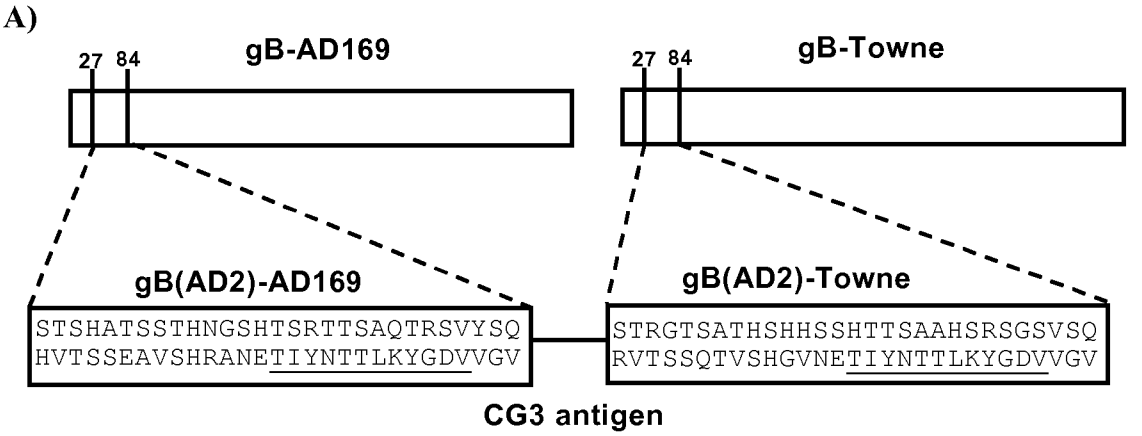
Fig. 1


A)
27 84
gB-AD169
27 84
gB-Towne
gB(AD2)-AD169
STSHATSSTHNGSHTSRTTSAQTRSVYSQ
HVTSSEAVSHRANETIYNTTLKYGDVVGV
gB(AD2)-Towne
STRGTSATHSHHSSHTTSAAHSRSGSVSQ
RVTSSQTVSHGVNETIYNTTLKYGDVVGV
CG3 antigen

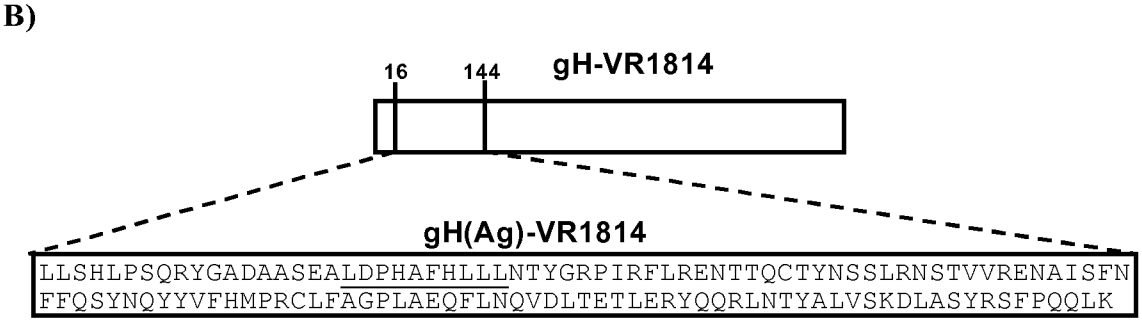

B)
16
144
gH-VR1814
gH(Ag)-VR1814
LLSHLPSQRYGADAASEALDPHAFHLLLNTYGRPIRFLRENTTQCTYNSSLRNSTVVRENAISFN
FFQSYNQYYVFHMPRCLFAGPLAEQFLNQVDLTETLERYQQRLNTYALVSKDLASYRSFPQQLK

Fig. 2

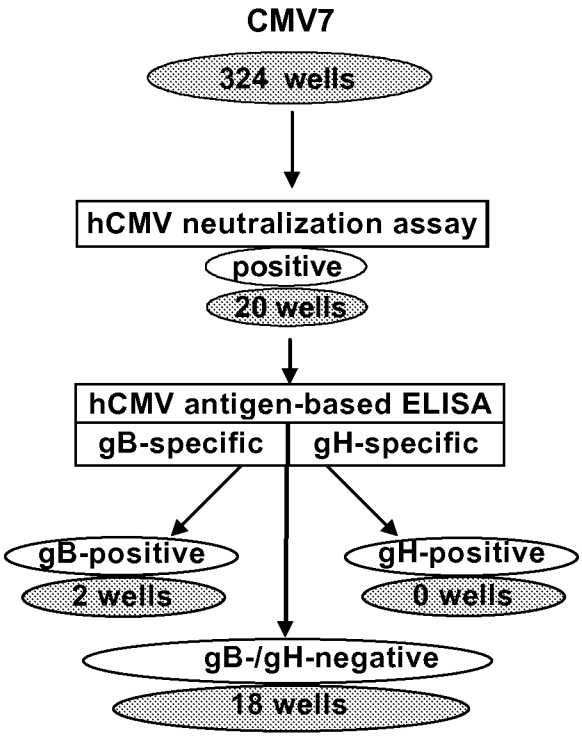

CMV7
324 wells
hCMV neutralization assay
positive
20 wells
hCMV antigen-based ELISA
gB-specific
gH-specific
gB-positive
2 wells
gH-positive
0 wells
gB-/gH-negative
18 wells

Fig. 3

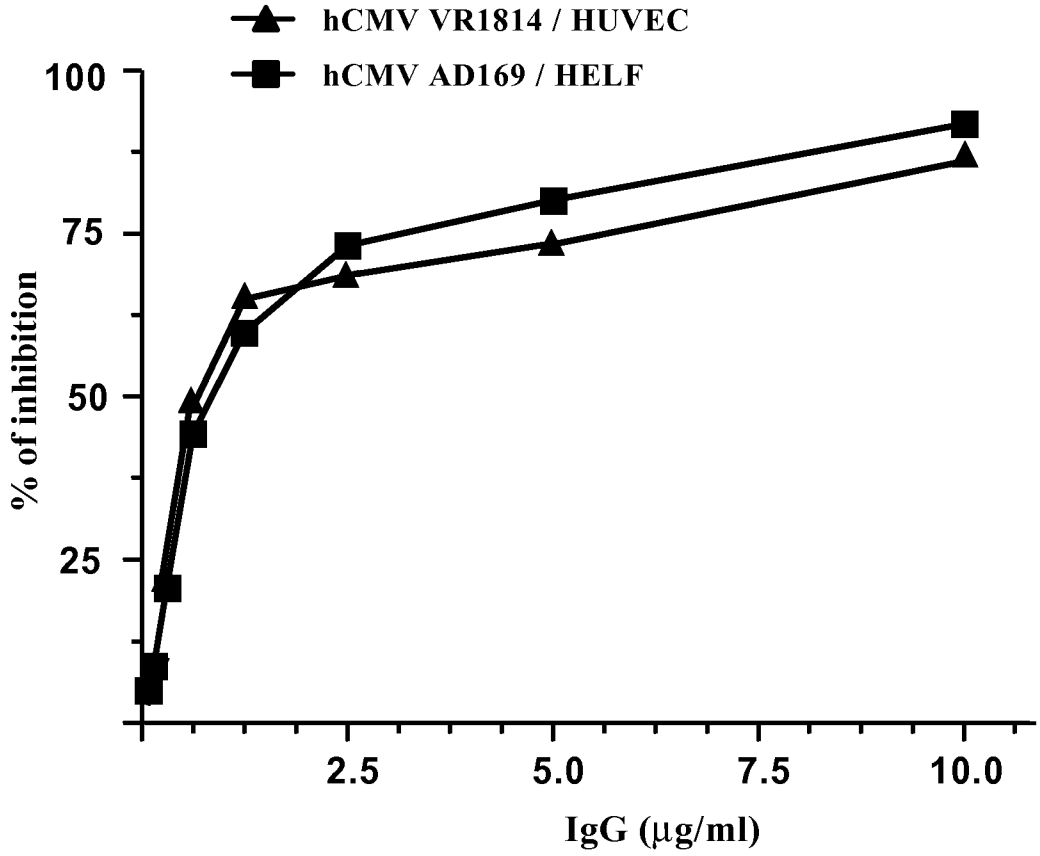
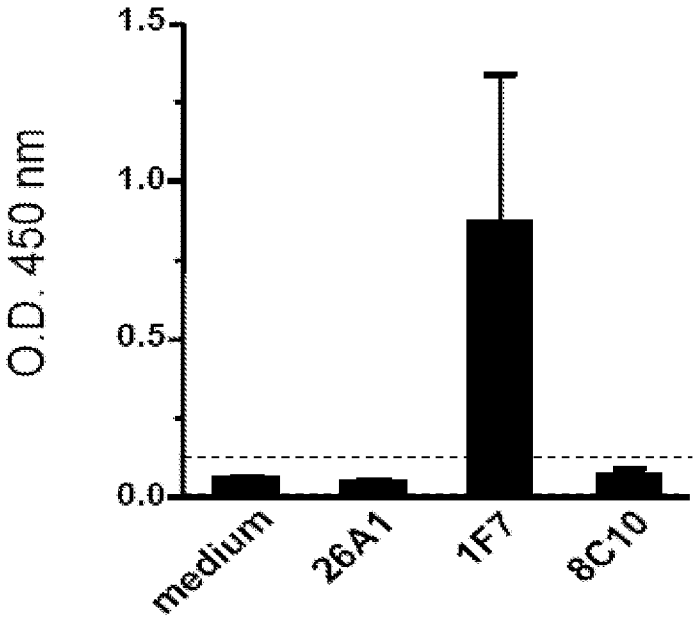

hCMV VR1814 / HUVEC
hCMV AD169 / HELF
100
75
50
25
% of inhibition
2.5
5.0
7.5
10.0
IgG (µg/ml)

Fig. 4

A)


O.D. 450 nm
1.5
1.0
0.5
0.0
medium
26A1
1F7
8C10

B)

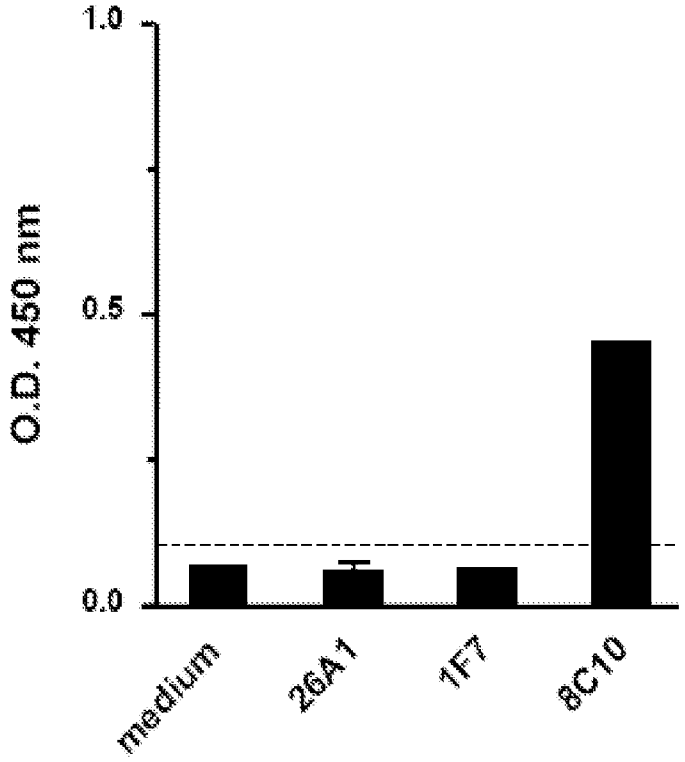

O.D. 450 nm
1.0
0.5
0.0
medium
26A1
1F7
8C10

Fig. 5

A)

```
                                10                                  20
 .  .  .  .  .  .  .  .  .  .  .¦.  .  .  .  .  .  .  .  .  .  .  .¦
 Q  V  Q  L  Q  E  S  G  P  G  L  V  K  P  S  Q  T  L  S  L
caggtgcagctgcaggagtcgggcccaggactggtgaagccttcacagaccctgtccctc

                                30                                  40
 .  .  .  .  .  .  .  .  .  .  .¦.  .  .  .  .  .  .  .  .  .  .  .¦
 I  C  T  V  S  G  G  S  V  S  S  G  G  D  Y  W  T  W  I  R
atatgcactgtctctggtggctccgtcagcagtggtggtgactactggacctggatccgc

                                50                                  60
 .  .  .  .  .  .  .  .  .  .  .¦.  .  .  .  .  .  .  .  .  .  .  .¦
 Q  H  P  G  K  G  L  E  W  L  G  Y  I  H  S  S  G  N  I  F
cagcacccagggaagggcctggagtggcttgggtacatccattccagtgggaatatcttc

                                70                                  80
 .  .  .  .  .  .  .  .  .  .  .¦.  .  .  .  .  .  .  .  .  .  .  .¦
 Y  N  P  S  L  K  S  R  L  T  L  S  M  D  T  S  K  N  Q  F
tacaacccgtccctcaagagtcgactgaccttatcaatggacacgtctaagaaccaattc

                                90                                 100
 .  .  .  .  .  .  .  .  .  .  .¦.  .  .  .  .  .  .  .  .  .  .  .¦
 F  L  K  L  T  S  V  T  A  A  D  T  A  V  Y  Y  C  A  R  V
ttcctgaagttgacctctgtgactgccgcggacacggccgtatattactgtgcgagagtc

                               110                                 120
 .  .  .  .  .  .  .  .  .  .  .¦.  .  .  .  .  .  .  .  .  .  .  .¦
 Y  H  K  D  F  V  V  V  P  G  A  F  P  F  E  F  W  F  D  P
tatcataaggattttgtagtagtaccaggtgctttccccttgaattctggttcgacccc

                               130
 .  .  .  .  .  .  .  .  .  .  .¦.  .
 W  G  Q  G  T  L  V  T  V  S  S
tggggccagggaaccctggtcaccgtctcctca
```

B)

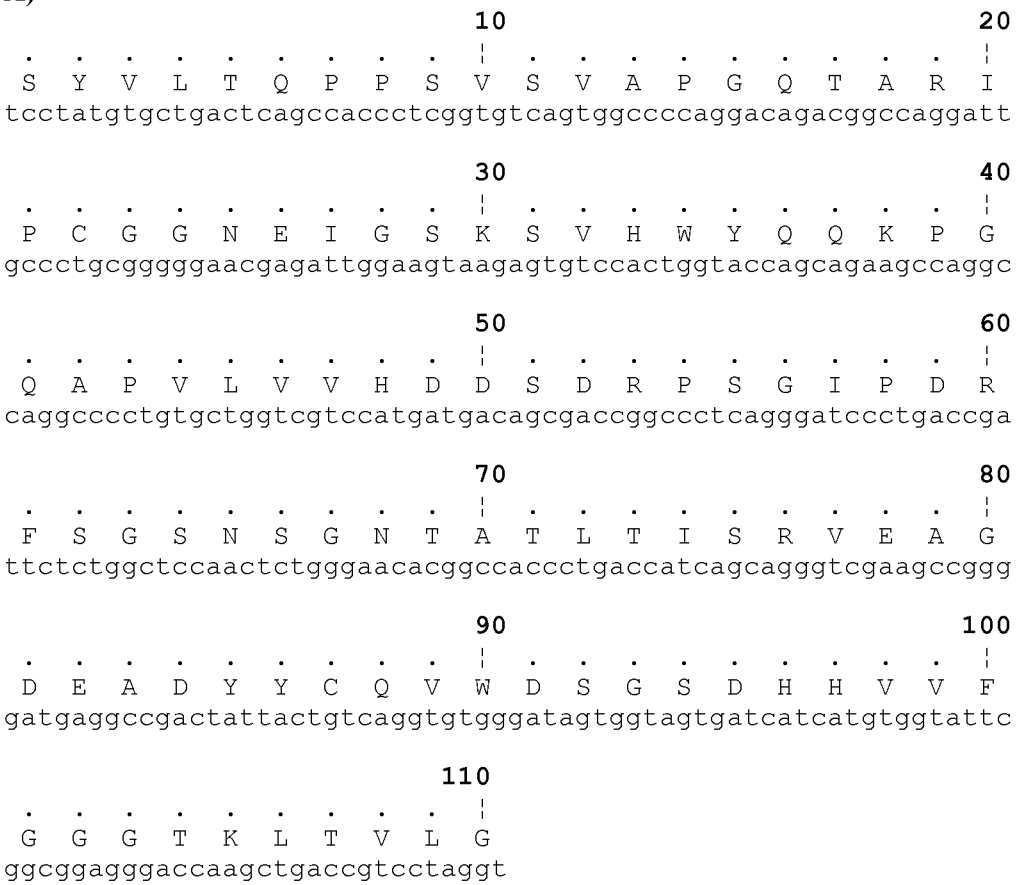
```
                10        20        30        40        50        60
        .........¦.........¦.........¦.........¦.........¦.........¦
VH 26A1 QVQLQESGPGLVKPSQTLSLICTVSGGSVSSGGDYWTWIRQHPGKGLEWLGYIHSSGNIF
                          T                   E         V   V
                                   HCDR1                  HCDR2

                70        80        90       100       110       120
        .........¦.........¦.........¦.........¦.........¦.........¦
VH 26A1 YNPSLKSRLTLSMDTSKNQFFLKLTSVTAADTAVYYCARVYHKDFVVVPGAFPFEFWFDP
                          L    T A             G                 S
                                                HCDR3

                130
        .........¦.
VH 26A1 WGQGTLVTVSS
          R
```

Fig. 6

A)


10 20
S Y V L T Q P P S V S V A P G Q T A R I
tcctatgtgctgactcagccaccctcggtgtcagtggccccaggacagacggccaggatt
30 40
P C G G N E I G S K S V H W Y Q Q K P G
gccctgcgggggaacgagattggaagtaagagtgtccactggtaccagcagaagccaggc
50 60
Q A P V L V V H D D S D R P S G I P D R
caggcccctgtgctggtcgtccatgatgacagcgaccggccctcagggatccctgaccga
70 80
F S G S N S G N T A T L T I S R V E A G
ttctctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggg
90 100
D E A D Y Y C Q V W D S G S D H H V V F
gatgaggccgactattactgtcaggtgtgggatagtggtagtgatcatcatgtggtattc
110
G G G T K L T V L G
ggcggagggaccaagctgaccgtcctaggt

B)

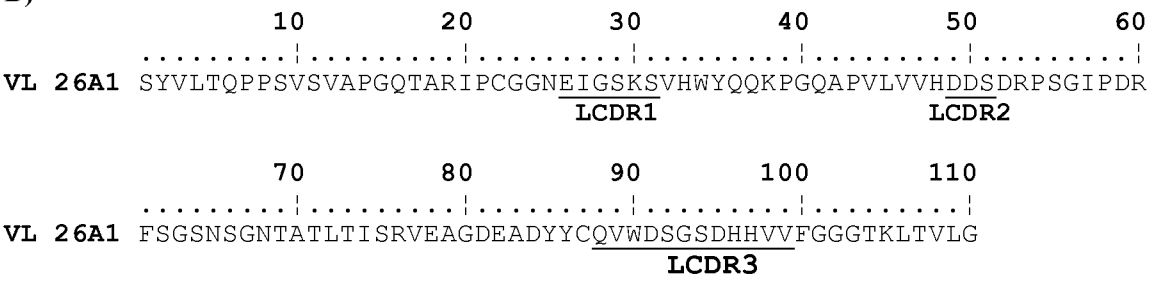

10 20 30 40 50 60
VL 26A1 SYVLTQPPSVSVAPGQTARIPCGGNEIGSKSVHWYQQKPGQAPVLVVHDDSDRPSGIPDR
LCDR1
LCDR2
70 80 90 100 110
VL 26A1 FSGSNSGNTATLTISRVEAGDEADYYCQVWDSGSDHHVVFGGGTKLTVLG
LCDR3

Fig. 7

```
atgaacatactgtggagcatgctcctgctggtggcagctcccagatgggtcctgtcccag
 M  N  I  L  W  S  M  L  L  L  V  A  A  P  R  W  V  L  S  Q   20

gtgcagctgcaggagtcgggcccaggactggtgaagccttcacagaccctgtccctcata
 V  Q  L  Q  E  S  G  P  G  L  V  K  P  S  Q  T  L  S  L  I   40

tgcactgtctctggtggctccgtcagcagtggtggtgactactggacctggatccgccag
 C  T  V  S  G  G  S  V  S  S  G  G  D  Y  W  T  W  I  R  Q   60

cacccagggaagggcctggagtggcttgggtacatccattccagtgggaatatcttctac
 H  P  G  K  G  L  E  W  L  G  Y  I  H  S  S  G  N  I  F  Y   80

aacccgtccctcaagagtcgactgaccttatcaatggacacgtctaagaaccaattcttc
 N  P  S  L  K  S  R  L  T  L  S  M  D  T  S  K  N  Q  F  F  100

ctgaagttgacctctgtgactgccgcggacacggccgtatattactgtgcgagagtctat
 L  K  L  T  S  V  T  A  A  D  T  A  V  Y  Y  C  A  R  V  Y  120

cataaggattttgtagtagtaccaggtgctttccccttgaattctggttcgacccctgg
 H  K  D  F  V  V  V  P  G  A  F  P  F  E  F  W  F  D  P  W  140

ggccagggaaccctggtcaccgtctcctcaggatccgcctccaccaagggcccatcggtc
 G  Q  G  T  L  V  T  V  S  S  G  S  A  S  T  K  G  P  S  V  160

ttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggctgcctg
 F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C  L  180

gtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccctgaccagc
 V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S  200

ggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctcagcagcgtg
 G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L  S  S  V  220

gtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaag
 V  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  240

cccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacaca
 P  S  N  T  K  V  D  K  K  V  E  P  K  S  C  D  K  T  H  T  260

tgcccaccgtgcccagcacctgaactcctgggggggaccgtcagtcttcctcttccccca
 C  P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  280

aaacccaaggacaccctcatgatctcccggaccctgaggtcacatgcgtggtggtggac
 K  P  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  300

gtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcat
 V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  320

aatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgggtggtcagcgtc
 N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  340

ctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaac
 L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  360

aaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaa
 K  A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  380

ccacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcctg
 P  Q  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  400

acctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatggg
 T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  420

cagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttc
 Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  440

ctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgc
 L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  460

tccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccg
 S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  480

ggtaaatga
 G  K stop                                                    482
```

8 / 10

Fig. 8

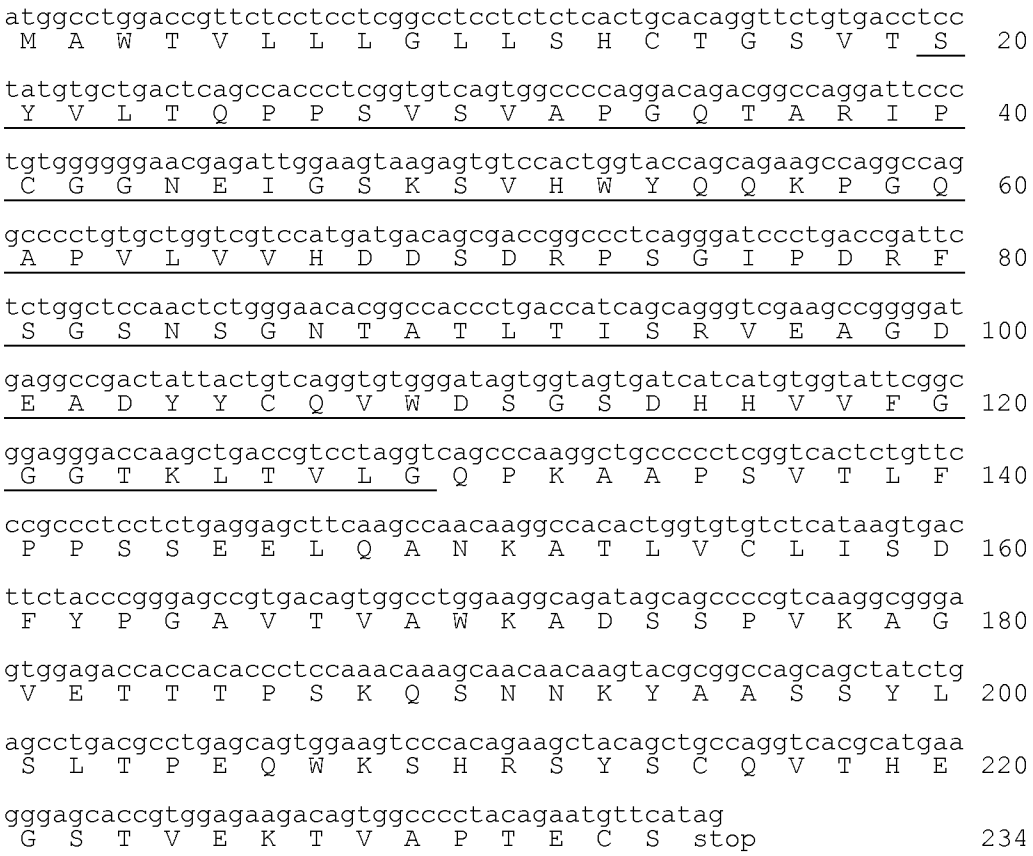
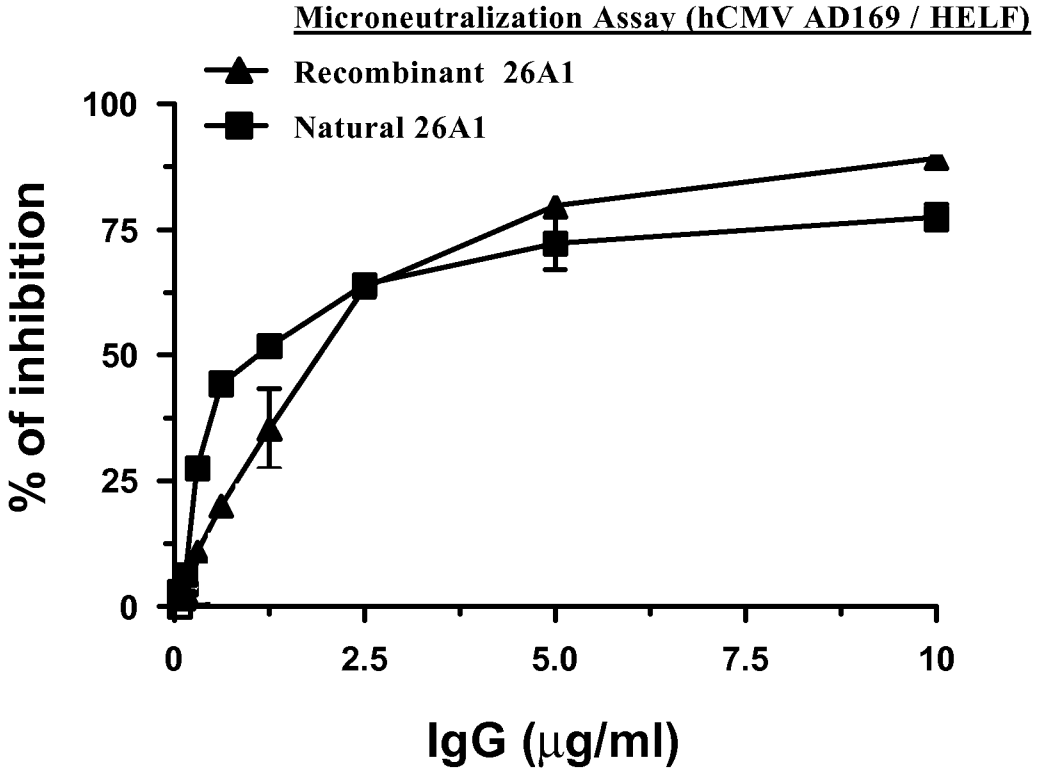

atggcctggaccgttctcctcctcggcctcctctctcactgcacaggttctgtgacctcc
M A W T V L L L G L L S H C T G S V T S 20
tatgtgctgactcagccaccctcggtgtcagtggccccaggacagacggccaggattccc
Y V L T Q P P S V S V A P G Q T A R I P 40
tgtgggggggaacgagattggaagtaagagtgtccactggtaccagcagaagccaggccag
C G G N E I G S K S V H W Y Q Q K P G Q 60
gcccctgtgctggtcgtccatgatgacagcgaccggccctcagggatccctgaccgattc
A P V L V V H D D S D R P S G I P D R F 80
tctggctccaactctgggaacacggccaccctgaccatcagcagggtcgaagccggggat
S G S N S G N T A T L T I S R V E A G D 100
gaggccgactattactgtcaggtgtgggatagtggtagtgatcatcatgtggtattcggc
E A D Y Y C Q V W D S G S D H H V V F G 120
ggagggaccaagctgaccgtcctaggtcagcccaaggctgccccctcggtcactctgttc
G G T K L T V L G Q P K A A P S V T L F 140
ccgccctcctctgaggagcttcaagccaacaaggccacactggtgtgtctcataagtgac
P P S S E E L Q A N K A T L V C L I S D 160
ttctacccgggagccgtgacagtggcctggaaggcagatagcagccccgtcaaggcggga
F Y P G A V T V A W K A D S S P V K A G 180
gtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggccagcagctatctg
V E T T T P S K Q S N N K Y A A S S Y L 200
agcctgacgcctgagcagtggaagtcccacagaagctacagctgccaggtcacgcatgaa
S L T P E Q W K S H R S Y S C Q V T H E 220
gggagcaccgtggagaagacagtggcccctacagaatgttcatag
G S T V E K T V A P T E C S stop 234

Fig. 9

A)


Microneutralization Assay (hCMV AD169 / HELF)
Recombinant 26A1
Natural 26A1
% of inhibition
100
75
50
25
0
0
2.5
5.0
7.5
10
IgG (µg/ml)

B)

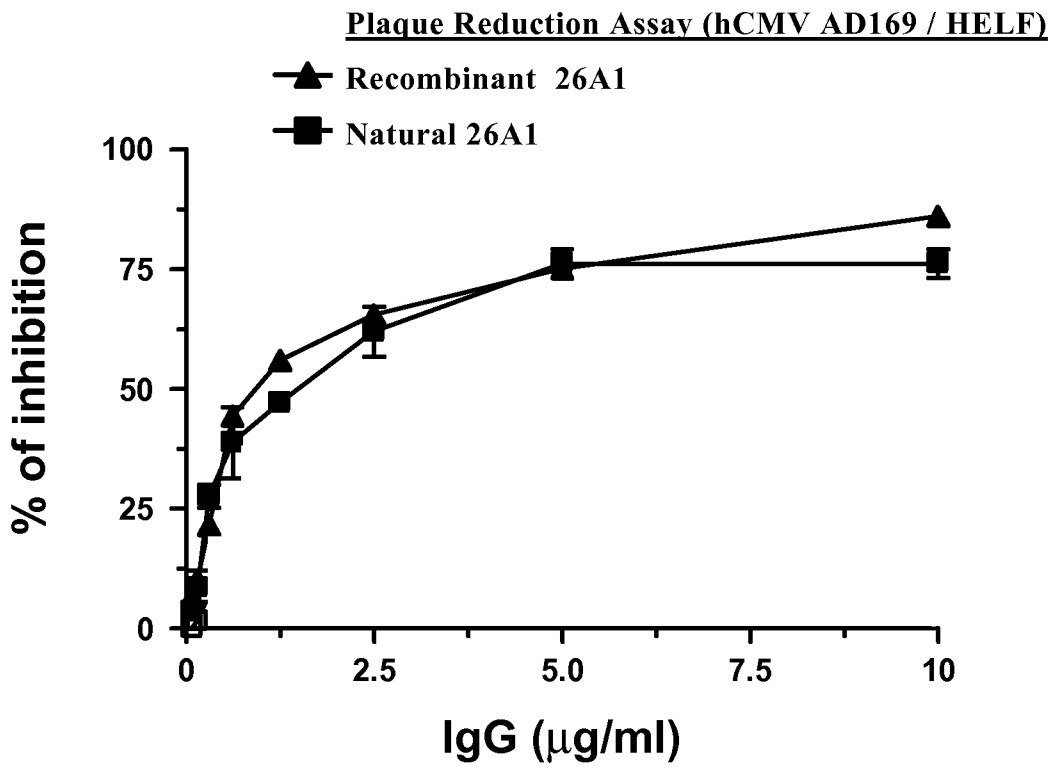
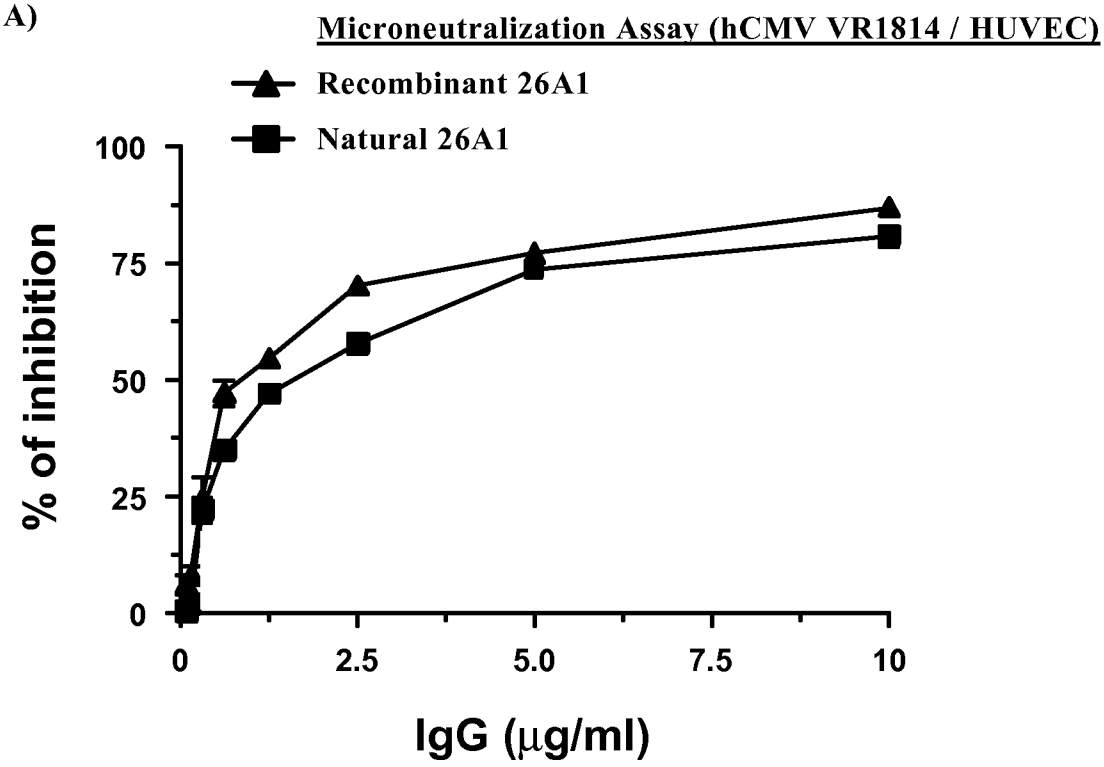
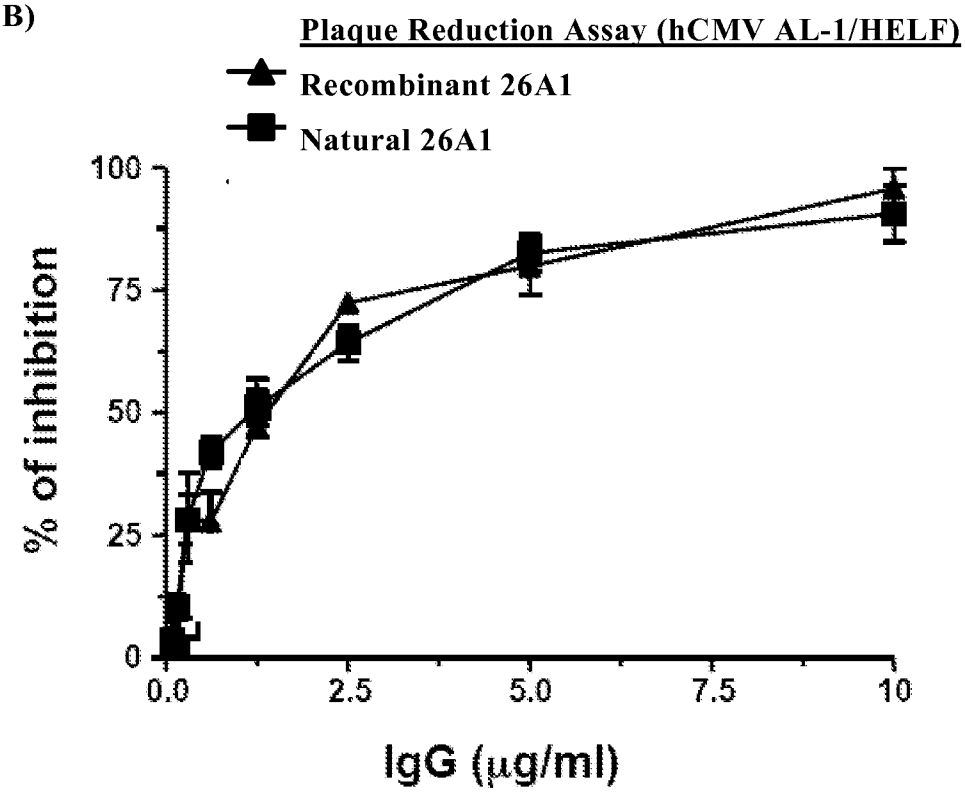

Plaque Reduction Assay (hCMV AD169 / HELF)
Recombinant 26A1
Natural 26A1
% of inhibition
100
75
50
25
0
0
2.5
5.0
7.5
10
IgG (µg/ml)

Fig. 10

A)


Microneutralization Assay (hCMV VR1814 / HUVEC)
Recombinant 26A1
Natural 26A1
% of inhibition
100
75
50
25
0
0
2.5
5.0
7.5
10
IgG (µg/ml)

B)


Plaque Reduction Assay (hCMV AL-1/HELF)
Recombinant 26A1
Natural 26A1
% of inhibition
100
75
50
25
0
0.0
2.5
5.0
7.5
10
IgG (µg/ml)

SEQUENCE LISTING

<110> Ribovax Biotechnologies SA

<120> ANTIBODIES AGAINST HUMAN CYTOMEGALOVIRUS (HCMV)

<130> PAF08_wo_aCMV_gX

<150> PCT/EP06/069780
<151> 2006-12-15

<150> EP07110693
<151> 2007-06-20

<160> 17

<170> PatentIn version 3.3

<210> 1
<211> 58
<212> PRT
<213> Human cytomegalovirus

<400> 1

Ser Thr Ser His Ala Thr Ser Ser Thr His Asn Gly Ser His Thr Ser
1 5 10 15

Arg Thr Thr Ser Ala Gln Thr Arg Ser Val Tyr Ser Gln His Val Thr
20 25 30

Ser Ser Glu Ala Val Ser His Arg Ala Asn Glu Thr Ile Tyr Asn Thr
35 40 45

Thr Leu Lys Tyr Gly Asp Val Val Gly Val
50 55

<210> 2
<211> 58
<212> PRT
<213> Human cytomegalovirus

<400> 2

Ser Thr Arg Gly Thr Ser Ala Thr His Ser His His Ser Ser His Thr
1 5 10 15

Thr Ser Ala Ala His Ser Arg Ser Gly Ser Val Ser Gln Arg Val Thr
20 25 30

Ser Ser Gln Thr Val Ser His Gly Val Asn Glu Thr Ile Tyr Asn Thr
35 40 45

Thr Leu Lys Tyr Gly Asp Val Val Gly Val
50 55

<210> 3
<211> 129
<212> PRT
<213> Human cytomegalovirus

<400> 3

Leu Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser
1 5 10 15

Glu Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly
20 25 30

Arg Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn
35 40 45

Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe
50 55 60

Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg
65 70 75 80

Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp
85 90 95

Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala
100 105 110

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

Lys

<210> 4
<211> 393
<212> DNA
<213> Homo sapiens

<400> 4
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

atatgcactg tctctggtgg ctccgtcagc agtggtggtg actactggac ctggatccgc 120

cagcacccag ggaagggcct ggagtggctt gggtacatcc attccagtgg gaatatcttc 180

tacaacccgt ccctcaagag tcgactgacc ttatcaatgg acacgtctaa gaaccaattc 240

ttcctgaagt tgacctctgt gactgccgcg gacacggccg tatattactg tgcgagagtc 300

tatcataagg attttgtagt agtaccaggt gctttcccct ttgaattctg gttcgacccc 360

tggggccagg gaaccctggt caccgtctcc tca 393

<210> 5
<211> 131
<212> PRT
<213> Homo sapiens

<400> 5

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

```
Thr Leu Ser Leu Ile Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
           20                  25                  30

Gly Asp Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Leu Gly Tyr Ile His Ser Ser Gly Asn Ile Phe Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Leu Ser Met Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Phe Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Tyr His Lys Asp Phe Val Val Val Pro Gly Ala Phe
            100                 105                 110

Pro Phe Glu Phe Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
        115                 120                 125

Val Ser Ser
    130
```

<210> 6
<211> 10
<212> PRT
<213> Homo sapiens

<400> 6

```
Gly Gly Ser Val Ser Ser Gly Gly Asp Tyr
1               5                   10
```

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

<400> 7

```
Ile His Ser Ser Gly Asn Ile
1               5
```

<210> 8
<211> 23
<212> PRT
<213> Homo sapiens

<400> 8

```
Ala Arg Val Tyr His Lys Asp Phe Val Val Val Pro Gly Ala Phe Pro
1               5                   10                  15

Phe Glu Phe Trp Phe Asp Pro
            20
```

<210> 9
<211> 330
<212> DNA
<213> Homo sapiens

<400> 9
tcctatgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt 60

gccctgcggg ggaacgagat tggaagtaag agtgtccact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcgt ccatgatgac agcgaccggc cctcagggat ccctgaccga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtggta gtgatcatca tgtggtattc 300

ggcggaggga ccaagctgac cgtcctaggt 330

<210> 10
<211> 110
<212> PRT
<213> Homo sapiens

<400> 10

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

Thr Ala Arg Ile Pro Cys Gly Gly Asn Glu Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val His
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

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

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Gly Ser Asp His
85 90 95

His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 11
<211> 6
<212> PRT
<213> Homo sapiens

<400> 11

Glu Ile Gly Ser Lys Ser
1 5

<210> 12
<211> 3
<212> PRT

<213> Homo sapiens

<400> 12

Asp Asp Ser
1

<210> 13
<211> 12
<212> PRT
<213> Homo sapiens

<400> 13

Gln Val Trp Asp Ser Gly Ser Asp His His Val Val
1 5 10

<210> 14
<211> 1449
<212> DNA
<213> Artificial

<220>
<223> Recombinant 26A1 IgG1 Heavy Chain

<400> 14
atgaacatac tgtggagcat gctcctgctg gtggcagctc ccagatgggt cctgtcccag 60

gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcata 120

tgcactgtct ctggtggctc cgtcagcagt ggtggtgact actggacctg gatccgccag 180

cacccaggga agggcctgga gtggcttggg tacatccatt ccagtgggaa tatcttctac 240

aacccgtccc tcaagagtcg actgacctta tcaatggaca cgtctaagaa ccaattcttc 300

ctgaagttga cctctgtgac tgccgcggac acggccgtat attactgtgc gagagtctat 360

cataaggatt ttgtagtagt accaggtgct ttccccctttg aattctggtt cgaccccctgg 420

ggccagggaa ccctggtcac cgtctcctca ggatccgcct ccaccaaggg cccatcggtc 480

ttcccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 540

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 600

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg 660

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 720

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgtgacaa aactcacaca 780

tgcccaccgt gcccagcacc tgaactcctg gggggaccgt cagtcttcct cttccccccca 840

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 900

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 960

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgggt ggtcagcgtc 1020

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1080

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1140

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1200

acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1260

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1320

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1380

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1440

ggtaaatga 1449

<210> 15
<211> 482
<212> PRT
<213> Artificial

<220>
<223> Recombinant 26A1 IgG1 Heavy Chain

<400> 15

Met Asn Ile Leu Trp Ser Met Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

Pro Ser Gln Thr Leu Ser Leu Ile Cys Thr Val Ser Gly Gly Ser Val
35 40 45

Ser Ser Gly Gly Asp Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys
50 55 60

Gly Leu Glu Trp Leu Gly Tyr Ile His Ser Ser Gly Asn Ile Phe Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Leu Ser Met Asp Thr Ser Lys
85 90 95

Asn Gln Phe Phe Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Val Tyr His Lys Asp Phe Val Val Val Pro
115 120 125

Gly Ala Phe Pro Phe Glu Phe Trp Phe Asp Pro Trp Gly Gln Gly Thr
130 135 140

Leu Val Thr Val Ser Ser Gly Ser Ala Ser Thr Lys Gly Pro Ser Val
145 150 155 160

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
165 170 175

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val

195 200 205

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
210 215 220

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
225 230 235 240

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Lys

<210> 16
<211> 705
<212> DNA
<213> Artificial

<220>
<223> Recombinant 26A1 IgG1 Light Chain

<400> 16
atggcctgga ccgttctcct cctcggcctc ctctctcact gcacaggttc tgtgacctcc 60

tatgtgctga ctcagccacc ctcggtgtca gtggccccag gacagacggc caggattccc 120

tgtgggggga acgagattgg aagtaagagt gtccactggt accagcagaa gccaggccag 180

gcccctgtgc tggtcgtcca tgatgacagc gaccggccct cagggatccc tgaccgattc 240

tctggctcca actctgggaa cacggccacc ctgaccatca gcagggtcga agccggggat 300

gaggccgact attactgtca ggtgtgggat agtggtagtg atcatcatgt ggtattcggc 360

ggagggacca agctgaccgt cctaggtcag cccaaggctg ccccctcggt cactctgttc 420

ccgccctcct ctgaggagct tcaagccaac aaggccacac tggtgtgtct cataagtgac 480

ttctacccgg gagccgtgac agtggcctgg aaggcagata gcagccccgt caaggcggga 540

gtggagacca ccacaccctc caaacaaagc aacaacaagt acgcggccag cagctatctg 600

agcctgacgc ctgagcagtg gaagtcccac agaagctaca gctgccaggt cacgcatgaa 660

gggagcaccg tggagaagac agtggccccct acagaatgtt catag 705

<210> 17
<211> 234
<212> PRT
<213> Artificial

<220>
<223> Recombinant 26A1 IgG1 Light Chain

<400> 17

Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly
1 5 10 15

Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala
20 25 30

Pro Gly Gln Thr Ala Arg Ile Pro Cys Gly Gly Asn Glu Ile Gly Ser
35 40 45

Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
50 55 60

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

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

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Gly
            100                 105                 110

Ser Asp His His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
        115                 120                 125

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
    130                 135                 140

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

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
                165                 170                 175

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
            180                 185                 190

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
        195                 200                 205

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
    210                 215                 220

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230
```