SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Removal of target cells by circulating virus-specific cytotoxic T-cells using MHC class I comprising complexes

<130> 27493

<150> EP11171027.3
<151> 2011-06-22

<160> 112

<170> PatentIn version 3.5

<210> 1
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 1

Asn Leu Val Pro Met Val Ala Thr Val
1 5

<210> 2
<211> 9
<212> PRT
<213> Human immunodeficiency virus

<400> 2

Ser Leu Tyr Asn Thr Val Ala Thr Leu
1 5

<210> 3
<211> 9
<212> PRT
<213> Human herpesvirus 4

<400> 3

Gly Leu Cys Thr Leu Val Ala Met Leu
1 5

<210> 4
<211> 9
<212> PRT
<213> Influenza A virus

<400> 4

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 5
<211> 9
<212> PRT
<213> Hepatitis B virus

<400> 5

Ser Thr Asn Arg Gln Ser Gly Arg Gln

1 5

<210> 6
<211> 9
<212> PRT
<213> Human T-cell lymphotropic virus type 1

<400> 6

Leu Leu Phe Gly Tyr Pro Val Tyr Val
1 5

<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> V-jun Sarcoma Virus 17 Oncogene Homolog (JUN)

<400> 7

Phe Ala Glu Gly Phe Val Arg Ala Leu
1 5

<210> 8
<211> 9
<212> PRT
<213> Human adenovirus type 3

<400> 8

Leu Ile Val Ile Gly Ile Leu Ile Leu
1 5

<210> 9
<211> 8
<212> PRT
<213> Hepatitis C virus

<400> 9

Ile Leu His Thr Pro Gly Cys Val
1 5

<210> 10
<211> 99
<212> PRT
<213> Homo sapiens

<400> 10

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu
1 5 10 15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro
20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys
35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu
50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys
65 70 75 80

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

Arg Asp Met

<210> 11
<211> 274
<212> PRT
<213> Homo sapiens

<400> 11

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg
35 40 45

Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr
50 55 60

Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr
65 70 75 80

Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln
85 90 95

Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly
100 105 110

Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu
115 120 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys
130 135 140

His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu
145 150 155 160

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

eolf-seql

Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His
180 185 190

Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe
195 200 205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
210 215 220

Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg
245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu
260 265 270

Arg Trp

<210> 12
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 1

<400> 12

Gly Ser
1

<210> 13
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 2

<400> 13

Gly Gly Ser
1

<210> 14
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 3

<400> 14

Gly Gly Gly Ser
1

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 4

<400> 15

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 16
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 5

<400> 16

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 17
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 6

<400> 17

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

<210> 18
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 7

<400> 18

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

Gly Gly Gly Ser
20

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> linker peptide 8

<400> 19

Gly Gly Gly Gly Ser
1 5

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 9

<400> 20

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 10

<400> 21

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

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 11

<400> 22

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

Gly Gly Gly Ser
20

<210> 23
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptide 12

<400> 23

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

eolf-seql
Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 24
<211> 15
<212> PRT
<213> Homo sapiens

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 25
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 heavy chain hinge region polypeptide variant

<400> 25

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 26
<211> 12
<212> PRT
<213> Homo sapiens

<400> 26

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1 5 10

<210> 27
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG2 heavy chain hinge region polypeptide variant 1

<400> 27

Glu Arg Lys Cys Ala Val Glu Cys Pro Pro Cys Pro
1 5 10

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG2 heavy chain hinge region polypeptide variant 2

<400> 28

Glu Arg Lys Ala Cys Val Glu Cys Pro Pro Cys Pro
1 5 10

<210> 29
<211> 62
<212> PRT
<213> Homo sapiens

<400> 29

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1 5 10 15

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
20 25 30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
35 40 45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
50 55 60

<210> 30
<211> 12
<212> PRT
<213> Homo sapiens

<400> 30

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1 5 10

<210> 31
<211> 107
<212> PRT
<213> Homo sapiens

<400> 31

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
1 5 10 15

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
20 25 30

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
50 55 60

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
65 70 75 80

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
85 90 95

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 32
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huamn IgG1 CH2 domain with the mutations L234A and L235A

<400> 32

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
1 5 10 15

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
20 25 30

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
50 55 60

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
65 70 75 80

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
85 90 95

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 33
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG CH2 domain with the mutations L234A, L235A and P329G

<400> 33

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
1 5 10 15

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
20 25 30

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
50 55 60

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
65 70 75 80

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
85 90 95

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 34
<211> 105
<212> PRT
<213> Homo sapiens

<400> 34

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 35
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 CH3 domain knob variant

<400> 35

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

```
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65                  70                  75                  80


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                85                  90                  95


Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105


<210>  36
<211>  105
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  human IgG1 CH3 domain hole variant

<400>  36

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
1               5                   10                  15


Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
            20                  25                  30


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


Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
    50                  55                  60


Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65                  70                  75                  80


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                85                  90                  95


Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105


<210>  37
<211>  232
<212>  PRT
<213>  Homo sapiens

<400>  37

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15


Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
```

35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 38
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 heavy chain Fc-region with the mutations L234A and L235A

<400> 38

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 39
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 heavy chain Fc-region wiith mutations L234A and L235A as hole variant

<400> 39

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

```
Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 40
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 heavy chain Fc region with mutations L234A and L235A knob variant

<400> 40

eolf-seql

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 41
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig Light Chain

<400> 41

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Tyr Asp Ala Ser Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ser Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 42
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig Heavy Chain (IgG1-L234A, L235A mutant)

<400> 42

eolf-seql

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

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

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

Ala Ile Ile Trp Phe Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Glu Leu Gly Arg Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270
```

eolf-seql

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 43
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig Heavy Chain (IgG1-L234A, L235A mutant with knob variation)

<400> 43

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

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

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

Ala Ile Ile Trp Phe Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Leu Gly Arg Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335
```

```
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210>  44
<211>  448
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ig Heavy Chain (IgG1-L234A, L235A mutant with hole variation)

<400>  44

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

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

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

Ala Ile Ile Trp Phe Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Glu Leu Gly Arg Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110
```

```
Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
            340                 345                 350

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

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
```

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 45
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig heavy chain Fc region (IgG1-L234A, L235A mutant Fc-region)

<400> 45

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

```
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 46
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> scFv

<400> 46

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

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

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

Ala Ile Ile Trp Phe Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Glu Leu Gly Arg Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Ser Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
    130                 135                 140

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
145                 150                 155                 160
```

eolf-seql

Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Lys Arg
180 185 190

Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr
210 215 220

Tyr Cys Gln Gln Arg Ser Lys Trp Pro Pro Trp Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ser Lys
245

<210> 47
<211> 10
<212> PRT
<213> Homo sapiens

<400> 47

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 48
<211> 7
<212> PRT
<213> Homo sapiens

<400> 48

Val Glu Cys Pro Pro Cys Pro
1 5

<210> 49
<211> 8
<212> PRT
<213> Homo sapiens

<400> 49

Ala Val Glu Cys Pro Pro Cys Pro
1 5

<210> 50
<211> 10
<212> PRT
<213> Homo sapiens

<400> 50

Asp Thr Thr His Thr Cys Pro Arg Cys Pro
1 5 10

<210> 51
<211> 7
<212> PRT
<213> Homo sapiens

<400> 51

Pro Pro Cys Pro Ser Cys Pro
1 5

<210> 52
<211> 9
<212> PRT
<213> Dengue virus

<400> 52

Trp Tyr Ala Gln Ile Gln Pro His Trp
1 5

<210> 53
<211> 9
<212> PRT
<213> Dengue virus

<400> 53

Ala Phe Ser Gly Val Ser Trp Thr Met
1 5

<210> 54
<211> 9
<212> PRT
<213> Dengue virus

<400> 54

Ile Leu Ile Gly Val Val Ile Thr Trp
1 5

<210> 55
<211> 9
<212> PRT
<213> Dengue virus

<400> 55

Met Met Ile Pro Thr Val Val Ala Phe
1 5

<210> 56
<211> 9
<212> PRT
<213> Dengue virus

<400> 56

Pro Phe Pro Gln Ser Asn Ala Pro Ile
1 5

<210> 57
<211> 9

<212> PRT
<213> Dengue virus

<400> 57

Leu Leu Leu Thr Leu Leu Ala Thr Val
1 5

<210> 58
<211> 9
<212> PRT
<213> Dengue virus

<400> 58

Ile Val Leu Glu His Gly Ser Cys Val
1 5

<210> 59
<211> 9
<212> PRT
<213> Dengue virus

<400> 59

Leu Leu Phe Lys Thr Glu Asn Gly Val
1 5

<210> 60
<211> 9
<212> PRT
<213> Dengue virus

<400> 60

Pro Leu Asn Glu Ala Ile Met Ala Val
1 5

<210> 61
<211> 9
<212> PRT
<213> Dengue virus

<400> 61

Asn Leu Val Arg Leu Gln Ser Gly Val
1 5

<210> 62
<211> 9
<212> PRT
<213> Dengue virus

<400> 62

Leu Val Ile Ser Gly Leu Phe Pro Val
1 5

<210> 63
<211> 9
<212> PRT
<213> Dengue virus

<400> 63

Leu Leu Leu Val Ala His Tyr Ala Ile
1 5

<210> 64
<211> 9
<212> PRT
<213> Dengue virus

<400> 64

Leu Ala Leu Leu Ala Ala Phe Lys Val
1 5

<210> 65
<211> 9
<212> PRT
<213> Dengue virus

<400> 65

Val Ile Leu Ala Gly Pro Met Pro Val
1 5

<210> 66
<211> 9
<212> PRT
<213> Dengue virus

<400> 66

His Val Leu Gly Arg Leu Ile Thr Val
1 5

<210> 67
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 67

Val Thr Glu His Asp Thr Leu Leu Tyr
1 5

<210> 68
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 68

Asn Thr Asp Phe Arg Val Leu Glu Leu
1 5

<210> 69
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 69

Cys Val Glu Thr Met Cys Asn Glu Tyr
1 5

<210> 70
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 70

Val Leu Glu Glu Thr Ser Val Met Leu
1 5

<210> 71
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 71

Asn Leu Val Pro Met Val Ala Thr Val
1 5

<210> 72
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 72

Arg Ile Phe Ala Glu Leu Glu Gly Val
1 5

<210> 73
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 73

Ile Ile Tyr Thr Arg Asn His Glu Val
1 5

<210> 74
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 74

Val Leu Ala Glu Leu Val Lys Gln Ile
1 5

<210> 75
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 75

Ala Val Gly Gly Ala Val Ala Ser Val

1 5

<210> 76
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 76

Thr Val Arg Ser His Cys Val Ser Lys
1 5

<210> 77
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 77

Ile Met Arg Glu Phe Asn Ser Tyr Lys
1 5

<210> 78
<211> 10
<212> PRT
<213> Human cytomegalovirus

<400> 78

Gly Pro Ile Ser His Gly His Val Leu Lys
1 5 10

<210> 79
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 79

Ala Thr Val Gln Gly Gln Asn Leu Lys
1 5

<210> 80
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 80

Val Tyr Ala Leu Pro Leu Lys Met Leu
1 5

<210> 81
<211> 10
<212> PRT
<213> Human cytomegalovirus

<400> 81

Ala Tyr Ala Gln Lys Ile Phe Lys Ile Leu
1 5 10

<210> 82
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 82

Gln Tyr Asp Pro Val Ala Ala Leu Phe
1 5

<210> 83
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 83

Tyr Val Lys Val Tyr Leu Glu Ser Phe
1 5

<210> 84
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 84

Asp Ile Tyr Arg Ile Phe Ala Glu Leu
1 5

<210> 85
<211> 10
<212> PRT
<213> Human cytomegalovirus

<400> 85

Val Phe Glu Thr Ser Gly Gly Leu Val Val
1 5 10

<210> 86
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 86

Lys Ala Arg Asp His Leu Ala Val Leu
1 5

<210> 87
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 87

Gln Ala Arg Leu Thr Val Ser Gly Leu
1 5

<210> 88

<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 88

Lys Ala Arg Ala Lys Lys Asp Glu Leu
1 5

<210> 89
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 89

Gln Ile Lys Val Arg Val Asp Met Val
1 5

<210> 90
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 90

Arg Arg Arg His Arg Gln Asp Ala Leu
1 5

<210> 91
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 91

Ala Arg Val Tyr Glu Ile Lys Cys Arg
1 5

<210> 92
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 92

Lys Met Gln Val Ile Gly Asp Gln Tyr
1 5

<210> 93
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 93

Asn Val Arg Arg Ser Trp Glu Glu Leu
1 5

<210> 94
<211> 12
<212> PRT

<213> Human cytomegalovirus

<400> 94

Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr Val Tyr
1 5 10

<210> 95
<211> 13
<212> PRT
<213> Human cytomegalovirus

<400> 95

Lys Pro Gly Lys Ile Ser His Ile Met Leu Asp Val Ala
1 5 10

<210> 96
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 96

Glu Leu Arg Arg Lys Met Met Tyr Met
1 5

<210> 97
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 97

Ile Pro Ser Ile Asn Val His His Tyr
1 5

<210> 98
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 98

Phe Glu Gln Pro Thr Glu Thr Pro Pro
1 5

<210> 99
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 99

Tyr Ala Tyr Ile Tyr Thr Thr Tyr Leu
1 5

<210> 100
<211> 11
<212> PRT
<213> Human cytomegalovirus

<400> 100

Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr
1 5 10

<210> 101
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 101

Tyr Glu Gln His Lys Ile Thr Ser Tyr
1 5

<210> 102
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 102

Gln Glu Pro Met Ser Ile Tyr Val Tyr
1 5

<210> 103
<211> 10
<212> PRT
<213> Human cytomegalovirus

<400> 103

Ser Glu His Pro Thr Phe Thr Ser Gln Tyr
1 5 10

<210> 104
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 104

Gln Ala Ile Arg Glu Thr Val Glu Leu
1 5

<210> 105
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 105

Thr Arg Ala Thr Lys Met Gln Val Ile
1 5

<210> 106
<211> 8
<212> PRT
<213> Human cytomegalovirus

<400> 106

Asp Ala Leu Pro Gly Pro Cys Ile
1 5

<210> 107
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 107

Cys Glu Asp Val Pro Ser Gly Lys Leu
1 5

<210> 108
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 108

His Glu Arg Asn Gly Phe Thr Val Leu
1 5

<210> 109
<211> 13
<212> PRT
<213> Human cytomegalovirus

<400> 109

Pro Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu
1 5 10

<210> 110
<211> 9
<212> PRT
<213> Human cytomegalovirus

<400> 110

Gln Met Trp Gln Ala Arg Leu Thr Val
1 5

<210> 111
<211> 12
<212> PRT
<213> Human cytomegalovirus

<400> 111

His Glu Leu Leu Val Leu Val Lys Lys Ala Gln Leu
1 5 10

<210> 112
<211> 12
<212> PRT
<213> Human cytomegalovirus

<400> 112

Asp Asp Tyr Ser Asn Thr His Ser Thr Arg Tyr Val
1 5 10