SEQUENCE LISTING

<110> University of Washington
Institute for Research in Biomedicine
KING, Neil P
BAKER, David
NICKERSON, Brooke
STEWART, Lance J
PEREZ, Laurent
LANZAVECCHIA, Antonio
MARCANDALLI, Jessica

<120> Self-assembling protein nanostructures displaying paramyxovirus and/or pneumovirus F proteins and their use

<130> 17-341-PCT

<150> US 62/481,331
<151> 2017-04-01

<160> 101

<170> PatentIn version 3.5

<210> 1
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-34A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 1

Met Glu Gly Met Asp Pro Leu Ala Val Leu Ala Glu Ser Arg Leu Leu
1 5 10 15

Pro Leu Leu Thr Val Arg Gly Gly Glu Asp Leu Ala Gly Leu Ala Thr
20 25 30

Val Leu Glu Leu Met Gly Val Gly Ala Leu Glu Ile Thr Leu Arg Thr
35 40 45

```
Glu Lys Gly Leu Glu Ala Leu Lys Ala Leu Arg Lys Ser Gly Leu Leu
    50                  55                  60

Leu Gly Ala Gly Thr Val Arg Ser Pro Lys Glu Ala Glu Ala Ala Leu
65                  70                  75                  80

Glu Ala Gly Ala Ala Phe Leu Val Ser Pro Gly Leu Leu Glu Glu Val
                85                  90                  95

Ala Ala Leu Ala Gln Ala Arg Gly Val Pro Tyr Leu Pro Gly Val Leu
            100                 105                 110

Thr Pro Thr Glu Val Glu Arg Ala Leu Ala Leu Gly Leu Ser Ala Leu
        115                 120                 125

Lys Phe Phe Pro Ala Glu Pro Phe Gln Gly Val Arg Val Leu Arg Ala
    130                 135                 140

Tyr Ala Glu Val Phe Pro Glu Val Arg Phe Leu Pro Thr Gly Gly Ile
145                 150                 155                 160

Lys Glu Glu His Leu Pro His Tyr Ala Ala Leu Pro Asn Leu Leu Ala
                165                 170                 175

Val Gly Gly Ser Trp Leu Leu Gln Gly Asp Leu Ala Ala Val Met Lys
            180                 185                 190

Lys Val Lys Ala Ala Lys Ala Leu Leu Ser Pro Gln Ala Pro Gly
        195                 200                 205
```

<210> 2
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-34B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 2

```
Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1               5                   10                  15


Met Ala Glu Ala Ala Ile Arg Thr Leu Lys Ala Leu Ser Pro Asn Ile
            20                  25                  30


Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
        35                  40                  45


Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
    50                  55                  60


Gly Met Pro Gly Lys Ala Glu Lys Asp Lys Val Cys Ala His Glu Ala
65                  70                  75                  80


Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
                85                  90                  95


Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Asp Glu Leu Asp
            100                 105                 110


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


Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
    130                 135                 140


Arg Gln Gly Arg Glu Asp Ala Gly Pro Ala Arg Glu
145                 150                 155
```

<210> 3
<211> 156

<212> PRT
<213> Artificial Sequence

<220>
<223> I53-40A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 3

```
Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1               5                  10                  15


Met Ala Ser Ala Ala Ile Leu Thr Leu Lys Met Glu Ser Pro Asn Ile
            20                  25                  30


Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
        35                  40                  45


Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
    50                  55                  60


Gly Met Pro Gly Lys Ala Glu Lys Asp Lys Val Cys Ala His Glu Ala
65                  70                  75                  80


Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
                85                  90                  95


Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Ala Glu Leu Lys
            100                 105                 110


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


Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
    130                 135                 140
```

```
Arg Gln Gly Phe Glu Asp Ala Gly Pro Ala Arg Glu
145                 150                 155


<210>  4
<211>  209
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-40B


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  4

Met Ser Thr Ile Asn Asn Gln Leu Lys Ala Leu Lys Val Ile Pro Val
1               5                   10                  15


Ile Ala Ile Asp Asn Ala Glu Asp Ile Ile Pro Leu Gly Lys Val Leu
            20                  25                  30


Ala Glu Asn Gly Leu Pro Ala Ala Glu Ile Thr Phe Arg Ser Ser Ala
        35                  40                  45


Ala Val Lys Ala Ile Met Leu Leu Arg Ser Ala Gln Pro Glu Met Leu
    50                  55                  60


Ile Gly Ala Gly Thr Ile Leu Asn Gly Val Gln Ala Leu Ala Ala Lys
65                  70                  75                  80


Glu Ala Gly Ala Thr Phe Val Val Ser Pro Gly Phe Asn Pro Asn Thr
                85                  90                  95


Val Arg Ala Cys Gln Ile Ile Gly Ile Asp Ile Val Pro Gly Val Asn
            100                 105                 110


Asn Pro Ser Thr Val Glu Ala Ala Leu Glu Met Gly Leu Thr Thr Leu
        115                 120                 125
```

```
Lys Phe Phe Pro Ala Glu Ala Ser Gly Gly Ile Ser Met Val Lys Ser
    130                 135                 140


Leu Val Gly Pro Tyr Gly Asp Ile Arg Leu Met Pro Thr Gly Gly Ile
145                 150                 155                 160


Thr Pro Ser Asn Ile Asp Asn Tyr Leu Ala Ile Pro Gln Val Leu Ala
                165                 170                 175


Cys Gly Gly Thr Trp Met Val Asp Lys Lys Leu Val Thr Asn Gly Glu
            180                 185                 190


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


Pro
```

<210> 5
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 5

```
Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Thr Asp Val Pro
1               5                   10                  15


Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
            20                  25                  30
```

```
Lys Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
        35                  40                  45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
    50                  55                  60

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

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
                85                  90                  95

Ile His Phe Val Asn Leu Asn Gly Asp Asp Val Gly Trp Asn Gly Thr
            100                 105                 110

Thr Phe
```

<210> 6
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 6

```
Met Asn Gln His Ser His Lys Asp Tyr Glu Thr Val Arg Ile Ala Val
1               5                   10                  15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
            20                  25                  30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45
```

```
Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95

Asp Gly Met Met Asn Val Gln Leu Ser Thr Gly Val Pro Val Leu Ser
            100                 105                 110

Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Ala Glu His His Arg
        115                 120                 125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
    130                 135                 140

Cys Ile Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145                 150                 155
```

<210> 7
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 7

```
Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1               5                   10                  15
```

```
Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
            20                  25                  30

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
        35                  40                  45

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

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65                  70                  75                  80

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
                85                  90                  95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
            100                 105                 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu
        115                 120                 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
    130                 135                 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
145                 150                 155                 160

Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly
                165                 170                 175

Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys
            180                 185                 190

Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
        195                 200                 205
```

<210> 8
<211> 157

<212> PRT
<213> Artificial Sequence

<220>
<223> I53-50B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 8

```
Met Asn Gln His Ser His Lys Asp Tyr Glu Thr Val Arg Ile Ala Val
1               5                   10                  15


Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
            20                  25                  30


Phe Glu Ala Ala Met Ala Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45


Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60


Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80


Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95


Asp Gly Met Met Asn Val Gln Leu Ser Thr Gly Val Pro Val Leu Ser
            100                 105                 110


Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Asp Ala His Thr Leu
        115                 120                 125


Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
    130                 135                 140
```

```
Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145                 150                 155


<210>  9
<211>  177
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-51A


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  9

Met Phe Thr Lys Ser Gly Asp Asp Gly Asn Thr Asn Val Ile Asn Lys
1               5                   10                  15


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


Glu Leu Asn Ser Phe Ile Gly Phe Ala Ile Ser Lys Ile Pro Trp Glu
        35                  40                  45


Asp Met Lys Lys Asp Leu Glu Arg Val Gln Val Glu Leu Phe Glu Ile
    50                  55                  60


Gly Glu Asp Leu Ser Thr Gln Ser Ser Lys Lys Lys Ile Asp Glu Ser
65                  70                  75                  80


Tyr Val Leu Trp Leu Leu Ala Ala Thr Ala Ile Tyr Arg Ile Glu Ser
                85                  90                  95


Gly Pro Val Lys Leu Phe Val Ile Pro Gly Gly Ser Glu Glu Ala Ser
            100                 105                 110


Val Leu His Val Thr Arg Ser Val Ala Arg Arg Val Glu Arg Asn Ala
        115                 120                 125
```

```
Val Lys Tyr Thr Lys Glu Leu Pro Glu Ile Asn Arg Met Ile Ile Val
    130                 135                 140

Tyr Leu Asn Arg Leu Ser Ser Leu Leu Phe Ala Met Ala Leu Val Ala
145                 150                 155                 160

Asn Lys Arg Arg Asn Gln Ser Glu Lys Ile Tyr Glu Ile Gly Lys Ser
                165                 170                 175

Trp
```

<210> 10
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-51B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 10

```
Met Asn Gln His Ser His Lys Asp Tyr Glu Thr Val Arg Ile Ala Val
1               5                   10                  15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Gln Cys Val Arg Ala
            20                  25                  30

Phe Glu Glu Ala Met Ala Asp Ala Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60
```

```
Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80


Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95


Asp Gly Met Met Asn Val Gln Leu Ser Thr Gly Val Pro Val Leu Ser
            100                 105                 110


Ala Val Leu Thr Pro His Arg Tyr Arg Ser Ser Arg Glu His His Glu
        115                 120                 125


Phe Phe Arg Glu His Phe Met Val Lys Gly Val Glu Ala Ala Ala Ala
    130                 135                 140


Cys Ile Thr Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145                 150                 155


<210>  11
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I52-03A


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  11

Met Gly His Thr Lys Gly Pro Thr Pro Gln Gln His Asp Gly Ser Ala
1               5                   10                  15


Leu Arg Ile Gly Ile Val His Ala Arg Trp Asn Lys Thr Ile Ile Met
            20                  25                  30


Pro Leu Leu Ile Gly Thr Ile Ala Lys Leu Leu Glu Cys Gly Val Lys
        35                  40                  45
```

```
Ala Ser Asn Ile Val Val Gln Ser Val Pro Gly Ser Trp Glu Leu Pro
    50                  55                  60

Ile Ala Val Gln Arg Leu Tyr Ser Ala Ser Gln Leu Gln Thr Pro Ser
65                  70                  75                  80

Ser Gly Pro Ser Leu Ser Ala Gly Asp Leu Leu Gly Ser Ser Thr Thr
                85                  90                  95

Asp Leu Thr Ala Leu Pro Thr Thr Thr Ala Ser Ser Thr Gly Pro Phe
            100                 105                 110

Asp Ala Leu Ile Ala Ile Gly Val Leu Ile Lys Gly Glu Thr Met His
        115                 120                 125

Phe Glu Tyr Ile Ala Asp Ser Val Ser His Gly Leu Met Arg Val Gln
    130                 135                 140

Leu Asp Thr Gly Val Pro Val Ile Phe Gly Val Leu Thr Val Leu Thr
145                 150                 155                 160

Asp Asp Gln Ala Lys Ala Arg Ala Gly Val Ile Glu Gly Ser His Asn
                165                 170                 175

His Gly Glu Asp Trp Gly Leu Ala Ala Val Glu Met Gly Val Arg Arg
            180                 185                 190

Arg Asp Trp Ala Ala Gly Lys Thr Glu
        195                 200
```

<210> 12
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> I52-03B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 12

```
Met Tyr Glu Val Asp His Ala Asp Val Tyr Asp Leu Phe Tyr Leu Gly
1               5                   10                  15


Arg Gly Lys Asp Tyr Ala Ala Glu Ala Ser Asp Ile Ala Asp Leu Val
            20                  25                  30


Arg Ser Arg Thr Pro Glu Ala Ser Ser Leu Leu Asp Val Ala Cys Gly
        35                  40                  45


Thr Gly Thr His Leu Glu His Phe Thr Lys Glu Phe Gly Asp Thr Ala
    50                  55                  60


Gly Leu Glu Leu Ser Glu Asp Met Leu Thr His Ala Arg Lys Arg Leu
65                  70                  75                  80


Pro Asp Ala Thr Leu His Gln Gly Asp Met Arg Asp Phe Gln Leu Gly
                85                  90                  95


Arg Lys Phe Ser Ala Val Val Ser Met Phe Ser Ser Val Gly Tyr Leu
            100                 105                 110


Lys Thr Val Ala Glu Leu Gly Ala Ala Val Ala Ser Phe Ala Glu His
        115                 120                 125


Leu Glu Pro Gly Gly Val Val Val Val Glu Pro Trp Trp Phe Pro Glu
    130                 135                 140


Thr Phe Ala Asp Gly Trp Val Ser Ala Asp Val Val Arg Arg Asp Gly
145                 150                 155                 160


Arg Thr Val Ala Arg Val Ser His Ser Val Arg Glu Gly Asn Ala Thr
                165                 170                 175
```

```
Arg Met Glu Val His Phe Thr Val Ala Asp Pro Gly Lys Gly Val Arg
            180                 185                 190


His Phe Ser Asp Val His Leu Ile Thr Leu Phe His Gln Arg Glu Tyr
        195                 200                 205


Glu Ala Ala Phe Met Ala Ala Gly Leu Arg Val Glu Tyr Leu Glu Gly
    210                 215                 220


Gly Pro Ser Gly Arg Gly Leu Phe Val Gly Val Pro Ala
225                 230                 235
```

<210> 13
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> I52-32A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 13

```
Met Gly Met Lys Glu Lys Phe Val Leu Ile Ile Thr His Gly Asp Phe
1               5                   10                  15


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


Asn Val His Thr Val Gly Leu Asn Leu Gly Asp Asn Ile Glu Lys Val
        35                  40                  45


Ala Lys Glu Val Met Arg Ile Ile Ile Ala Lys Leu Ala Glu Asp Lys
    50                  55                  60
```

```
Glu Ile Ile Ile Val Val Asp Leu Phe Gly Gly Ser Pro Phe Asn Ile
65                  70                  75                  80


Ala Leu Glu Met Met Lys Thr Phe Asp Val Lys Val Ile Thr Gly Ile
                85                  90                  95


Asn Met Pro Met Leu Val Glu Leu Leu Thr Ser Ile Asn Val Tyr Asp
            100                 105                 110


Thr Thr Glu Leu Leu Glu Asn Ile Ser Lys Ile Gly Lys Asp Gly Ile
        115                 120                 125


Lys Val Ile Glu Lys Ser Ser Leu Lys Met
    130                 135


<210>  14
<211>  154
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I52-32B


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  14

Met Lys Tyr Asp Gly Ser Lys Leu Arg Ile Gly Ile Leu His Ala Arg
1               5                   10                  15


Trp Asn Leu Glu Ile Ile Ala Ala Leu Val Ala Gly Ala Ile Lys Arg
            20                  25                  30


Leu Gln Glu Phe Gly Val Lys Ala Glu Asn Ile Ile Ile Glu Thr Val
        35                  40                  45


Pro Gly Ser Phe Glu Leu Pro Tyr Gly Ser Lys Leu Phe Val Glu Lys
    50                  55                  60
```

```
Gln Lys Arg Leu Gly Lys Pro Leu Asp Ala Ile Ile Pro Ile Gly Val
65                  70                  75                  80


Leu Ile Lys Gly Ser Thr Met His Phe Glu Tyr Ile Cys Asp Ser Thr
                85                  90                  95


Thr His Gln Leu Met Lys Leu Asn Phe Glu Leu Gly Ile Pro Val Ile
            100                 105                 110


Phe Gly Val Leu Thr Cys Leu Thr Asp Glu Gln Ala Glu Ala Arg Ala
        115                 120                 125


Gly Leu Ile Glu Gly Lys Met His Asn His Gly Glu Asp Trp Gly Ala
    130                 135                 140


Ala Ala Val Glu Met Ala Thr Lys Phe Asn
145                 150


<210>  15
<211>  164
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I52-33A


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  15

Met Ala Val Lys Gly Leu Gly Glu Val Asp Gln Lys Tyr Asp Gly Ser
1               5                   10                  15


Lys Leu Arg Ile Gly Ile Leu His Ala Arg Trp Asn Arg Lys Ile Ile
            20                  25                  30
```

```
Leu Ala Leu Val Ala Gly Ala Val Leu Arg Leu Leu Glu Phe Gly Val
        35                  40                  45

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

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

Pro Leu Asp Ala Ile Ile Pro Ile Gly Val Leu Ile Lys Gly Ser Thr
                85                  90                  95

Met His Phe Glu Tyr Ile Cys Asp Ser Thr Thr His Gln Leu Met Lys
            100                 105                 110

Leu Asn Phe Glu Leu Gly Ile Pro Val Ile Phe Gly Val Leu Thr Cys
        115                 120                 125

Leu Thr Asp Glu Gln Ala Glu Ala Arg Ala Gly Leu Ile Glu Gly Lys
    130                 135                 140

Met His Asn His Gly Glu Asp Trp Gly Ala Ala Ala Val Glu Met Ala
145                 150                 155                 160

Thr Lys Phe Asn
```

<210> 16
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> I52-33B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 16

```
Met Gly Ala Asn Trp Tyr Leu Asp Asn Glu Ser Ser Arg Leu Ser Phe
1               5                  10                  15

Thr Ser Thr Lys Asn Ala Asp Ile Ala Glu Val His Arg Phe Leu Val
            20                  25                  30

Leu His Gly Lys Val Asp Pro Lys Gly Leu Ala Glu Val Glu Val Glu
        35                  40                  45

Thr Glu Ser Ile Ser Thr Gly Ile Pro Leu Arg Asp Met Leu Leu Arg
    50                  55                  60

Val Leu Val Phe Gln Val Ser Lys Phe Pro Val Ala Gln Ile Asn Ala
65                  70                  75                  80

Gln Leu Asp Met Arg Pro Ile Asn Asn Leu Ala Pro Gly Ala Gln Leu
                85                  90                  95

Glu Leu Arg Leu Pro Leu Thr Val Ser Leu Arg Gly Lys Ser His Ser
            100                 105                 110

Tyr Asn Ala Glu Leu Leu Ala Thr Arg Leu Asp Glu Arg Arg Phe Gln
        115                 120                 125

Val Val Thr Leu Glu Pro Leu Val Ile His Ala Gln Asp Phe Asp Met
    130                 135                 140

Val Arg Ala Phe Asn Ala Leu Arg Leu Val Ala Gly Leu Ser Ala Val
145                 150                 155                 160

Ser Leu Ser Val Pro Val Gly Ala Val Leu Ile Phe Thr Ala Arg
                165                 170                 175
```

<210> 17
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> I32-06A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 17

```
Met Thr Asp Tyr Ile Arg Asp Gly Ser Ala Ile Lys Ala Leu Ser Phe
1               5                   10                  15


Ala Ile Ile Leu Ala Glu Ala Asp Leu Arg His Ile Pro Gln Asp Leu
            20                  25                  30


Gln Arg Leu Ala Val Arg Val Ile His Ala Cys Gly Met Val Asp Val
        35                  40                  45


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


Ala Leu Leu Ala Gly Ala Pro Ile Leu Cys Asp Ala Arg Met Val Ala
65                  70                  75                  80


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


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


Thr Arg Ser Ala Ala Ala Leu Asp Leu Trp Leu Pro His Ile Glu Gly
        115                 120                 125


Ser Ile Val Ala Ile Gly Asn Ala Pro Thr Ala Leu Phe Arg Leu Phe
    130                 135                 140


Glu Leu Leu Asp Ala Gly Ala Pro Lys Pro Ala Leu Ile Ile Gly Met
145                 150                 155                 160
```

Pro Val Gly Phe Val Gly Ala Ala Glu Ser Lys Asp Glu Leu Ala Ala
165 170 175

Asn Ser Arg Gly Val Pro Tyr Val Ile Val Arg Gly Arg Arg Gly Gly
180 185 190

Ser Ala Met Thr Ala Ala Ala Val Asn Ala Leu Ala Ser Glu Arg Glu
195 200 205

<210> 18
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> I32-06B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 18

Met Ile Thr Val Phe Gly Leu Lys Ser Lys Leu Ala Pro Arg Arg Glu
1 5 10 15

Lys Leu Ala Glu Val Ile Tyr Ser Ser Leu His Leu Gly Leu Asp Ile
20 25 30

Pro Lys Gly Lys His Ala Ile Arg Phe Leu Cys Leu Glu Lys Glu Asp
35 40 45

Phe Tyr Tyr Pro Phe Asp Arg Ser Asp Asp Tyr Thr Val Ile Glu Ile
50 55 60

Asn Leu Met Ala Gly Arg Ser Glu Glu Thr Lys Met Leu Leu Ile Phe
65 70 75 80

```
Leu Leu Phe Ile Ala Leu Glu Arg Lys Leu Gly Ile Arg Ala His Asp
                85                  90                  95


Val Glu Ile Thr Ile Lys Glu Gln Pro Ala His Cys Trp Gly Phe Arg
            100                 105                 110


Gly Arg Thr Gly Asp Ser Ala Arg Asp Leu Asp Tyr Asp Ile Tyr Val
        115                 120                 125


<210>  19
<211>  235
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I32-19A


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  19

Met Gly Ser Asp Leu Gln Lys Leu Gln Arg Phe Ser Thr Cys Asp Ile
1               5                   10                  15


Ser Asp Gly Leu Leu Asn Val Tyr Asn Ile Pro Thr Gly Gly Tyr Phe
            20                  25                  30


Pro Asn Leu Thr Ala Ile Ser Pro Pro Gln Asn Ser Ser Ile Val Gly
        35                  40                  45


Thr Ala Tyr Thr Val Leu Phe Ala Pro Ile Asp Asp Pro Arg Pro Ala
    50                  55                  60


Val Asn Tyr Ile Asp Ser Val Pro Pro Asn Ser Ile Leu Val Leu Ala
65                  70                  75                  80


Leu Glu Pro His Leu Gln Ser Gln Phe His Pro Phe Ile Lys Ile Thr
                85                  90                  95
```

```
Gln Ala Met Tyr Gly Gly Leu Met Ser Thr Arg Ala Gln Tyr Leu Lys
            100                 105                 110

Ser Asn Gly Thr Val Val Phe Gly Arg Ile Arg Asp Val Asp Glu His
        115                 120                 125

Arg Thr Leu Asn His Pro Val Phe Ala Tyr Gly Val Gly Ser Cys Ala
    130                 135                 140

Pro Lys Ala Val Val Lys Ala Val Gly Thr Asn Val Gln Leu Lys Ile
145                 150                 155                 160

Leu Thr Ser Asp Gly Val Thr Gln Thr Ile Cys Pro Gly Asp Tyr Ile
                165                 170                 175

Ala Gly Asp Asn Asn Gly Ile Val Arg Ile Pro Val Gln Glu Thr Asp
            180                 185                 190

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

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

Thr Ala Arg Arg Met Val Leu Lys Asp Tyr Ile
225                 230                 235
```

<210> 20
<211> 162
<212> PRT
<213> Artificial Sequence

<220>
<223> I32-19B

<220>
<221> MISC_FEATURE
<222> (1)..(1)

<223> optionally absent

<400> 20

```
Met Ser Gly Met Arg Val Tyr Leu Gly Ala Asp His Ala Gly Tyr Glu
1               5                  10                  15


Leu Lys Gln Ala Ile Ile Ala Phe Leu Lys Met Thr Gly His Glu Pro
            20                  25                  30


Ile Asp Cys Gly Ala Leu Arg Tyr Asp Ala Asp Asp Asp Tyr Pro Ala
        35                  40                  45


Phe Cys Ile Ala Ala Ala Thr Arg Thr Val Ala Asp Pro Gly Ser Leu
    50                  55                  60


Gly Ile Val Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn
65                  70                  75                  80


Lys Val Pro Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Gln Thr Ala
                85                  90                  95


Ala Leu Ala Arg Glu His Asn Asn Ala Gln Leu Ile Gly Ile Gly Gly
            100                 105                 110


Arg Met His Thr Leu Glu Glu Ala Leu Arg Ile Val Lys Ala Phe Val
        115                 120                 125


Thr Thr Pro Trp Ser Lys Ala Gln Arg His Gln Arg Arg Ile Asp Ile
    130                 135                 140


Leu Ala Glu Tyr Glu Arg Thr His Glu Ala Pro Pro Val Pro Gly Ala
145                 150                 155                 160


Pro Ala
```

<210> 21
<211> 157

<212> PRT
<213> Artificial Sequence

<220>
<223> I32-28A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 21

Met Gly Asp Asp Ala Arg Ile Ala Ala Ile Gly Asp Val Asp Glu Leu
1 5 10 15

Asn Ser Gln Ile Gly Val Leu Leu Ala Glu Pro Leu Pro Asp Asp Val
20 25 30

Arg Ala Ala Leu Ser Ala Ile Gln His Asp Leu Phe Asp Leu Gly Gly
35 40 45

Glu Leu Cys Ile Pro Gly His Ala Ala Ile Thr Glu Asp His Leu Leu
50 55 60

Arg Leu Ala Leu Trp Leu Val His Tyr Asn Gly Gln Leu Pro Pro Leu
65 70 75 80

Glu Glu Phe Ile Leu Pro Gly Gly Ala Arg Gly Ala Ala Leu Ala His
85 90 95

Val Cys Arg Thr Val Cys Arg Arg Ala Glu Arg Ser Ile Lys Ala Leu
100 105 110

Gly Ala Ser Glu Pro Leu Asn Ile Ala Pro Ala Ala Tyr Val Asn Leu
115 120 125

Leu Ser Asp Leu Leu Phe Val Leu Ala Arg Val Leu Asn Arg Ala Ala
130 135 140

Gly Gly Ala Asp Val Leu Trp Asp Arg Thr Arg Ala His
145 150 155

<210> 22
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I32-28B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 22

Met Ile Leu Ser Ala Glu Gln Ser Phe Thr Leu Arg His Pro His Gly
1 5 10 15

Gln Ala Ala Ala Leu Ala Phe Val Arg Glu Pro Ala Ala Ala Leu Ala
20 25 30

Gly Val Gln Arg Leu Arg Gly Leu Asp Ser Asp Gly Glu Gln Val Trp
35 40 45

Gly Glu Leu Leu Val Arg Val Pro Leu Leu Gly Glu Val Asp Leu Pro
50 55 60

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

Leu Thr Leu Thr Gly Glu Arg Ala Trp Val Ala Val Ser Gly Gln Ala
85 90 95

Thr Ala Ala Glu Gly Gly Glu Met Ala Phe Ala Phe Gln Phe Gln Ala
100 105 110

His Leu Ala Thr Pro Glu Ala Glu Gly Glu Gly Gly Ala Ala Phe Glu
115 120 125

```
Val Met Val Gln Ala Ala Ala Gly Val Thr Leu Leu Leu Val Ala Met
    130                 135                 140


Ala Leu Pro Gln Gly Leu Ala Ala Gly Leu Pro Pro Ala
145                 150                 155


<210>  23
<211>  156
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-40A.1


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  23

Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1               5                   10                  15


Met Ala Ser Ala Ala Ile Leu Thr Leu Lys Met Glu Ser Pro Asn Ile
            20                  25                  30


Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
        35                  40                  45


Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
    50                  55                  60


Gly Met Pro Gly Lys Lys Glu Lys Asp Lys Val Cys Ala His Glu Ala
65                  70                  75                  80


Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
                85                  90                  95
```

Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Ala Glu Leu Lys
100 105 110

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

Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
130 135 140

Arg Gln Gly Phe Glu Asp Ala Gly Pro Ala Arg Glu
145 150 155

<210> 24
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-40B.1

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 24

Met Asp Asp Ile Asn Asn Gln Leu Lys Arg Leu Lys Val Ile Pro Val
1 5 10 15

Ile Ala Ile Asp Asn Ala Glu Asp Ile Ile Pro Leu Gly Lys Val Leu
20 25 30

Ala Glu Asn Gly Leu Pro Ala Ala Glu Ile Thr Phe Arg Ser Ser Ala
35 40 45

Ala Val Lys Ala Ile Met Leu Leu Arg Ser Ala Gln Pro Glu Met Leu
50 55 60

Ile Gly Ala Gly Thr Ile Leu Asn Gly Val Gln Ala Leu Ala Ala Lys
65 70 75 80

```
Glu Ala Gly Ala Asp Phe Val Val Ser Pro Gly Phe Asn Pro Asn Thr
                85                  90                  95

Val Arg Ala Cys Gln Ile Ile Gly Ile Asp Ile Val Pro Gly Val Asn
            100                 105                 110

Asn Pro Ser Thr Val Glu Gln Ala Leu Glu Met Gly Leu Thr Thr Leu
        115                 120                 125

Lys Phe Phe Pro Ala Glu Ala Ser Gly Gly Ile Ser Met Val Lys Ser
    130                 135                 140

Leu Val Gly Pro Tyr Gly Asp Ile Arg Leu Met Pro Thr Gly Gly Ile
145                 150                 155                 160

Thr Pro Asp Asn Ile Asp Asn Tyr Leu Ala Ile Pro Gln Val Leu Ala
                165                 170                 175

Cys Gly Gly Thr Trp Met Val Asp Lys Lys Leu Val Arg Asn Gly Glu
            180                 185                 190

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

Pro
```

<210> 25
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47A.1

<220>
<221> MISC_FEATURE
<222> (1)..(1)

<223> optionally absent

<400> 25

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Asp Asp Val Pro
1   5   10   15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
            20   25   30

Lys Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
        35   40   45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
    50   55   60

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

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
                85   90   95

Ile His Phe Val Asn Leu Asn Gly Asp Asp Val Gly Trp Asn Gly Thr
            100   105   110

Thr Phe

<210> 26
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47A.1NegT2

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 26

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Asp Asp Val Pro
1 5 10 15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
20 25 30

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

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
50 55 60

Ile Gly Gly Ile Glu Pro Asp Lys Asn Glu Asp His Ser Ala Val Leu
65 70 75 80

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
85 90 95

Ile His Phe Val Asp Leu Asp Gly Asp Asp Val Gly Trp Asn Gly Thr
100 105 110

Thr Phe

<210> 27
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47B.1

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 27

```
Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1               5                   10                  15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
            20                  25                  30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
            100                 105                 110

Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Asp Glu His His Arg
        115                 120                 125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
    130                 135                 140

Cys Ile Glu Ile Leu Asn Ala Arg Glu Lys Ile Ala Ala
145                 150                 155
```

<210> 28
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47B.1NegT2

<220>

<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 28

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
20 25 30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asp Gly Gly Ile Tyr Asp His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Glu Tyr Glu Asp Ser Asp Glu Asp His Glu
115 120 125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
130 135 140

Cys Ile Glu Ile Leu Asn Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 29
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-50A.1

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 29

```
Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1               5                   10                  15


Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
            20                  25                  30


Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
        35                  40                  45


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


Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65                  70                  75                  80


Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
                85                  90                  95


Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
            100                 105                 110


Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Asp Ile Leu
        115                 120                 125


Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
    130                 135                 140


Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
145                 150                 155                 160
```

```
Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly
                165                 170                 175


Val Gly Asp Ala Leu Val Lys Gly Asp Pro Asp Glu Val Arg Glu Lys
            180                 185                 190


Ala Lys Lys Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
        195                 200                 205


<210>  30
<211>  205
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-50A.1NegT2


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  30

Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1               5                   10                  15


Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
            20                  25                  30


Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
        35                  40                  45


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


Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65                  70                  75                  80
```

```
Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
                85                  90                  95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
            100                 105                 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Asp Ile Leu
        115                 120                 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Glu Phe Val Glu Ala Met
    130                 135                 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asp
145                 150                 155                 160

Leu Asp Asp Val Cys Glu Trp Phe Asp Ala Gly Val Leu Ala Val Gly
                165                 170                 175

Val Gly Asp Ala Leu Val Glu Gly Asp Pro Asp Glu Val Arg Glu Asp
            180                 185                 190

Ala Lys Glu Phe Val Glu Glu Ile Arg Gly Cys Thr Glu
        195                 200                 205


<210>  31
<211>  205
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-50A.1PosT1


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  31

Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1               5                   10                  15
```

```
Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
            20                  25                  30

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
        35                  40                  45

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

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65                  70                  75                  80

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
                85                  90                  95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
            100                 105                 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Asp Ile Leu
        115                 120                 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
    130                 135                 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
145                 150                 155                 160

Leu Asp Asn Val Cys Lys Trp Phe Lys Ala Gly Val Leu Ala Val Gly
                165                 170                 175

Val Gly Lys Ala Leu Val Lys Gly Lys Pro Asp Glu Val Arg Glu Lys
            180                 185                 190

Ala Lys Lys Phe Val Lys Lys Ile Arg Gly Cys Thr Glu
        195                 200                 205
```

<210> 32
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-50B.1

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 32

```
Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1               5                   10                  15


Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
            20                  25                  30


Phe Glu Ala Ala Met Arg Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45


Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60


Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80


Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95


Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
            100                 105                 110


Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Asp Ala His Thr Leu
        115                 120                 125


Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
    130                 135                 140
```

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 33
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-50B.1NegT2

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 33

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
20 25 30

Phe Glu Ala Ala Met Arg Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asp Gly Gly Ile Tyr Asp His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
100 105 110

```
Ala Val Leu Thr Pro His Glu Tyr Glu Asp Ser Asp Ala Asp Thr Leu
        115                 120                 125


Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
    130                 135                 140


Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145                 150                 155


<210>  34
<211>  157
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-50B.4PosT1


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  34

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1               5                   10                  15


Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
            20                  25                  30


Phe Glu Ala Ala Met Arg Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45


Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60


Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80


Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95
```

```
Asn Gly Met Met Asn Val Gln Leu Asn Thr Gly Val Pro Val Leu Ser
            100                 105                 110


Ala Val Leu Thr Pro His Asn Tyr Asp Lys Ser Lys Ala His Thr Leu
        115                 120                 125


Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
    130                 135                 140


Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145                 150                 155


<210>  35
<211>  156
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-40 A genus


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<220>
<221>  MISC_FEATURE
<222>  (70)..(70)
<223>  Xaa is A or K

<400>  35

Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1               5                   10                  15


Met Ala Ser Ala Ala Ile Leu Thr Leu Lys Met Glu Ser Pro Asn Ile
            20                  25                  30


Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
        35                  40                  45
```

```
Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
    50                  55                  60

Gly Met Pro Gly Lys Xaa Glu Lys Asp Lys Val Cys Ala His Glu Ala
65                  70                  75                  80

Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
                85                  90                  95

Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Ala Glu Leu Lys
            100                 105                 110

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

Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
    130                 135                 140

Arg Gln Gly Phe Glu Asp Ala Gly Pro Ala Arg Glu
145                 150                 155
```

<210> 36
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-40 B genus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is S or D

<220>
<221> MISC_FEATURE

<222> (3)..(3)
<223> Xaa is T or D

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is A or R

<220>
<221> MISC_FEATURE
<222> (85)..(85)
<223> Xaa is T or D

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa is A or Q

<220>
<221> MISC_FEATURE
<222> (163)..(163)
<223> Xaa is S or D

<220>
<221> MISC_FEATURE
<222> (189)..(189)
<223> Xaa is T or R

<400> 36

```
Met Xaa Xaa Ile Asn Asn Gln Leu Lys Xaa Leu Lys Val Ile Pro Val
1               5                   10                  15


Ile Ala Ile Asp Asn Ala Glu Asp Ile Ile Pro Leu Gly Lys Val Leu
            20                  25                  30


Ala Glu Asn Gly Leu Pro Ala Ala Glu Ile Thr Phe Arg Ser Ser Ala
        35                  40                  45


Ala Val Lys Ala Ile Met Leu Leu Arg Ser Ala Gln Pro Glu Met Leu
    50                  55                  60


Ile Gly Ala Gly Thr Ile Leu Asn Gly Val Gln Ala Leu Ala Ala Lys
65                  70                  75                  80
```

```
Glu Ala Gly Ala Xaa Phe Val Val Ser Pro Gly Phe Asn Pro Asn Thr
                85                  90                  95

Val Arg Ala Cys Gln Ile Ile Gly Ile Asp Ile Val Pro Gly Val Asn
            100                 105                 110

Asn Pro Ser Thr Val Glu Xaa Ala Leu Glu Met Gly Leu Thr Thr Leu
        115                 120                 125

Lys Phe Phe Pro Ala Glu Ala Ser Gly Gly Ile Ser Met Val Lys Ser
    130                 135                 140

Leu Val Gly Pro Tyr Gly Asp Ile Arg Leu Met Pro Thr Gly Gly Ile
145                 150                 155                 160

Thr Pro Xaa Asn Ile Asp Asn Tyr Leu Ala Ile Pro Gln Val Leu Ala
                165                 170                 175

Cys Gly Gly Thr Trp Met Val Asp Lys Lys Leu Val Xaa Asn Gly Glu
            180                 185                 190

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

Pro
```

<210> 37
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47A genus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is T or D

<220>
<221> MISC_FEATURE
<222> (33)..(33)
<223> Xaa is K or E

<220>
<221> MISC_FEATURE
<222> (71)..(71)
<223> Xaa is S or D

<220>
<221> MISC_FEATURE
<222> (74)..(74)
<223> Xaa is R or E

<220>
<221> MISC_FEATURE
<222> (101)..(101)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (103)..(103)
<223> Xaa is N or D

<400> 37

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Xaa Asp Val Pro
1   5   10   15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
            20   25   30

Xaa Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
        35   40   45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
    50   55   60

Ile Gly Gly Ile Glu Pro Xaa Lys Asn Xaa Asp His Ser Ala Val Leu
65   70   75   80

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
85 90 95

Ile His Phe Val Xaa Leu Xaa Gly Asp Asp Val Gly Trp Asn Gly Thr
100 105 110

Thr Phe

<210> 38
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-47B genus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Y or H

<220>
<221> MISC_FEATURE
<222> (82)..(82)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (87)..(87)
<223> Xaa is R or D

<220>
<221> MISC_FEATURE
<222> (105)..(105)
<223> Xaa is S or D

<220>
<221> MISC_FEATURE

<222> (119)..(119)
<223> Xaa is R or E

<220>
<221> MISC_FEATURE
<222> (121)..(121)
<223> Xaa is R or E

<220>
<221> MISC_FEATURE
<222> (124)..(124)
<223> Xaa is A or D

<220>
<221> MISC_FEATURE
<222> (126)..(126)
<223> Xaa is H or D

<220>
<221> MISC_FEATURE
<222> (128)..(128)
<223> Xaa is R or E

<220>
<221> MISC_FEATURE
<222> (150)..(150)
<223> Xaa is A or N

<400> 38

```
Met Asn Gln His Ser His Lys Asp Xaa Glu Thr Val Arg Ile Ala Val
1               5                   10                  15


Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
            20                  25                  30


Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45


Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60


Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80
```

```
Val Xaa Gly Gly Ile Tyr Xaa His Glu Phe Val Ala Ser Ala Val Ile
                85                  90                  95


Asp Gly Met Met Asn Val Gln Leu Xaa Thr Gly Val Pro Val Leu Ser
            100                 105                 110


Ala Val Leu Thr Pro His Xaa Tyr Xaa Asp Ser Xaa Glu Xaa His Xaa
        115                 120                 125


Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
    130                 135                 140


Cys Ile Glu Ile Leu Xaa Ala Arg Glu Lys Ile Ala Ala
145                 150                 155


<210>  39
<211>  205
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  I53-50A genus


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<220>
<221>  MISC_FEATURE
<222>  (126)..(126)
<223>  Xaa is T or D

<220>
<221>  MISC_FEATURE
<222>  (139)..(139)
<223>  Xaa is Q or E

<220>
<221>  MISC_FEATURE
<222>  (142)..(142)
<223>  Xaa is K or E

<220>
```

<221> MISC_FEATURE
<222> (160)..(160)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (163)..(163)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (166)..(166)
<223> Xaa is E or K

<220>
<221> MISC_FEATURE
<222> (169)..(169)
<223> Xaa is D or K

<220>
<221> MISC_FEATURE
<222> (179)..(179)
<223> Xaa is S, D or K

<220>
<221> MISC_FEATURE
<222> (183)..(183)
<223> Xaa is K or E

<220>
<221> MISC_FEATURE
<222> (185)..(185)
<223> Xaa is T, D, or K

<220>
<221> MISC_FEATURE
<222> (192)..(192)
<223> Xaa is D or K

<220>
<221> MISC_FEATURE
<222> (195)..(195)
<223> Xaa is A, E, or K

<220>
<221> MISC_FEATURE
<222> (198)..(198)
<223> Xaa is E or K

<220>

<221> MISC_FEATURE
<222> (199)..(199)
<223> Xaa is E or K

<400> 39

```
Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1               5                  10                  15


Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
            20                  25                  30


Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
        35                  40                  45


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


Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65                  70                  75                  80


Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
                85                  90                  95


Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
            100                 105                 110


Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Xaa Ile Leu
        115                 120                 125


Lys Leu Phe Pro Gly Glu Val Val Gly Pro Xaa Phe Val Xaa Ala Met
    130                 135                 140


Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Xaa
145                 150                 155                 160


Leu Asp Xaa Val Cys Xaa Trp Phe Xaa Ala Gly Val Leu Ala Val Gly
                165                 170                 175
```

Val Gly Xaa Ala Leu Val Xaa Gly Xaa Pro Asp Glu Val Arg Glu Xaa
            180   185   190

Ala Lys Xaa Phe Val Xaa Xaa Ile Arg Gly Cys Thr Glu
        195   200   205

<210> 40
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> I53-50B genus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Y or H

<220>
<221> MISC_FEATURE
<222> (38)..(38)
<223> Xaa is A or R

<220>
<221> MISC_FEATURE
<222> (82)..(82)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (87)..(87)
<223> Xaa is R or D

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (105)..(105)

<223> Xaa is S, N, or D

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa is R, E, or N

<220>
<221> MISC_FEATURE
<222> (121)..(121)
<223> Xaa is R, E, or D

<220>
<221> MISC_FEATURE
<222> (122)..(122)
<223> Xaa is K or D

<220>
<221> MISC_FEATURE
<222> (124)..(124)
<223> Xaa is K or D

<220>
<221> MISC_FEATURE
<222> (126)..(126)
<223> Xaa is H or D

<400> 40

```
Met Asn Gln His Ser His Lys Asp Xaa Glu Thr Val Arg Ile Ala Val
1               5                   10                  15


Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
            20                  25                  30


Phe Glu Ala Ala Met Xaa Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
        35                  40                  45


Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50                  55                  60


Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65                  70                  75                  80


Val Xaa Gly Gly Ile Tyr Xaa His Glu Phe Val Ala Ser Ala Val Ile
```

```
                85                  90                  95

Xaa Gly Met Met Asn Val Gln Leu Xaa Thr Gly Val Pro Val Leu Ser
            100                 105                 110

Ala Val Leu Thr Pro His Xaa Tyr Xaa Xaa Ser Xaa Ala Xaa Thr Leu
        115                 120                 125

Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
    130                 135                 140

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145                 150                 155
```

<210> 41
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> T32-28A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 41

```
Met Gly Glu Val Pro Ile Gly Asp Pro Lys Glu Leu Asn Gly Met Glu
1               5                   10                  15

Ile Ala Ala Val Tyr Leu Gln Pro Ile Glu Met Glu Pro Arg Gly Ile
            20                  25                  30

Asp Leu Ala Ala Ser Leu Ala Asp Ile His Leu Glu Ala Asp Ile His
        35                  40                  45

Ala Leu Lys Asn Asn Pro Asn Gly Phe Pro Glu Gly Phe Trp Met Pro
    50                  55                  60
```

```
Tyr Leu Thr Ile Ala Tyr Ala Leu Ala Asn Ala Asp Thr Gly Ala Ile
65                  70                  75                  80


Lys Thr Gly Thr Leu Met Pro Met Val Ala Asp Asp Gly Pro His Tyr
                85                  90                  95


Gly Ala Asn Ile Ala Met Glu Lys Asp Lys Lys Gly Gly Phe Gly Val
            100                 105                 110


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


Phe Gly Arg His Val Asp Glu Glu Thr Gly Val Gly Lys Trp Phe Glu
    130                 135                 140


Pro Phe Val Val Thr Tyr Phe Phe Lys Tyr Thr Gly Thr Pro Lys
145                 150                 155


<210>  42
<211>  184
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  T32-28B


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  42

Met Ser Gln Ala Ile Gly Ile Leu Glu Leu Thr Ser Ile Ala Lys Gly
1               5                   10                  15


Met Glu Leu Gly Asp Ala Met Leu Lys Ser Ala Asn Val Asp Leu Leu
            20                  25                  30


Val Ser Lys Thr Ile Ser Pro Gly Lys Phe Leu Leu Met Leu Gly Gly
```

```
        35                  40                  45

Asp Ile Gly Ala Ile Gln Gln Ala Ile Glu Thr Gly Thr Ser Gln Ala
    50                  55                  60

Gly Glu Met Leu Val Asp Ser Leu Val Leu Ala Asn Ile His Pro Ser
65                  70                  75                  80

Val Leu Pro Ala Ile Ser Gly Leu Asn Ser Val Asp Lys Arg Gln Ala
                85                  90                  95

Val Gly Ile Val Glu Thr Trp Ser Val Ala Ala Cys Ile Ser Ala Ala
            100                 105                 110

Asp Leu Ala Val Lys Gly Ser Asn Val Thr Leu Val Arg Val His Met
        115                 120                 125

Ala Phe Gly Ile Gly Gly Lys Cys Tyr Met Val Val Ala Gly Asp Val
    130                 135                 140

Leu Asp Val Ala Ala Ala Val Ala Thr Ala Ser Leu Ala Ala Gly Ala
145                 150                 155                 160

Lys Gly Leu Leu Val Tyr Ala Ser Ile Ile Pro Arg Pro His Glu Ala
                165                 170                 175

Met Trp Arg Gln Met Val Glu Gly
            180


<210>  43
<211>  103
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  T33-09A


<220>
<221>  MISC_FEATURE
```

<222> (1)..(1)
<223> optionally absent

<400> 43

Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val
1   5   10   15

Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn
            20   25   30

Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Trp Gln Gly Ser Val Val
        35   40   45

Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr His Ala Phe
    50   55   60

Pro Lys Leu Lys Glu Arg Val Lys Ala Leu His Pro Tyr Thr Val Pro
65   70   75   80

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

Trp Leu Arg Glu Asn Thr Gly
            100

<210> 44
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-09B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 44

Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val Glu Glu Asp Thr Pro

```
1               5                   10                  15


Ala Ala Ile Leu Ala Ala Thr Ile Glu Leu Leu Leu Lys Met Leu Glu
            20                  25                  30


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


Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Leu
    50                  55                  60


Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val
65                  70                  75                  80


Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr
                85                  90                  95


Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Asn Glu Ala Val
            100                 105                 110


Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
        115                 120


<210>  45
<211>  177
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  T33-15A


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  optionally absent

<400>  45

Met Ser Lys Ala Lys Ile Gly Ile Val Thr Val Ser Asp Arg Ala Ser
1               5                   10                  15
```

```
Ala Gly Ile Thr Ala Asp Ile Ser Gly Lys Ala Ile Ile Leu Ala Leu
            20                  25                  30

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

Asp Glu Gln Asp Val Ile Glu Thr Thr Leu Ile Lys Met Ala Asp Glu
    50                  55                  60

Gln Asp Cys Cys Leu Ile Val Thr Thr Gly Gly Thr Gly Pro Ala Lys
65                  70                  75                  80

Arg Asp Val Thr Pro Glu Ala Thr Glu Ala Val Cys Asp Arg Met Met
                85                  90                  95

Pro Gly Phe Gly Glu Leu Met Arg Ala Glu Ser Leu Lys Glu Val Pro
            100                 105                 110

Thr Ala Ile Leu Ser Arg Gln Thr Ala Gly Leu Arg Gly Asp Ser Leu
        115                 120                 125

Ile Val Asn Leu Pro Gly Asp Pro Ala Ser Ile Ser Asp Cys Leu Leu
    130                 135                 140

Ala Val Phe Pro Ala Ile Pro Tyr Cys Ile Asp Leu Met Glu Gly Pro
145                 150                 155                 160

Tyr Leu Glu Cys Asn Glu Ala Met Ile Lys Pro Phe Arg Pro Lys Ala
                165                 170                 175

Lys
```

<210> 46
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-15B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 46

Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn Ser Asp Thr Pro
1   5   10   15

Thr Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu Lys Met Leu Glu
            20   25   30

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

Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Gln
    50   55   60

Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val
65   70   75   80

Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr
                85   90   95

Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Ser Glu Ala Val
            100   105   110

Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
        115   120

<210> 47
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-21A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 47

```
Met Arg Ile Thr Thr Lys Val Gly Asp Lys Gly Ser Thr Arg Leu Phe
1               5                   10                  15


Gly Gly Glu Glu Val Trp Lys Asp Ser Pro Ile Ile Glu Ala Asn Gly
            20                  25                  30


Thr Leu Asp Glu Leu Thr Ser Phe Ile Gly Glu Ala Lys His Tyr Val
        35                  40                  45


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


Lys Ile Met Gly Glu Ile Gly Ser Lys Gly Lys Ile Glu Gly Ile Ser
65                  70                  75                  80


Glu Glu Arg Ile Ala Trp Leu Leu Lys Leu Ile Leu Arg Tyr Met Glu
                85                  90                  95


Met Val Asn Leu Lys Ser Phe Val Leu Pro Gly Gly Thr Leu Glu Ser
            100                 105                 110


Ala Lys Leu Asp Val Cys Arg Thr Ile Ala Arg Arg Ala Leu Arg Lys
        115                 120                 125


Val Leu Thr Val Thr Arg Glu Phe Gly Ile Gly Ala Glu Ala Ala Ala
    130                 135                 140


Tyr Leu Leu Ala Leu Ser Asp Leu Leu Phe Leu Leu Ala Arg Val Ile
145                 150                 155                 160


Glu Ile Glu Lys Asn Lys Leu Lys Glu Val Arg Ser
```

165 170

<210> 48
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-21B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 48

Met Pro His Leu Val Ile Glu Ala Thr Ala Asn Leu Arg Leu Glu Thr
1 5 10 15

Ser Pro Gly Glu Leu Leu Glu Gln Ala Asn Lys Ala Leu Phe Ala Ser
20 25 30

Gly Gln Phe Gly Glu Ala Asp Ile Lys Ser Arg Phe Val Thr Leu Glu
35 40 45

Ala Tyr Arg Gln Gly Thr Ala Ala Val Glu Arg Ala Tyr Leu His Ala
50 55 60

Cys Leu Ser Ile Leu Asp Gly Arg Asp Ile Ala Thr Arg Thr Leu Leu
65 70 75 80

Gly Ala Ser Leu Cys Ala Val Leu Ala Glu Ala Val Ala Gly Gly Gly
85 90 95

Glu Glu Gly Val Gln Val Ser Val Glu Val Arg Glu Met Glu Arg Leu
100 105 110

Ser Tyr Ala Lys Arg Val Val Ala Arg Gln Arg
115 120

<210> 49
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-28A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 49

Met Glu Ser Val Asn Thr Ser Phe Leu Ser Pro Ser Leu Val Thr Ile
1 5 10 15

Arg Asp Phe Asp Asn Gly Gln Phe Ala Val Leu Arg Ile Gly Arg Thr
20 25 30

Gly Phe Pro Ala Asp Lys Gly Asp Ile Asp Leu Cys Leu Asp Lys Met
35 40 45

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

Gly Phe Lys Gly Pro His Ile Arg Ile Arg Cys Val Asp Ile Asp Asp
65 70 75 80

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

Gly Ala Ser Glu Val Glu Arg Glu Thr Ala Glu Glu Glu Ala Lys Leu
100 105 110

Ala Leu Arg Val Ala Leu Gln Val Asp Ile Ala Asp Glu His Ser Cys
115 120 125

Val Thr Gln Phe Glu Met Lys Leu Arg Glu Glu Leu Leu Ser Ser Asp

130 135 140

Ser Phe His Pro Asp Lys Asp Glu Tyr Tyr Lys Asp Phe Leu
145 150 155

<210> 50
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-28B

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 50

Met Pro Val Ile Gln Thr Phe Val Ser Thr Pro Leu Asp His His Lys
1 5 10 15

Arg Leu Leu Leu Ala Ile Ile Tyr Arg Ile Val Thr Arg Val Val Leu
20 25 30

Gly Lys Pro Glu Asp Leu Val Met Met Thr Phe His Asp Ser Thr Pro
35 40 45

Met His Phe Phe Gly Ser Thr Asp Pro Val Ala Cys Val Arg Val Glu
50 55 60

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

Val Thr Ala Ala Ile Thr Ala Val Cys Gly Ile Val Ala Asp Arg Ile
85 90 95

Phe Val Leu Tyr Phe Ser Pro Leu His Cys Gly Trp Asn Gly Thr Asn
100 105 110

Phe

<210> 51
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> T33-31A

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> optionally absent

<400> 51

Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val
1 5 10 15

Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn
20 25 30

Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu Glu Gly Ser Val Val
35 40 45

Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr Asp Ala Phe
50 55 60

Pro Lys Leu Lys Glu Arg Val Lys Glu Leu His Pro Tyr Glu Val Pro
65 70 75 80

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

Trp Leu Arg Glu Asn Thr Gly
100

<210> 52

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 52

Gln Asn Ile Thr Glu Glu Phe
1 5

<210> 53
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (508)..(513)
<223> optionally absent

<400> 53

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

```
Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270
```

```
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460
```

```
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480


Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495


Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510


Leu
```

<210> 54
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> T4 fibritin foldon domain

<400> 54

```
Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
1               5                   10                  15


Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
            20                  25
```

<210> 55
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 55

```
Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
1               5                   10                  15
```

<210> 56
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 56

Gly Gly Ser Gly Gly Ser Gly Ser
1 5

<210> 57
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 57

Gly Ser Gly Gly Ser Gly Ser Gly
1 5

<210> 58
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Helical extension

<400> 58

Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg
1 5 10

<210> 59
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 59

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1   5   10   15

Ala Val Thr Phe Cys Phe Ala Ser Gly
            20   25

<210> 60
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-foldon

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 60

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1   5   10   15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35   40   45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50   55   60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65   70   75   80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100   105   110

```
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300
```

```
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510
```

Leu Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
515 520 525

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
530 535 540

<210> 61
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> sc9-10 DS-Cav1 A149C Y458C

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (468)..(474)
<223> optionally absent

<400> 61

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
            100                 105                 110

Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140

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

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser
                165                 170                 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
        195                 200                 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
```

```
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305                 310                 315                 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385                 390                 395                 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
                405                 410                 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly
            420                 425                 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
        435                 440                 445

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

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu
465                 470
```

<210> 62
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> sc9-10 DS-Cav1 A149C Y458C S46G K465Q S215P E92D

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (468)..(474)
<223> optionally absent

<400> 62

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1   5   10   15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Gly Ala Leu
        35   40   45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50   55   60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65   70   75   80

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
            100   105   110

```
Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140

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

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Pro
                165                 170                 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
        195                 200                 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305                 310                 315                 320
```

```
Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385                 390                 395                 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
                405                 410                 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Gln Ser Leu Tyr Val Lys Gly
            420                 425                 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
        435                 440                 445

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

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu
465                 470
```

<210> 63
<211> 522
<212> PRT
<213> Artificial Sequence

<220>
<223> SC-DM (N67I, S215P)

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (486)..(522)
<223> optionally absent

<400> 63

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                   10                  15


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


Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45


Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60


Lys Lys Ile Lys Cys Asn Gly Thr Asp Ala Lys Ile Lys Leu Ile Lys
65                  70                  75                  80


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


Met Gln Ser Thr Pro Ala Thr Asn Asn Gln Ala Arg Gly Ser Gly Ser
            100                 105                 110


Gly Arg Ser Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser
        115                 120                 125


Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys
    130                 135                 140


Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser
```

```
145                 150                 155                 160

Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
                165                 170                 175

Ile Asp Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile
            180                 185                 190

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

Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro
    210                 215                 220

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

Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val
                245                 250                 255

Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu
            260                 265                 270

Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp
        275                 280                 285

Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr
    290                 295                 300

Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr
305                 310                 315                 320

Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys
                325                 330                 335

Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr
            340                 345                 350
```

```
Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys
        355                 360                 365


Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val
    370                 375                 380


Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys
385                 390                 395                 400


Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly
                405                 410                 415


Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn
            420                 425                 430


Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys
        435                 440                 445


Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
    450                 455                 460


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


Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Ser Ala Ile Gly Gly
                485                 490                 495


Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
            500                 505                 510


Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
        515                 520


<210>  64
<211>  522
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> SC-TM (N67I, S215P, and E487Q)

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (486)..(522)
<223> optionally absent

<400> 64

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                   10                  15


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


Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45


Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60


Lys Lys Ile Lys Cys Asn Gly Thr Asp Ala Lys Ile Lys Leu Ile Lys
65                  70                  75                  80


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


Met Gln Ser Thr Pro Ala Thr Asn Asn Gln Ala Arg Gly Ser Gly Ser
            100                 105                 110


Gly Arg Ser Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser
        115                 120                 125


Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys
    130                 135                 140
```

```
Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser
145                 150                 155                 160


Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
                165                 170                 175


Ile Asp Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile
            180                 185                 190


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


Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro
    210                 215                 220


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


Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val
                245                 250                 255


Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu
            260                 265                 270


Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp
        275                 280                 285


Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr
    290                 295                 300


Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr
305                 310                 315                 320


Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys
                325                 330                 335
```

```
Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr
            340                 345                 350

Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys
        355                 360                 365

Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val
    370                 375                 380

Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys
385                 390                 395                 400

Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly
                405                 410                 415

Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn
            420                 425                 430

Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys
        435                 440                 445

Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
    450                 455                 460

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

Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Ser Ala Ile Gly Gly
                485                 490                 495

Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
            500                 505                 510

Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
        515                 520
```

<210> 65
<211> 490

<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV F protein, strain CAN97-83 (A2)

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 65

```
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30


Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45


Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
    50                  55                  60


Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80


Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95


Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110


Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125


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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350
```

```
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly
                485                 490
```

<210> 66
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPVF with A113C, A339C, T160F, I177L

<220>
<221> MISC_FEATURE
<222> (1)..(18)

<223> optionally absent

<400> 66

```
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30


Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45


Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
    50                  55                  60


Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80


Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95


Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110


Cys Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125


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


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


Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175


Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190
```

```
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380
```

```
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400


Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415


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


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


Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460


Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480


Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly
                485                 490


<210>  67
<211>  490
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HMPV- F with A113C, A120C, A339C, T160F, I177L, and Q426C


<220>
<221>  MISC_FEATURE
<222>  (1)..(18)
<223>  optionally absent

<400>  67

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30
```

```
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
    50                  55                  60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95

Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Cys Thr Ala Ala Ala Val Thr Cys Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220
```

```
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240


Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255


Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270


Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285


Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300


Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320


Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335


Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350


Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365


Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380


Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400


Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415


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

```
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
        435                 440                 445


Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460


Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480


Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly
                485                 490


<210>  68
<211>  542
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  115-BV (A185P)


<220>
<221>  MISC_FEATURE
<222>  (1)..(18)
<223>  optionally absent

<220>
<221>  MISC_FEATURE
<222>  (490)..(542)
<223>  optionally absent

<400>  68

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30


Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45
```

```
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
    50                  55                  60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80

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

Asn Pro Arg Arg Arg Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Ile Asn Lys Asn Lys Cys Asp Ile Pro Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
```

```
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
        435                 440                 445
```

```
Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460


Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480


Leu Ser Ser Ala Glu Lys Gly Asn Thr Ser Gly Arg Glu Asn Leu Tyr
                485                 490                 495


Phe Gln Gly Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp
            500                 505                 510


Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr
        515                 520                 525


Phe Leu Gly Gly Ile Glu Gly Arg His His His His His His
    530                 535                 540
```

<210> 69
<211> 646
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-foldon-T33-31A

<220>
<221> MISC_FEATURE
<222> (1)..(26)
<223> optionally absent

<400> 69

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


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


Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
```

```
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240
```

```
Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
```

```
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
        515                 520                 525

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Met
    530                 535                 540

Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val Lys
545                 550                 555                 560

Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn Ile
                565                 570                 575

Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu Glu Gly Ser Val Val Ser
            580                 585                 590

Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr Asp Ala Phe Pro
        595                 600                 605

Lys Leu Lys Glu Arg Val Lys Glu Leu His Pro Tyr Glu Val Pro Glu
    610                 615                 620

Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg Glu Tyr Leu Asp Trp
625                 630                 635                 640
```

Leu Arg Glu Asn Thr Gly
645

<210> 70
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-T33-31A

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 70

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr

```
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320
```

```
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Gly Ser Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala
```

```
        515                 520                 525

Leu Val Ala Val Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala
    530                 535                 540

Ala Cys Val Asn Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu Glu
545                 550                 555                 560

Gly Ser Val Val Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr
                565                 570                 575

Thr Asp Ala Phe Pro Lys Leu Lys Glu Arg Val Lys Glu Leu His Pro
            580                 585                 590

Tyr Glu Val Pro Glu Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg
        595                 600                 605

Glu Tyr Leu Asp Trp Leu Arg Glu Asn Thr Gly
    610                 615


<210>  71
<211>  665
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DS-Cav1-foldon-T33-15B


<220>
<221>  MISC_FEATURE
<222>  (1)..(25)
<223>  optionally absent

<400>  71

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1               5                   10                  15

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

```
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
```

```
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430
```

```
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
        515                 520                 525

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Met
    530                 535                 540

Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn Ser Asp Thr Pro Thr
545                 550                 555                 560

Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu Lys Met Leu Glu Ala
                565                 570                 575

Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala Val Ile Phe Thr Val
            580                 585                 590

Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Gln Ile
        595                 600                 605

Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val Pro
    610                 615                 620

Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr Asp
```

625 630 635 640

Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Ser Glu Ala Val Arg
645 650 655

Leu Arg Pro Asp Leu Glu Ser Ala Gln
660 665

<210> 72
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-T33-15B

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 72

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

```
Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
```

```
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495
```

```
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Gly Ser Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn
        515                 520                 525

Ser Asp Thr Pro Thr Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu
    530                 535                 540

Lys Met Leu Glu Ala Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala
545                 550                 555                 560

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

Ala Ala Arg Gln Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg
            580                 585                 590

Glu Val Pro Val Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala
        595                 600                 605

Leu Trp Asn Thr Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu
    610                 615                 620

Ser Glu Ala Val Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
625                 630                 635
```

<210> 73
<211> 769
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-foldon-I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 73

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                   10                  15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190
```

```
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
```

```
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
        515                 520                 525

Leu Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His
    530                 535                 540

His His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala
545                 550                 555                 560

Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile
                565                 570                 575

Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala
            580                 585                 590
```

```
Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr
        595                 600                 605

Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu
    610                 615                 620

Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys
625                 630                 635                 640

Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu
                645                 650                 655

Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met
            660                 665                 670

Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly
        675                 680                 685

His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe
    690                 695                 700

Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr
705                 710                 715                 720

Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val
                725                 730                 735

Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu
            740                 745                 750

Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr
        755                 760                 765

Glu
```

<210> 74

<211> 730
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 74

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

```
Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
```

```
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met
        515                 520                 525

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

```
Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly
545                 550                 555                 560


Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val
                565                 570                 575


Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala
            580                 585                 590


Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly
        595                 600                 605


Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe
    610                 615                 620


Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr
625                 630                 635                 640


Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe
                645                 650                 655


Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro
            660                 665                 670


Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn
        675                 680                 685


Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser
    690                 695                 700


Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala
705                 710                 715                 720


Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
                725                 730
```

<210> 75

<211> 676
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-I32-28A

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 75

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

```
Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
```

```
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Gly Ser Gly Gly Ser Gly Ser Asp Asp Ala Arg Ile Ala Ala
        515                 520                 525

Ile Gly Asp Val Asp Glu Leu Asn Ser Gln Ile Gly Val Leu Leu Ala
    530                 535                 540
```

```
Glu Pro Leu Pro Asp Asp Val Arg Ala Ala Leu Ser Ala Ile Gln His
545                 550                 555                 560


Asp Leu Phe Asp Leu Gly Gly Glu Leu Cys Ile Pro Gly His Ala Ala
                565                 570                 575


Ile Thr Glu Asp His Leu Leu Arg Leu Ala Leu Trp Leu Val His Tyr
            580                 585                 590


Asn Gly Gln Leu Pro Pro Leu Glu Glu Phe Ile Leu Pro Gly Gly Ala
        595                 600                 605


Arg Gly Ala Ala Leu Ala His Val Cys Arg Thr Val Cys Arg Arg Ala
    610                 615                 620


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


Pro Ala Ala Tyr Val Asn Leu Leu Ser Asp Leu Leu Phe Val Leu Ala
                645                 650                 655


Arg Val Leu Asn Arg Ala Ala Gly Gly Ala Asp Val Leu Trp Asp Arg
            660                 665                 670


Thr Arg Ala His
        675


<210>  76
<211>  730
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DS-Cav1-8GS-HelExt-I53-50A (F10)


<220>
<221>  MISC_FEATURE
<222>  (1)..(25)
<223>  optionally absent
```

<400> 76

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                  10                  15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190
```

```
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
```

```
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Gly Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met
        515                 520                 525

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

Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly
545                 550                 555                 560

Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val
                565                 570                 575

Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala
            580                 585                 590
```

```
Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly
        595                 600                 605


Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe
    610                 615                 620


Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr
625                 630                 635                 640


Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe
                645                 650                 655


Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro
            660                 665                 670


Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn
        675                 680                 685


Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser
    690                 695                 700


Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala
705                 710                 715                 720


Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
                725                 730


<210>  77
<211>  764
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DS-Cav1-foldon-15GS-HelExt-I53-50A (F14)


<220>
<221>  MISC_FEATURE
<222>  (1)..(25)
<223>  optionally absent
```

<400> 77

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                  10                  15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190
```

```
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
```

```
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
        515                 520                 525

Leu Leu Ser Thr Phe Leu Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly
    530                 535                 540

Gly Ser Gly Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg
545                 550                 555                 560

Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg
                565                 570                 575

Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala
            580                 585                 590
```

```
Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp
        595                 600                 605

Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile
    610                 615                 620

Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu
625                 630                 635                 640

Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser
                645                 650                 655

Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr
            660                 665                 670

Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys
        675                 680                 685

Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys
    690                 695                 700

Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu
705                 710                 715                 720

Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val
                725                 730                 735

Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala
            740                 745                 750

Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
        755                 760
```

<210> 78
<211> 774
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV F wt_CAN97-83 strain-I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 78

```
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30


Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45


Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
    50                  55                  60


Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80


Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95


Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110


Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125


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


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

```
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
```

```
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
                485                 490                 495

Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
            500                 505                 510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
        515                 520                 525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Ser Gly Ser Gly Ser His
    530                 535                 540

His His His His His His His Gly Gly Ser Gly Gly Ser Gly Ser Glu
545                 550                 555                 560
```

```
Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe
               565                 570                 575

Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu
            580                 585                 590

Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His Leu Ile
        595                 600                 605

Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu
    610                 615                 620

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

Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile
               645                 650                 655

Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys
            660                 665                 670

Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys
        675                 680                 685

Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val
    690                 695                 700

Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val
705                 710                 715                 720

Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp
               725                 730                 735

Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys
            740                 745                 750

Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys
```

```
        755                 760                 765


Ile Arg Gly Cys Thr Glu
    770


<210>  79
<211>  725
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HMPV F A113C_A339C_T160F_I177L-I53-50A


<220>
<221>  MISC_FEATURE
<222>  (1)..(18)
<223>  optionally absent

<400>  79

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30


Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45


Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
    50                  55                  60


Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80


Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95


Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
```

```
Cys Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
```

```
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Gly Ser Gly Ser His His
                485                 490                 495

His His His His His His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys
            500                 505                 510
```

```
Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys
        515                 520                 525

Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala
    530                 535                 540

Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu
545                 550                 555                 560

Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser
                565                 570                 575

Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser
            580                 585                 590

Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val
        595                 600                 605

Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly
    610                 615                 620

Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala
625                 630                 635                 640

Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val
                645                 650                 655

Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys
            660                 665                 670

Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe
        675                 680                 685

Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly
    690                 695                 700

Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile
```

705 710 715 720

Arg Gly Cys Thr Glu
725

<210> 80
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV F A113C_A339C_T160F_I177L_A120C, Q426C - I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 80

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95

Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110

```
Cys Thr Ala Ala Ala Val Thr Cys Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
```

```
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Gly Ser Gly Ser His His
                485                 490                 495

His His His His His His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys
            500                 505                 510
```

```
Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys
        515                 520                 525

Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala
    530                 535                 540

Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu
545                 550                 555                 560

Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser
                565                 570                 575

Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser
            580                 585                 590

Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val
        595                 600                 605

Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly
    610                 615                 620

Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala
625                 630                 635                 640

Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val
                645                 650                 655

Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys
            660                 665                 670

Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe
        675                 680                 685

Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly
    690                 695                 700

Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile
```

705 710 715 720

Arg Gly Cys Thr Glu
725

<210> 81
<211> 703
<212> PRT
<213> Artificial Sequence

<220>
<223> sc-DS2-I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 81

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Cys Ile Ala Ser Gly
100 105 110

```
Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140

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

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser
                165                 170                 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
        195                 200                 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
```

```
305                 310                 315                 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385                 390                 395                 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
                405                 410                 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly
            420                 425                 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
        435                 440                 445

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

Ala Phe Ile Arg Gly Ser Gly Ser His His His His His His His His
465                 470                 475                 480

Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu
                485                 490                 495

Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala
            500                 505                 510
```

```
Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala
        515                 520                 525

Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro
    530                 535                 540

Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly
545                 550                 555                 560

Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys
                565                 570                 575

Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu
            580                 585                 590

Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly
        595                 600                 605

Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr
    610                 615                 620

Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys
625                 630                 635                 640

Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly
                645                 650                 655

Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala
            660                 665                 670

Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg
        675                 680                 685

Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
    690                 695                 700
```

<210> 82

<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> tc-DS2-I53-50A

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 82

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

```
Gly Ser Cys Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160


Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175


Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190


Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205


Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220


Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240


Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255


Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270


Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285


Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300


Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320


Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335


Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
```

```
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Cys Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Gly Ser Gly Ser His
            500                 505                 510

His His His His His His His Gly Gly Ser Gly Gly Ser Gly Ser Glu
        515                 520                 525

Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe
    530                 535                 540
```

```
Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu
545                 550                 555                 560


Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His Leu Ile
                565                 570                 575


Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu
            580                 585                 590


Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr
        595                 600                 605


Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile
    610                 615                 620


Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys
625                 630                 635                 640


Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys
                645                 650                 655


Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val
            660                 665                 670


Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val
        675                 680                 685


Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp
    690                 695                 700


Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys
705                 710                 715                 720


Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys
                725                 730                 735


Ile Arg Gly Cys Thr Glu
```

740

<210> 83
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-12GS-HelExt-I53-50A (F11)

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 83

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

```
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
```

```
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Gly Ser Gly Ser Gly Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu Ala
        515                 520                 525
```

```
Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val
    530                 535                 540

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

Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp
                565                 570                 575

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

Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala
        595                 600                 605

Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu
    610                 615                 620

Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val
625                 630                 635                 640

Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile
                645                 650                 655

Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala
            660                 665                 670

Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val
        675                 680                 685

Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val
    690                 695                 700

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

Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
```

725 730

<210> 84
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-16GS-HelExt-I53-50A (F12)

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 84

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

```
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
```

```
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Glu Lys Ala Ala Lys
        515                 520                 525
```

```
Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys
    530                 535                 540

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

Ala Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe
                565                 570                 575

Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys
            580                 585                 590

Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln
        595                 600                 605

Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His
    610                 615                 620

Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr
625                 630                 635                 640

Met Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu
                645                 650                 655

Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln
            660                 665                 670

Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro
        675                 680                 685

Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly
    690                 695                 700

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

Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys
```

725 730 735

Thr Glu

<210> 85
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-foldon-10GS-HelExt-I53-50A (F13)

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 85

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

```
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
```

```
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Gly Tyr Ile Pro Glu
            500                 505                 510
```

```
Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
        515                 520                 525

Leu Leu Ser Thr Phe Leu Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly
    530                 535                 540

Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu
545                 550                 555                 560

Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val Glu
                565                 570                 575

Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His Leu
            580                 585                 590

Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala
        595                 600                 605

Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr Val
    610                 615                 620

Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe
625                 630                 635                 640

Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu
                645                 650                 655

Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu Val
            660                 665                 670

Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu
        675                 680                 685

Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn
    690                 695                 700

Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu
```

705 710 715 720

Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu Val
725 730 735

Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu
740 745 750

Lys Ile Arg Gly Cys Thr Glu
755

<210> 86
<211> 769
<212> PRT
<213> Artificial Sequence

<220>
<223> DS-Cav1-foldon-20GS-HelExt-I53-50A (F15)

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<400> 86

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145                 150                 155                 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
            180                 185                 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
        195                 200                 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
```

```
        275                 280                 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480
```

```
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

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

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
        515                 520                 525

Leu Leu Ser Thr Phe Leu Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly
    530                 535                 540

Gly Ser Gly Ser Gly Gly Ser Ser Gly Ser Glu Lys Ala Ala Lys Ala
545                 550                 555                 560

Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile
                565                 570                 575

Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala
            580                 585                 590

Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr
        595                 600                 605

Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu
    610                 615                 620

Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys
625                 630                 635                 640

Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu
                645                 650                 655

Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met
            660                 665                 670

Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly
```

```
        675                 680                 685

His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe
    690                 695                 700

Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr
705                 710                 715                 720

Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val
                725                 730                 735

Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu
            740                 745                 750

Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr
        755                 760                 765

Glu
```

<210> 87
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> sc9-10 DS-Cav1 A149C Y458C-foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (469)..(474)
<223> optionally absent

<400> 87

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                   10                  15
```

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
            100                 105                 110

Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140

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

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser
                165                 170                 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
        195                 200                 205
```

```
Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305                 310                 315                 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385                 390                 395                 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
                405                 410                 415
```

```
Leu Tyr Cys Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly
            420                 425                 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
        435                 440                 445

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

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Tyr Ile Pro Glu Ala
465                 470                 475                 480

Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
                485                 490                 495

Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His His
            500                 505                 510

His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu
        515                 520                 525

Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val
    530                 535                 540

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

Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val
                565                 570                 575

Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys
            580                 585                 590

Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg
        595                 600                 605
```

```
Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp
    610                 615                 620

Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro
625                 630                 635                 640

Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His
                645                 650                 655

Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val
            660                 665                 670

Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly
        675                 680                 685

Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu
    690                 695                 700

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

Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
                725                 730                 735
```

<210> 88
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> sc9-10 DS-Cav1 A149C Y458C - F10 embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (469)..(474)
<223> optionally absent

<400> 88

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                  10                  15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
            100                 105                 110

Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140

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

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser
                165                 170                 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190
```

```
Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
        195                 200                 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305                 310                 315                 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
```

385 390 395 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
405 410 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly
420 425 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
435 440 445

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

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Ser Gly Gly Ser Gly
465 470 475 480

Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu
485 490 495

Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser
500 505 510

Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val
515 520 525

His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile
530 535 540

Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly
545 550 555 560

Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala
565 570 575

Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys
580 585 590

```
Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu
        595                 600                 605

Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro
    610                 615                 620

Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe
625                 630                 635                 640

Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val
                645                 650                 655

Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala
            660                 665                 670

Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe
        675                 680                 685

Val Glu Lys Ile Arg Gly Cys Thr Glu
    690                 695
```

<210> 89
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> sc9-10 DS-Cav1 A149C Y458C S46G K465Q S215P E92D -foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (469)..(474)
<223> optionally absent

<400> 89

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                  10                  15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Gly Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
            100                 105                 110

Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140

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

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Pro
                165                 170                 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
```

```
        195                 200                 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305                 310                 315                 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385                 390                 395                 400
```

```
Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
                405                 410                 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Gln Ser Leu Tyr Val Lys Gly
            420                 425                 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
        435                 440                 445

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

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Tyr Ile Pro Glu Ala
465                 470                 475                 480

Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
                485                 490                 495

Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His His
            500                 505                 510

His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu
        515                 520                 525

Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val
    530                 535                 540

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

Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val
                565                 570                 575

Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys
            580                 585                 590

Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg
```

```
        595                 600                 605

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

Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro
625                 630                 635                 640

Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His
                645                 650                 655

Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val
            660                 665                 670

Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly
        675                 680                 685

Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu
    690                 695                 700

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

Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
                725                 730                 735


<210>  90
<211>  697
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  sc9-10 DS-Cav1 A149C Y458C S46G K465Q S215P E92D - F10 embodiment


<220>
<221>  MISC_FEATURE
<222>  (1)..(25)
<223>  optionally absent

<220>
```

<221> MISC_FEATURE
<222> (469)..(474)
<223> optionally absent

<400> 90

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                  10                  15


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


Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Gly Ala Leu
        35                  40                  45


Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60


Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80


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


Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
            100                 105                 110


Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
        115                 120                 125


Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
    130                 135                 140


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


Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Pro
                165                 170                 175
```

```
Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
            180                 185                 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
        195                 200                 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
    210                 215                 220

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

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
                245                 250                 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
            260                 265                 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
        275                 280                 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
    290                 295                 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305                 310                 315                 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
                325                 330                 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
            340                 345                 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
        355                 360                 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
    370                 375                 380
```

```
Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385                 390                 395                 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
                405                 410                 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Gln Ser Leu Tyr Val Lys Gly
            420                 425                 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
        435                 440                 445

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

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Ser Gly Gly Ser Gly
465                 470                 475                 480

Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu
                485                 490                 495

Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser
            500                 505                 510

Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val
        515                 520                 525

His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile
    530                 535                 540

Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly
545                 550                 555                 560

Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala
                565                 570                 575
```

```
Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys
            580                 585                 590

Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu
        595                 600                 605

Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro
    610                 615                 620

Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe
625                 630                 635                 640

Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val
                645                 650                 655

Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala
            660                 665                 670

Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe
        675                 680                 685

Val Glu Lys Ile Arg Gly Cys Thr Glu
    690                 695
```

<210> 91
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<223> SC-DM (N67I, S215P) - foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (486)..(491)
<223> optionally absent

<400> 91

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                  10                  15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60

Lys Lys Ile Lys Cys Asn Gly Thr Asp Ala Lys Ile Lys Leu Ile Lys
65                  70                  75                  80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Gln Ala Arg Gly Ser Gly Ser
            100                 105                 110

Gly Arg Ser Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser
        115                 120                 125

Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys
    130                 135                 140

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

Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
                165                 170                 175

Ile Asp Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile
            180                 185                 190
```

```
Pro Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu
        195                 200                 205

Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro
    210                 215                 220

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

Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val
                245                 250                 255

Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu
            260                 265                 270

Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp
        275                 280                 285

Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr
    290                 295                 300

Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr
305                 310                 315                 320

Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys
                325                 330                 335

Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr
            340                 345                 350

Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys
        355                 360                 365

Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val
    370                 375                 380

Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys
```

```
385                 390                 395                 400

Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly
                405                 410                 415

Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn
            420                 425                 430

Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys
        435                 440                 445

Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
    450                 455                 460

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

Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Tyr Ile Pro Glu
                485                 490                 495

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
            500                 505                 510

Leu Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His
        515                 520                 525

His His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala
    530                 535                 540

Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile
545                 550                 555                 560

Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala
                565                 570                 575

Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr
            580                 585                 590
```

```
Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu
        595                 600                 605

Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys
    610                 615                 620

Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu
625                 630                 635                 640

Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met
                645                 650                 655

Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly
            660                 665                 670

His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe
        675                 680                 685

Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr
    690                 695                 700

Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val
705                 710                 715                 720

Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu
                725                 730                 735

Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr
            740                 745                 750

Glu
```

<210> 92
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> SC-DM (N67I, S215P) - F10 embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (486)..(491)
<223> optionally absent

<400> 92

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                   10                  15


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


Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45


Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60


Lys Lys Ile Lys Cys Asn Gly Thr Asp Ala Lys Ile Lys Leu Ile Lys
65                  70                  75                  80


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


Met Gln Ser Thr Pro Ala Thr Asn Asn Gln Ala Arg Gly Ser Gly Ser
            100                 105                 110


Gly Arg Ser Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser
        115                 120                 125


Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys
    130                 135                 140
```

```
Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser
145                 150                 155                 160


Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
                165                 170                 175


Ile Asp Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile
            180                 185                 190


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


Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro
    210                 215                 220


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


Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val
                245                 250                 255


Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu
            260                 265                 270


Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp
        275                 280                 285


Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr
    290                 295                 300


Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr
305                 310                 315                 320


Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys
                325                 330                 335
```

```
Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr
            340                 345                 350

Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys
        355                 360                 365

Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val
    370                 375                 380

Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys
385                 390                 395                 400

Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly
                405                 410                 415

Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn
            420                 425                 430

Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys
        435                 440                 445

Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
    450                 455                 460

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

Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Ser Gly Gly Ser
                485                 490                 495

Gly Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met
            500                 505                 510

Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn
        515                 520                 525

Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly
    530                 535                 540
```

```
Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val
545                 550                 555                 560


Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala
                565                 570                 575


Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly
            580                 585                 590


Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe
        595                 600                 605


Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr
    610                 615                 620


Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe
625                 630                 635                 640


Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro
                645                 650                 655


Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn
            660                 665                 670


Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser
        675                 680                 685


Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala
    690                 695                 700


Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
705                 710
```

<210> 93
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<223> SC-TM (N67I, S215P, and E487Q) - foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (486)..(491)
<223> optionally absent

<400> 93

```
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1               5                   10                  15


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


Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45


Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60


Lys Lys Ile Lys Cys Asn Gly Thr Asp Ala Lys Ile Lys Leu Ile Lys
65                  70                  75                  80


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


Met Gln Ser Thr Pro Ala Thr Asn Asn Gln Ala Arg Gly Ser Gly Ser
            100                 105                 110


Gly Arg Ser Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser
        115                 120                 125


Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys
```

```
    130                 135                 140

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

Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
                165                 170                 175

Ile Asp Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile
            180                 185                 190

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

Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro
    210                 215                 220

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

Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val
                245                 250                 255

Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu
            260                 265                 270

Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp
        275                 280                 285

Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr
    290                 295                 300

Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr
305                 310                 315                 320

Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys
                325                 330                 335
```

```
Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr
            340                 345                 350

Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys
        355                 360                 365

Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val
    370                 375                 380

Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys
385                 390                 395                 400

Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly
                405                 410                 415

Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn
            420                 425                 430

Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys
        435                 440                 445

Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
    450                 455                 460

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

Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Tyr Ile Pro Glu
                485                 490                 495

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
            500                 505                 510

Leu Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His
        515                 520                 525

His His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala
```

```
    530                 535                 540

Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile
545                 550                 555                 560

Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala
                565                 570                 575

Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr
            580                 585                 590

Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu
        595                 600                 605

Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys
    610                 615                 620

Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu
625                 630                 635                 640

Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met
                645                 650                 655

Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly
            660                 665                 670

His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe
        675                 680                 685

Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr
    690                 695                 700

Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val
705                 710                 715                 720

Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu
                725                 730                 735
```

Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr
            740   745   750

Glu

<210> 94
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> SC-TM (N67I, S215P, and E487Q)-I53-50A - F10 embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> optionally absent

<220>
<221> MISC_FEATURE
<222> (486)..(491)
<223> optionally absent

<400> 94

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1   5   10   15

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

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35   40   45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50   55   60

Lys Lys Ile Lys Cys Asn Gly Thr Asp Ala Lys Ile Lys Leu Ile Lys
65   70   75   80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Gln Ala Arg Gly Ser Gly Ser
            100                 105                 110

Gly Arg Ser Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser
        115                 120                 125

Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys
    130                 135                 140

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

Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
                165                 170                 175

Ile Asp Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile
            180                 185                 190

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

Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro
    210                 215                 220

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

Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val
                245                 250                 255

Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu
            260                 265                 270

Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp
        275                 280                 285
```

```
Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr
    290                 295                 300

Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr
305                 310                 315                 320

Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys
                325                 330                 335

Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr
            340                 345                 350

Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys
        355                 360                 365

Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val
    370                 375                 380

Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys
385                 390                 395                 400

Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly
                405                 410                 415

Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn
            420                 425                 430

Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys
        435                 440                 445

Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
    450                 455                 460

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

```
Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Gly Ser Gly Gly Ser
                485                 490                 495

Gly Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met
            500                 505                 510

Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn
        515                 520                 525

Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly
    530                 535                 540

Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val
545                 550                 555                 560

Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala
                565                 570                 575

Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly
            580                 585                 590

Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe
        595                 600                 605

Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr
    610                 615                 620

Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe
625                 630                 635                 640

Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro
                645                 650                 655

Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn
            660                 665                 670

Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser
        675                 680                 685
```

Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala
690 695 700

Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
705 710

<210> 95
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV-F with A113C, A339C, T160F, I177L - foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 95

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95

```
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Cys Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
```

```
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Gly Tyr Ile Pro Glu Ala
                485                 490                 495
```

```
Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
            500                 505                 510

Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His His
        515                 520                 525

His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu
    530                 535                 540

Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val
545                 550                 555                 560

Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val
                565                 570                 575

Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val
            580                 585                 590

Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys
        595                 600                 605

Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg
    610                 615                 620

Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp
625                 630                 635                 640

Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro
                645                 650                 655

Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His
            660                 665                 670

Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val
        675                 680                 685

Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly
```

690 695 700

Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu
705 710 715 720

Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val
725 730 735

Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
740 745 750

<210> 96
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV-F with A113C, A339C, T160F, I177L-I53-50A F10 embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 96

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80

```
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95

Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Cys Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
```

```
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480
```

```
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Gly Ser Gly Gly Ser Gly
                485                 490                 495

Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu
            500                 505                 510

Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser
        515                 520                 525

Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val
    530                 535                 540

His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile
545                 550                 555                 560

Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly
                565                 570                 575

Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala
            580                 585                 590

Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys
        595                 600                 605

Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu
    610                 615                 620

Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro
625                 630                 635                 640

Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe
                645                 650                 655

Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val
            660                 665                 670

Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala
```

675 680 685

Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe
690 695 700

Val Glu Lys Ile Arg Gly Cys Thr Glu
705 710

<210> 97
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV-F with A113C, A120C, A339C, T160F, I177L, and Q426C - foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 97

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95

```
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Cys Thr Ala Ala Ala Val Thr Cys Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285
```

```
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Gly Tyr Ile Pro Glu Ala
                485                 490                 495
```

```
Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
            500                 505                 510

Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His His
        515                 520                 525

His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu
    530                 535                 540

Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val
545                 550                 555                 560

Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val
                565                 570                 575

Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val
            580                 585                 590

Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys
        595                 600                 605

Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg
    610                 615                 620

Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp
625                 630                 635                 640

Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro
                645                 650                 655

Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His
            660                 665                 670

Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val
        675                 680                 685
```

Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly
690 695 700

Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu
705 710 715 720

Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val
725 730 735

Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
740 745 750

<210> 98
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV-F with A113C, A120C, A339C, T160F, I177L, and Q426C - F10 embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 98

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu

```
65                  70                  75                  80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95

Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Cys Thr Ala Ala Ala Val Thr Cys Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270
```

```
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Cys Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
```

```
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Gly Ser Gly Gly Ser Gly
                485                 490                 495

Ser Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu
            500                 505                 510

Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser
        515                 520                 525

Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val
    530                 535                 540

His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile
545                 550                 555                 560

Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly
                565                 570                 575

Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala
            580                 585                 590

Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys
        595                 600                 605

Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu
    610                 615                 620

Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro
625                 630                 635                 640

Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe
                645                 650                 655

Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val
            660                 665                 670
```

Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala
        675   680   685

Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe
    690   695   700

Val Glu Lys Ile Arg Gly Cys Thr Glu
705   710

<210> 99
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV-F 115-BV (A185P) -foldon-I53-50A embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 99

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1   5   10   15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20   25   30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35   40   45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
    50   55   60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65   70   75   80

Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu

```
                85                  90                  95

Asn Pro Arg Arg Arg Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Ile Asn Lys Asn Lys Cys Asp Ile Pro Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285
```

```
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Tyr Ile Pro Glu Ala Pro
```

```
                485                 490                 495

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
            500                 505                 510

Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His His His
        515                 520                 525

Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu
    530                 535                 540

Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala
545                 550                 555                 560

Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala
                565                 570                 575

Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro
            580                 585                 590

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

Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys
    610                 615                 620

Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu
625                 630                 635                 640

Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly
                645                 650                 655

Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr
            660                 665                 670

Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys
        675                 680                 685
```

```
Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly
    690                 695                 700


Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala
705                 710                 715                 720


Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg
                725                 730                 735


Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
            740                 745                 750
```

<210> 100
<211> 712
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV-F 115-BV (A185P)-I53-50A - F10 embodiment

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 100

```
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15


His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30


Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45


Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
    50                  55                  60


Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
```

```
65                  70                  75                  80

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

Asn Pro Arg Arg Arg Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Ile Asn Lys Asn Lys Cys Asp Ile Pro Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270
```

```
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285

Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
```

```
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Ser Gly Gly Ser Gly Ser
                485                 490                 495

Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu
            500                 505                 510

Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val
        515                 520                 525

Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His
    530                 535                 540

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

Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr
                565                 570                 575

Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu
            580                 585                 590

Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys
        595                 600                 605

Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu
    610                 615                 620

Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly
625                 630                 635                 640

Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro
                645                 650                 655

Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys
            660                 665                 670
```

Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu
        675   680   685

Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val
    690   695   700

Glu Lys Ile Arg Gly Cys Thr Glu
705   710

<210> 101
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> HMPV F >AAK62968.2 fusion protein [Human metapneumovirus]

<220>
<221> MISC_FEATURE
<222> (1)..(18)
<223> optionally absent

<400> 101

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1   5   10   15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20   25   30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35   40   45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
    50   55   60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65   70   75   80

Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu

```
                85                  90                  95

Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125

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

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175

Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
            180                 185                 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255

Gly Phe Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285
```

```
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415

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

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

Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460

Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly
```

485 490