leu Phe Leu Asp Val
                165                 170                 175

Leu Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu Ser
            180                 185                 190

Ala His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly Met
        195                 200                 205

Pro Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys Gln
    210                 215                 220

Gly Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser Ile
225                 230                 235                 240

Ala Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys Phe
                245                 250                 255

Asp Ser Glu Arg Ser Ile Ser Phe Ile Pro Pro Asp Gly Glu Phe Glu
            260                 265                 270

Leu Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg Val
        275                 280                 285

Ile Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys Val
    290                 295                 300

Val Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile Glu
305                 310                 315                 320

Val Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile Cys
                325                 330                 335

Met Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val Trp
            340                 345                 350

Lys Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala Glu
        355                 360                 365
```

```
Ile Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro Pro
    370                 375                 380

Ile Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys Val
385                 390                 395                 400

Arg Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His Asp
                405                 410                 415

Val Ile Lys Trp Val Arg Tyr Ile Gly Arg Ser Gly Ile Tyr Glu Thr
            420                 425                 430

Arg Cys
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<210> 2490
<211> 142
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID: P53680; "

<220>
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<400> 2490

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Met Ile Arg Phe Ile Leu Ile Gln Asn Arg Ala Gly Lys Thr Arg Leu
1               5                   10                  15

Ala Lys Trp Tyr Met Gln Phe Asp Asp Asp Glu Lys Gln Lys Leu Ile
            20                  25                  30
```

```
Glu Glu Val His Ala Val Val Thr Val Arg Asp Ala Lys His Thr Asn
        35                  40                  45

Phe Val Glu Phe Arg Asn Phe Lys Ile Ile Tyr Arg Arg Tyr Ala Gly
    50                  55                  60

Leu Tyr Phe Cys Ile Cys Val Asp Val Asn Asp Asn Asn Leu Ala Tyr
65                  70                  75                  80

Leu Glu Ala Ile His Asn Phe Val Glu Val Leu Asn Glu Tyr Phe His
                85                  90                  95

Asn Val Cys Glu Leu Asp Leu Val Phe Asn Phe Tyr Lys Val Tyr Thr
            100                 105                 110

Val Val Asp Glu Met Phe Leu Ala Gly Glu Ile Arg Glu Thr Ser Gln
        115                 120                 125

Thr Lys Val Leu Lys Gln Leu Leu Met Leu Gln Ser Leu Glu
    130                 135                 140


<210> 2491
<211> 156
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Gene Symbol: AP2S1; "

<220>
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      subunit; "

<220>
<221> source
<223> /note="ENSP ID: ENSP00000263271"

<400> 2491
Met Ile Arg Phe Ile Leu Ile Gln Asn Arg Ala Gly Lys Thr Arg Leu
1               5                   10                  15

Ala Lys Trp Tyr Met Gln Phe Asp Asp Asp Glu Lys Gln Lys Leu Ile
```

```
            20                  25                  30

Glu Glu Val His Ala Val Val Thr Val Arg Asp Ala Lys His Thr Asn
        35                  40                  45

Phe Val Glu Val Leu Ala Ile Ser Val Ala Asp Ser Leu Ser Val Leu
    50                  55                  60

Gln Phe Arg Asn Phe Lys Ile Ile Tyr Arg Arg Tyr Ala Gly Leu Tyr
65                  70                  75                  80

Phe Cys Ile Cys Val Asp Val Asn Asp Asn Asn Leu Ala Tyr Leu Glu
                85                  90                  95

Ala Ile His Asn Phe Val Glu Val Leu Asn Glu Tyr Phe His Asn Val
            100                 105                 110

Cys Glu Leu Asp Leu Val Phe Asn Phe Tyr Lys Val Tyr Thr Val Val
        115                 120                 125

Asp Glu Met Phe Leu Ala Gly Glu Ile Arg Glu Thr Ser Gln Thr Lys
    130                 135                 140

Val Leu Lys Gln Leu Leu Met Leu Gln Ser Leu Glu
145                 150                 155


<210> 2492
<211> 158
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Symbol: AP2S1; "

<220>
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<220>
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<223> /note="ENSP ID: ENSP00000470176"
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<400> 2492
Met Lys Leu Lys Gly Leu Gly Lys Arg Cys Lys Arg Arg Glu Asp Leu
1 5 10 15

Glu Ile Arg Phe Ile Leu Ile Gln Asn Arg Ala Gly Lys Thr Arg Leu
20 25 30

Ala Lys Trp Tyr Met Gln Phe Asp Asp Asp Glu Lys Gln Lys Leu Ile
35 40 45

Glu Glu Val His Ala Val Val Thr Val Arg Asp Ala Lys His Thr Asn
50 55 60

Phe Val Glu Phe Arg Asn Phe Lys Ile Ile Tyr Arg Arg Tyr Ala Gly
65 70 75 80

Leu Tyr Phe Cys Ile Cys Val Asp Val Asn Asp Asn Asn Leu Ala Tyr
85 90 95

Leu Glu Ala Ile His Asn Phe Val Glu Val Leu Asn Glu Tyr Phe His
100 105 110

Asn Val Cys Glu Leu Asp Leu Val Phe Asn Phe Tyr Lys Val Tyr Thr
115 120 125

Val Val Asp Glu Met Phe Leu Ala Gly Glu Ile Arg Glu Thr Ser Gln
130 135 140

Thr Lys Val Leu Lys Gln Leu Leu Met Leu Gln Ser Leu Glu
145 150 155

<210> 2493
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Payload ID: 597; "

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<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000470235"

<400> 2493
Met Gln Phe Asp Asp Asp Glu Lys Gln Lys Leu Ile Glu Glu Val His
1 5 10 15

Ala Val Val Thr Val Arg Asp Ala Lys His Thr Asn Phe Val Glu Phe
20 25 30

Arg Asn Phe Lys Ile Ile Tyr Arg Arg Tyr Ala Gly Leu Tyr Phe Cys
35 40 45

Ile Cys Val Asp Val Asn Asp Asn Asn Leu Ala Tyr Leu Glu Ala Ile
50 55 60

His Asn Phe Val Glu Val Leu Asn Glu Tyr Phe His Asn Val Cys Glu
65 70 75 80

Leu Asp Leu Val Phe Asn Phe Tyr Lys Val Tyr Thr Val Val Asp Glu
85 90 95

Met Phe Leu Ala Gly Glu Ile Arg Glu Thr Ser Gln Thr Lys Val Leu
100 105 110

Lys Gln Leu Leu Met Leu Gln Ser Leu Glu
115 120

<210> 2494
<211> 104
<212> PRT
<213> Homo sapiens

<220>
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<223> /note="Gene Name:

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<220>
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<223> /note="Uniprot ID: P53680; "

<220>
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<400> 2494
Met Ile Arg Phe Ile Leu Ile Gln Asn Arg Ala Gly Lys Thr Arg Leu
1   5   10   15

Ala Lys Trp Tyr Met Gln Phe Asp Asp Asp Glu Lys Gln Lys Leu Ile
            20   25   30

Glu Glu Val His Ala Val Val Thr Val Arg Asp Ala Lys His Thr Asn
        35   40   45

Phe Val Glu Val Leu Asn Glu Tyr Phe His Asn Val Cys Glu Leu Asp
    50   55   60

Leu Val Phe Asn Phe Tyr Lys Val Tyr Thr Val Val Asp Glu Met Phe
65   70   75   80

Leu Ala Gly Glu Ile Arg Glu Thr Ser Gln Thr Lys Val Leu Lys Gln
                85   90   95

Leu Leu Met Leu Gln Ser Leu Glu
            100

<210> 2495
<211> 144
<212> PRT
<213> Homo sapiens

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<220>
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<223> /note="ENSP ID: ENSP00000471340"

<400> 2495
Met Val Trp Ile Arg Phe Ile Leu Ile Gln Asn Arg Ala Gly Lys Thr
1   5   10   15

Arg Leu Ala Lys Trp Tyr Met Gln Phe Asp Asp Asp Glu Lys Gln Lys
            20   25   30

Leu Ile Glu Glu Val His Ala Val Val Thr Val Arg Asp Ala Lys His
        35   40   45

Thr Asn Phe Val Glu Phe Arg Asn Phe Lys Ile Ile Tyr Arg Arg Tyr
    50   55   60

Ala Gly Leu Tyr Phe Cys Ile Cys Val Asp Val Asn Asp Asn Asn Leu
65   70   75   80

Ala Tyr Leu Glu Ala Ile His Asn Phe Val Glu Val Leu Asn Glu Tyr
                85   90   95

Phe His Asn Val Cys Glu Leu Asp Leu Val Phe Asn Phe Tyr Lys Val
            100   105   110

Tyr Thr Val Val Asp Glu Met Phe Leu Ala Gly Glu Ile Arg Glu Thr
        115   120   125

Ser Gln Thr Lys Val Leu Lys Gln Leu Leu Met Leu Gln Ser Leu Glu
    130   135   140

<210> 2496
<211> 92
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>

<221> source
<223> /note="Gene Name:
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<220>
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<223> /note="ENSP ID: ENSP00000472080"

<400> 2496
Met Phe Arg Asn Phe Lys Ile Ile Tyr Arg Arg Tyr Ala Gly Leu Tyr
1 5 10 15

Phe Cys Ile Cys Val Asp Val Asn Asp Asn Asn Leu Ala Tyr Leu Glu
20 25 30

Ala Ile His Asn Phe Val Glu Val Leu Asn Glu Tyr Phe His Asn Val
35 40 45

Cys Glu Leu Asp Leu Val Phe Asn Phe Tyr Lys Val Tyr Thr Val Val
50 55 60

Asp Glu Met Phe Leu Ala Gly Glu Ile Arg Glu Thr Ser Gln Thr Lys
65 70 75 80

Val Leu Lys Gln Leu Leu Met Leu Gln Ser Leu Glu
85 90

<210> 2497
<211> 1094
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> /note="Uniprot ID: O00203; "

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<400> 2497
Met Ser Ser Asn Ser Phe Pro Tyr Asn Glu Gln Ser Gly Gly Gly Glu
1   5   10   15

Ala Thr Glu Leu Gly Gln Glu Ala Thr Ser Thr Ile Ser Pro Ser Gly
            20   25   30

Ala Phe Gly Leu Phe Ser Ser Asp Leu Lys Lys Asn Glu Asp Leu Lys
        35   40   45

Gln Met Leu Glu Ser Asn Lys Asp Ser Ala Lys Leu Asp Ala Met Lys
    50   55   60

Arg Ile Val Gly Met Ile Ala Lys Gly Lys Asn Ala Ser Glu Leu Phe
65   70   75   80

Pro Ala Val Val Lys Asn Val Ala Ser Lys Asn Ile Glu Ile Lys Lys
                85   90   95

Leu Val Tyr Val Tyr Leu Val Arg Tyr Ala Glu Glu Gln Gln Asp Leu
            100   105   110

Ala Leu Leu Ser Ile Ser Thr Phe Gln Arg Ala Leu Lys Asp Pro Asn
        115   120   125

Gln Leu Ile Arg Ala Ser Ala Leu Arg Val Leu Ser Ser Ile Arg Val
    130   135   140

Pro Ile Ile Val Pro Ile Met Met Leu Ala Ile Lys Glu Ala Ser Ala
145   150   155   160

Asp Leu Ser Pro Tyr Val Arg Lys Asn Ala Ala His Ala Ile Gln Lys
                165   170   175

Leu Tyr Ser Leu Asp Pro Glu Gln Lys Glu Met Leu Ile Glu Val Ile
            180   185   190

Glu Lys Leu Leu Lys Asp Lys Ser Thr Leu Val Ala Gly Ser Val Val
        195   200   205

```
Met Ala Phe Glu Glu Val Cys Pro Asp Arg Ile Asp Leu Ile His Lys
    210                 215                 220

Asn Tyr Arg Lys Leu Cys Asn Leu Leu Val Asp Val Glu Glu Trp Gly
225                 230                 235                 240

Gln Val Val Ile Ile His Met Leu Thr Arg Tyr Ala Arg Thr Gln Phe
                245                 250                 255

Val Ser Pro Trp Lys Glu Gly Asp Glu Leu Glu Asp Asn Gly Lys Asn
            260                 265                 270

Phe Tyr Glu Ser Asp Asp Asp Gln Lys Glu Lys Thr Asp Lys Lys Lys
        275                 280                 285

Lys Pro Tyr Thr Met Asp Pro Asp His Arg Leu Leu Ile Arg Asn Thr
    290                 295                 300

Lys Pro Leu Leu Gln Ser Arg Asn Ala Ala Val Val Met Ala Val Ala
305                 310                 315                 320

Gln Leu Tyr Trp His Ile Ser Pro Lys Ser Glu Ala Gly Ile Ile Ser
                325                 330                 335

Lys Ser Leu Val Arg Leu Leu Arg Ser Asn Arg Glu Val Gln Tyr Ile
            340                 345                 350

Val Leu Gln Asn Ile Ala Thr Met Ser Ile Gln Arg Lys Gly Met Phe
        355                 360                 365

Glu Pro Tyr Leu Lys Ser Phe Tyr Val Arg Ser Thr Asp Pro Thr Met
    370                 375                 380

Ile Lys Thr Leu Lys Leu Glu Ile Leu Thr Asn Leu Ala Asn Glu Ala
385                 390                 395                 400

Asn Ile Ser Thr Leu Leu Arg Glu Phe Gln Thr Tyr Val Lys Ser Gln
                405                 410                 415

Asp Lys Gln Phe Ala Ala Ala Thr Ile Gln Thr Ile Gly Arg Cys Ala
            420                 425                 430

Thr Asn Ile Leu Glu Val Thr Asp Thr Cys Leu Asn Gly Leu Val Cys
```

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        435                 440                 445

Leu Leu Ser Asn Arg Asp Glu Ile Val Val Ala Glu Ser Val Val Val
    450                 455                 460

Ile Lys Lys Leu Leu Gln Met Gln Pro Ala Gln His Gly Glu Ile Ile
465                 470                 475                 480

Lys His Met Ala Lys Leu Leu Asp Ser Ile Thr Val Pro Val Ala Arg
                485                 490                 495

Ala Ser Ile Leu Trp Leu Ile Gly Glu Asn Cys Glu Arg Val Pro Lys
            500                 505                 510

Ile Ala Pro Asp Val Leu Arg Lys Met Ala Lys Ser Phe Thr Ser Glu
        515                 520                 525

Asp Asp Leu Val Lys Leu Gln Ile Leu Asn Leu Gly Ala Lys Leu Tyr
    530                 535                 540

Leu Thr Asn Ser Lys Gln Thr Lys Leu Leu Thr Gln Tyr Ile Leu Asn
545                 550                 555                 560

Leu Gly Lys Tyr Asp Gln Asn Tyr Asp Ile Arg Asp Arg Thr Arg Phe
                565                 570                 575

Ile Arg Gln Leu Ile Val Pro Asn Val Lys Ser Gly Ala Leu Ser Lys
            580                 585                 590

Tyr Ala Lys Lys Ile Phe Leu Ala Gln Lys Pro Ala Pro Leu Leu Glu
        595                 600                 605

Ser Pro Phe Lys Asp Arg Asp His Phe Gln Leu Gly Thr Leu Ser His
    610                 615                 620

Thr Leu Asn Ile Lys Ala Thr Gly Tyr Leu Glu Leu Ser Asn Trp Pro
625                 630                 635                 640

Glu Val Ala Pro Asp Pro Ser Val Arg Asn Val Glu Val Ile Glu Leu
                645                 650                 655

Ala Lys Glu Trp Thr Pro Ala Gly Lys Ala Lys Gln Glu Asn Ser Ala
            660                 665                 670
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Lys Lys Phe Tyr Ser Glu Ser Glu Glu Glu Glu Asp Ser Ser Asp Ser
        675                 680                 685

Ser Ser Asp Ser Glu Ser Glu Ser Gly Ser Glu Ser Gly Glu Gln Gly
    690                 695                 700

Glu Ser Gly Glu Glu Gly Asp Ser Asn Glu Asp Ser Ser Glu Asp Ser
705                 710                 715                 720

Ser Ser Glu Gln Asp Ser Glu Ser Gly Arg Glu Ser Gly Leu Glu Asn
                725                 730                 735

Lys Arg Thr Ala Lys Arg Asn Ser Lys Ala Lys Gly Lys Ser Asp Ser
            740                 745                 750

Glu Asp Gly Glu Lys Glu Asn Glu Lys Ser Lys Thr Ser Asp Ser Ser
        755                 760                 765

Asn Asp Glu Ser Ser Ser Ile Glu Asp Ser Ser Ser Asp Ser Glu Ser
    770                 775                 780

Glu Ser Glu Pro Glu Ser Glu Ser Glu Ser Arg Arg Val Thr Lys Glu
785                 790                 795                 800

Lys Glu Lys Lys Thr Lys Gln Asp Arg Thr Pro Leu Thr Lys Asp Val
                805                 810                 815

Ser Leu Leu Asp Leu Asp Asp Phe Asn Pro Val Ser Thr Pro Val Ala
            820                 825                 830

Leu Pro Thr Pro Ala Leu Ser Pro Ser Leu Met Ala Asp Leu Glu Gly
        835                 840                 845

Leu His Leu Ser Thr Ser Ser Ser Val Ile Ser Val Ser Thr Pro Ala
    850                 855                 860

Phe Val Pro Thr Lys Thr His Val Leu Leu His Arg Met Ser Gly Lys
865                 870                 875                 880

Gly Leu Ala Ala His Tyr Phe Phe Pro Arg Gln Pro Cys Ile Phe Gly
                885                 890                 895
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Asp Lys Met Val Ser Ile Gln Ile Thr Leu Asn Asn Thr Thr Asp Arg
            900                 905                 910

Lys Ile Glu Asn Ile His Ile Gly Glu Lys Lys Leu Pro Ile Gly Met
        915                 920                 925

Lys Met His Val Phe Asn Pro Ile Asp Ser Leu Glu Pro Glu Gly Ser
    930                 935                 940

Ile Thr Val Ser Met Gly Ile Asp Phe Cys Asp Ser Thr Gln Thr Ala
945                 950                 955                 960

Ser Phe Gln Leu Cys Thr Lys Asp Asp Cys Phe Asn Val Asn Ile Gln
                965                 970                 975

Pro Pro Val Gly Glu Leu Leu Leu Pro Val Ala Met Ser Glu Lys Asp
            980                 985                 990

Phe Lys Lys Glu Gln Gly Val Leu  Thr Gly Met Asn Glu  Thr Ser
Ala
        995                 1000                1005

Val Ile  Ile Ala Ala Pro Gln  Asn Phe Thr Pro Ser  Val Ile Phe
    1010                1015                1020

Gln Lys  Val Val Asn Val Ala  Asn Val Gly Ala Val  Pro Ser Gly
    1025                1030                1035

Gln Asp  Asn Ile His Arg Phe  Ala Ala Lys Thr Val  His Ser Gly
    1040                1045                1050

Ser Leu  Met Leu Val Thr Val  Glu Leu Lys Glu Gly  Ser Thr Ala
    1055                1060                1065

Gln Leu  Ile Ile Asn Thr Glu  Lys Thr Val Ile Gly  Ser Val Leu
    1070                1075                1080

Leu Arg  Glu Leu Lys Pro Val  Leu Ser Gln Gly
    1085                1090
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