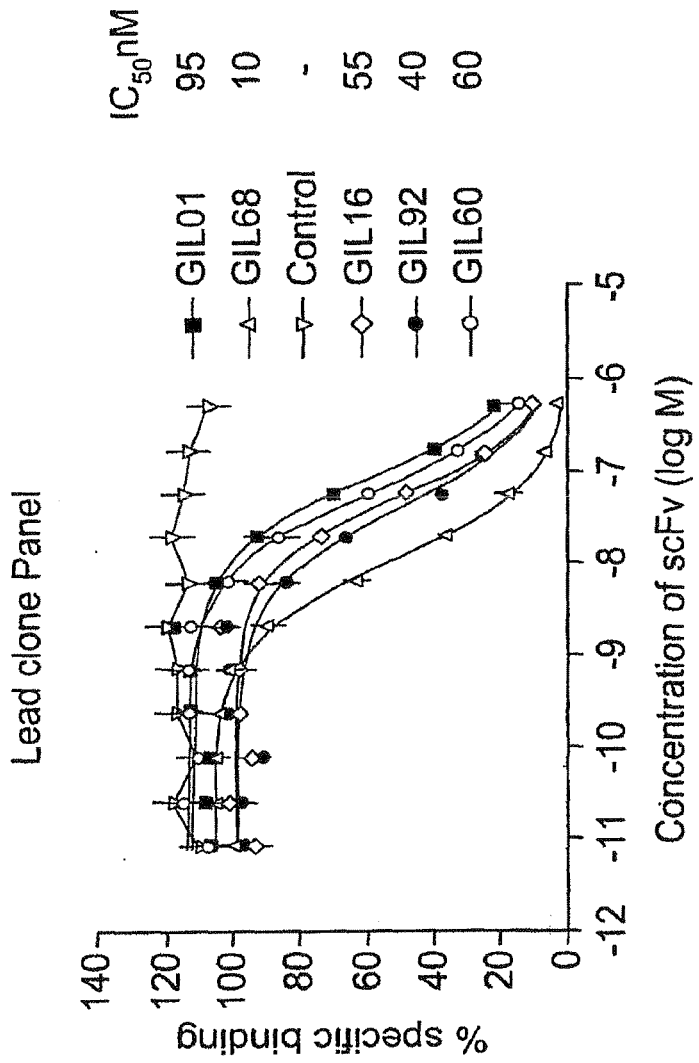

Lead clone Panel
IC_{50}nM
GIL01 95
GIL68 10
Control -
GIL16 55
GIL92 40
GIL60 60
% specific binding
140
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
Concentration of scFv (log M)

FIG. 1

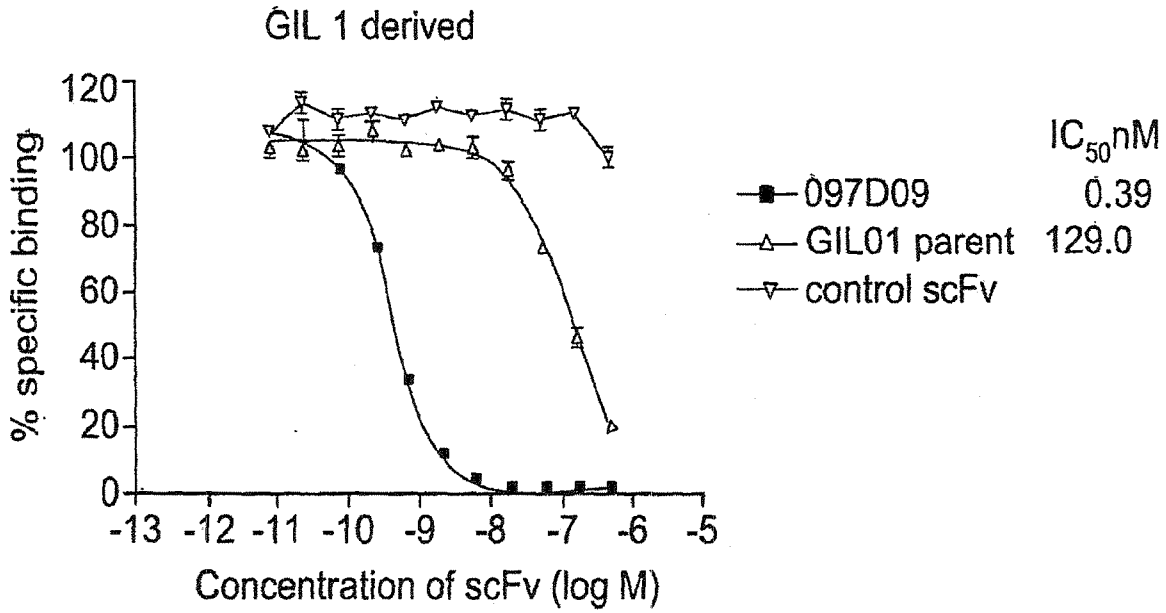

GIL 1 derived
% specific binding
120
100
80
60
40
20
0
-13 -12 -11 -10 -9 -8 -7 -6 -5
Concentration of scFv (log M)
IC50nM
097D09 0.39
GIL01 parent 129.0
control scFv

FIG. 2A

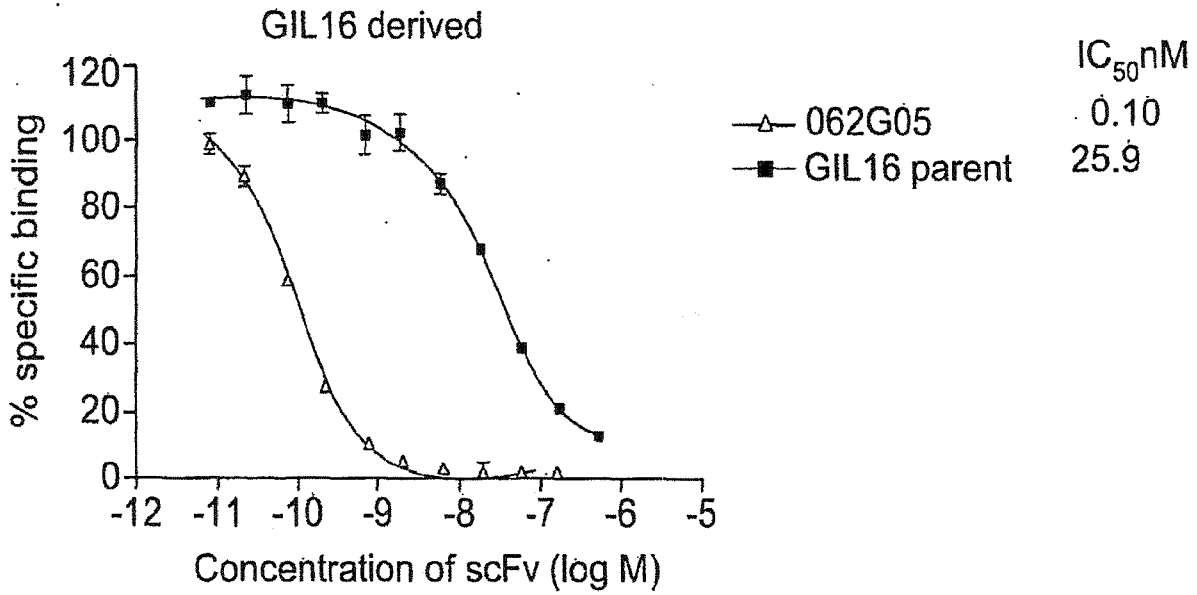

GIL16 derived
% specific binding
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
Concentration of scFv (log M)
IC50nM
062G05
0.10
GIL16 parent
25.9

FIG. 2B

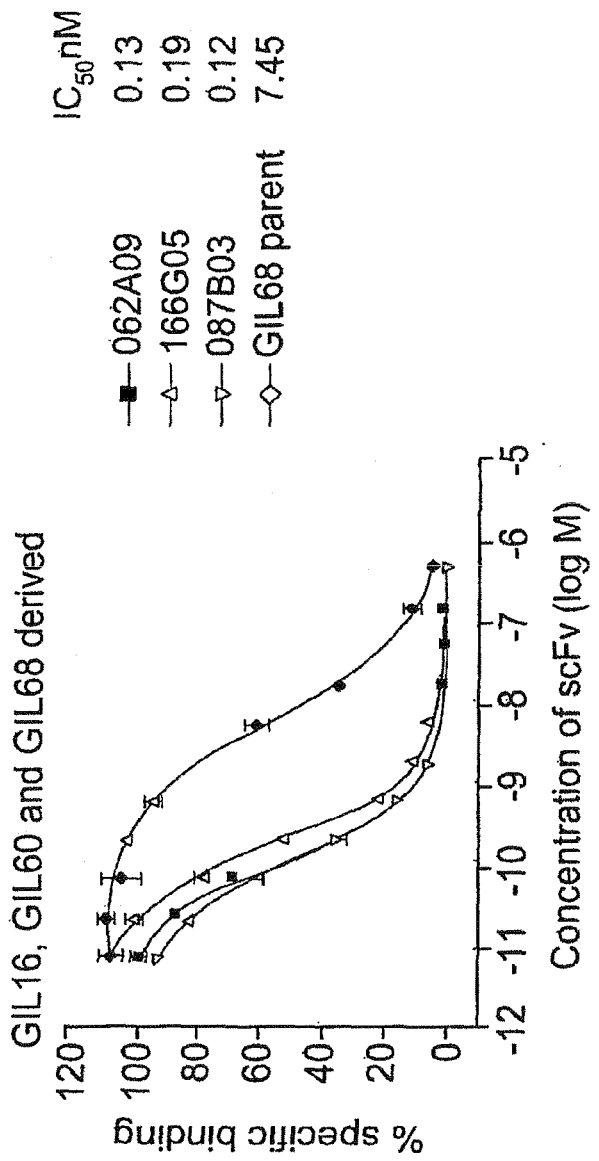

GIL16, GIL60 and GIL68 derived
% specific binding
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
Concentration of scFv (log M)
IC50nM
062A09 0.13
166G05 0.19
087B03 0.12
GIL68 parent 7.45

FIG. 2C

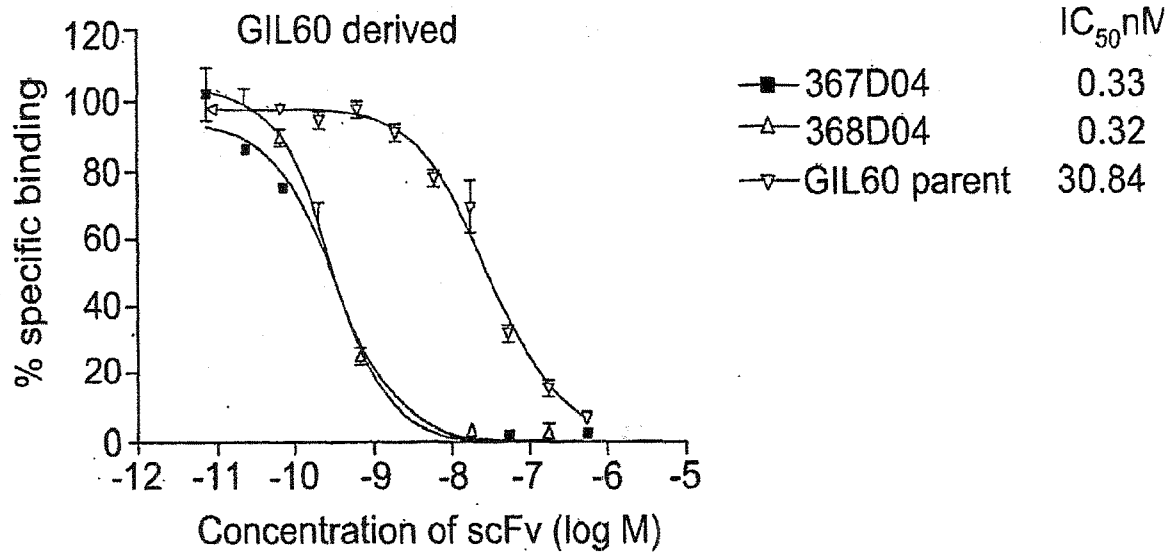

GIL60 derived
% specific binding
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
Concentration of scFv (log M)
IC50nM
367D04 0.33
368D04 0.32
GIL60 parent 30.84

FIG. 2D

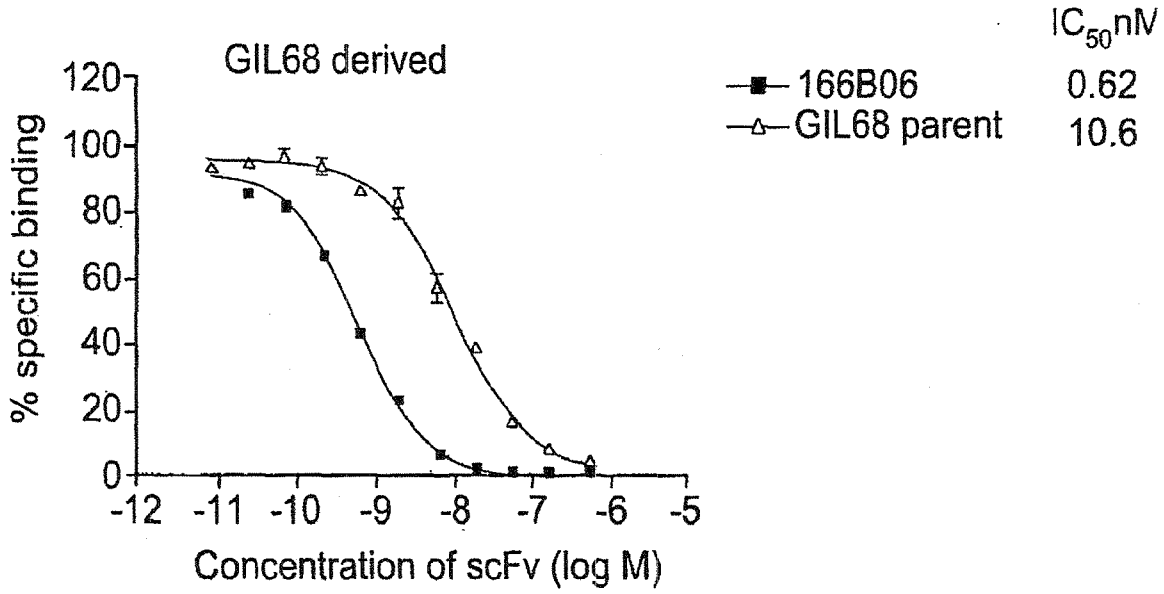

GIL68 derived
% specific binding
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
Concentration of scFv (log M)
IC50nM
166B06
0.62
GIL68 parent
10.6

FIG. 2E

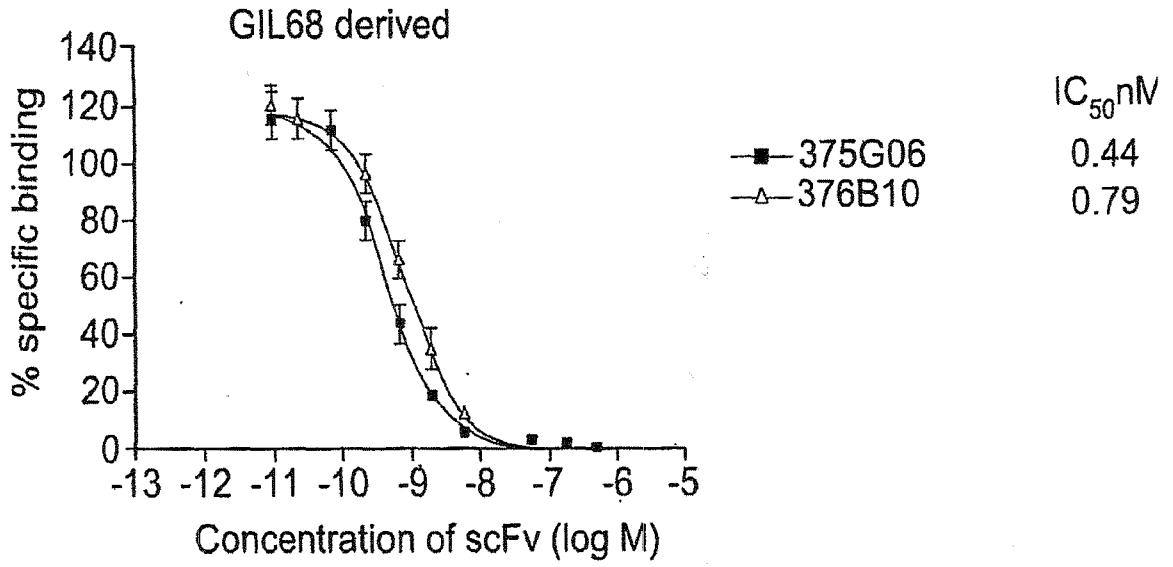

GIL68 derived
% specific binding
140
120
100
80
60
40
20
0
-13 -12 -11 -10 -9 -8 -7 -6 -5
Concentration of scFv (log M)
IC50nM
375G06 0.44
376B10 0.79

FIG. 2F

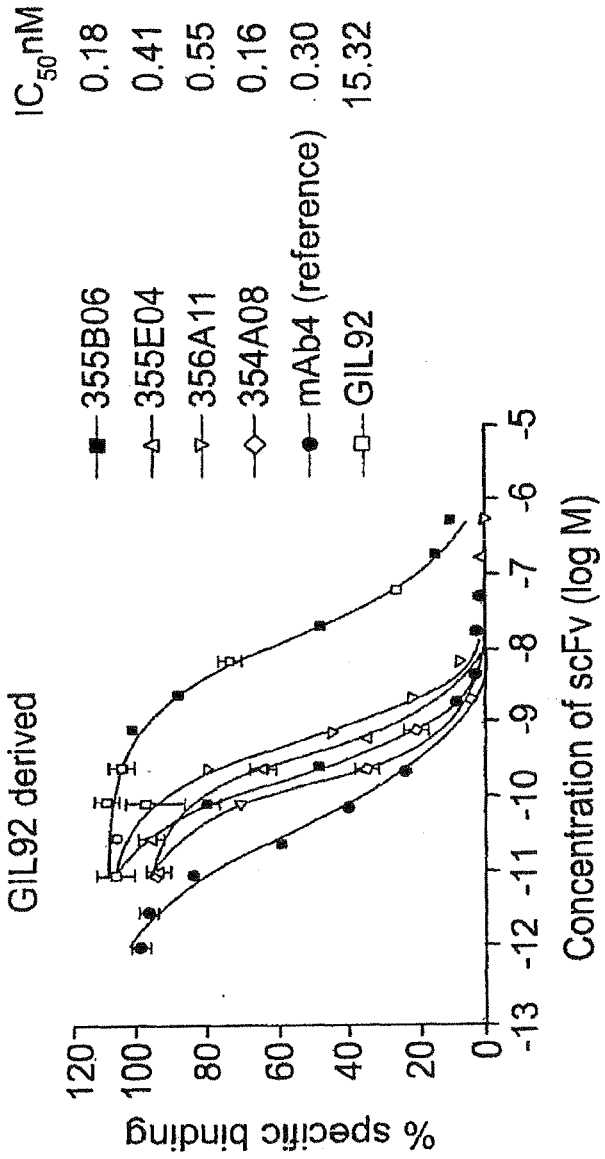

GIL92 derived
IC_{50}nM
355B06 0.18
355E04 0.41
356A11 0.55
354A08 0.16
mAb4 (reference) 0.30
GIL92 15.32
% specific binding
120
100
80
60
40
20
0
-13 -12 -11 -10 -9 -8 -7 -6 -5
Concentration of scFv (log M)

FIG. 2G

Germlined IgG

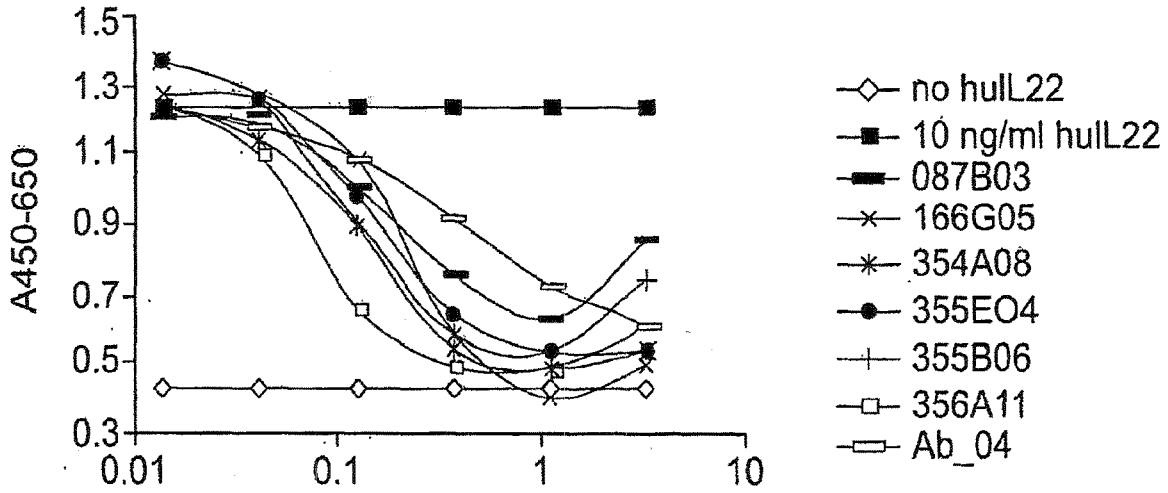


FIG. 3A

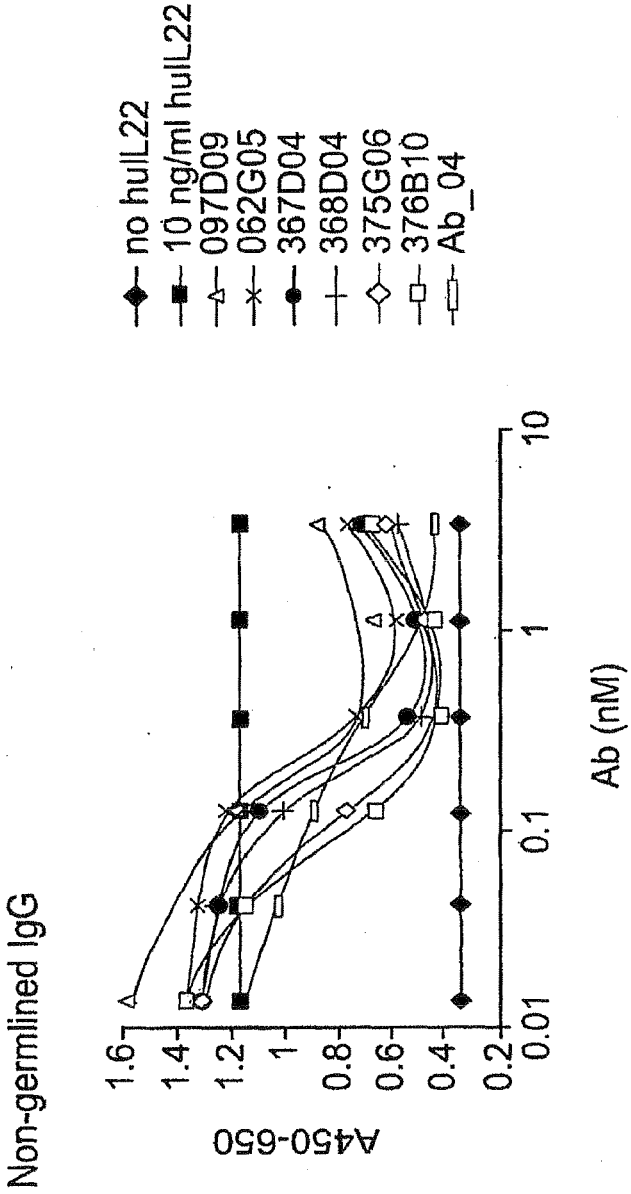

Non-germlined IgG
A450-650
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0.01
0.1
1
10
Ab (nM)
no hulL22
10 ng/ml hulL22
097D09
062G05
367D04
368D04
375G06
376B10
Ab_04

FIG. 3B

Germlined IgG

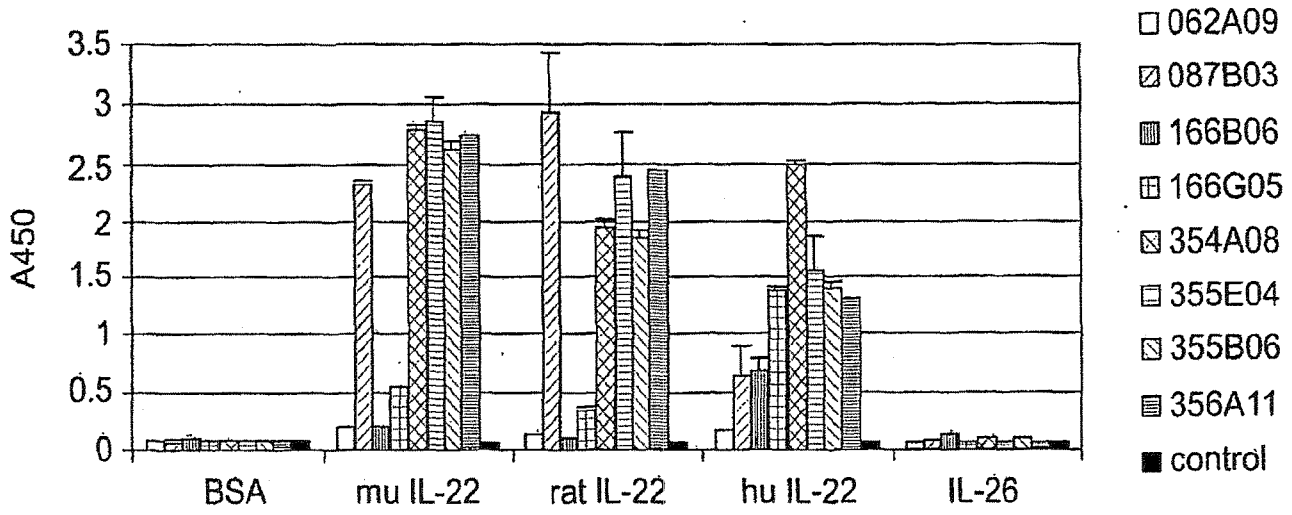


FIG. 4A

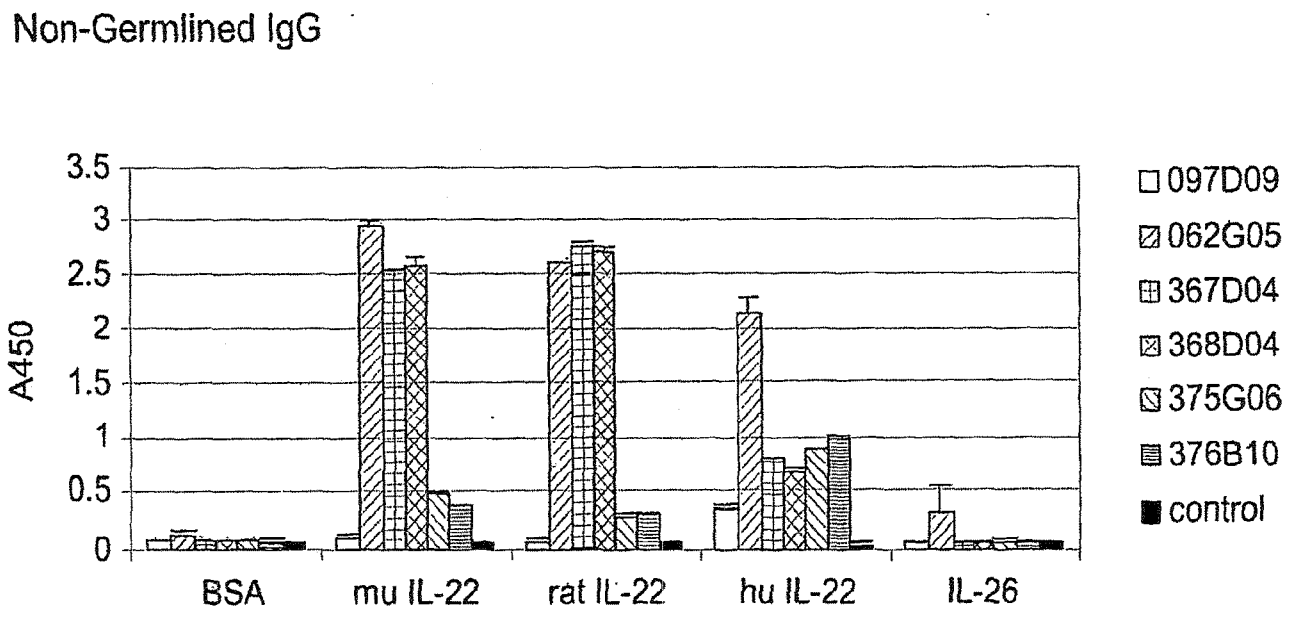

Non-Germlined IgG
A450
3.5
3
2.5
2
1.5
1
0.5
0
BSA
mu IL-22
rat IL-22
hu IL-22
IL-26
097D09
062G05
367D04
368D04
375G06
376B10
control

FIG. 4B

SEQ ID NO:1

```
  1 MAALQKSVSS FLMGTLATSC LLLLALLVQG GAAAPISSHC RLDKSNFQQP
 51 YITNRTFMLA KEASLADNNT DVRLIGEKLF HGVSMSERCY LMKQVLNFTL
101 EEVLFPQSDR FQPYMQEWPF LARLSNRLST CHIEGDDLHI QRNVQKLKD
151 TVKKLGESGE IKAIGELDLL FMSLRNACI
```

SEQ ID NO:2

```
   1 GAATTCGGCC AAAGAGGCCT ACAGGTTCTC CTTCCCCAGT CACCAGTTGC
  51 TCGAGTTAGA ATTGTCTGCA ATGGCCGCCC TGCAGAAATC TGTGAGCTCT
 101 TTCCTTATGG GGACCCTGGC CACCAGCTGC CTCCTTCTCT TGGCCCTCTT
 151 GGTACAGGGA GGAGCAGCTG CGCCCATCAG CTCCCACTGC AGGCTTGACA
 201 AGTCCAACTT CCAGCAGCCC TATATCACCA ACCGCACCTT CATGCTGGCT
 251 AAGGAGGCTA GCTTGGCTGA TAACAACACA GACGTTCGTC TCATTGGGGA
 301 GAAACTGTTC CACGGAGTCA GTATGAGTGA GCGCTGCTAT CTGATGAAGC
 351 AGGTGCTGAA CTTCACCCTT GAAGAAGTGC TGTTCCCTCA ATCTGATAGG
 401 TTCCAGCCTT ATATGCAGGA GGTGGTGCCC TTCCTGGCCA GGCTCAGCAA
 451 CAGGCTAAGC ACATGTCATA TTGAAGGTGA TGACCTGCAT ATCCAGAGGA
 501 ATGTGCAAAA GCTGAAGGAC ACAGTGAAAA AGCTTGGAGA GAGTGGAGAG
 551 ATCAAAGCAA TTGGAGAACT GGATTTGCTG TTTATGTCTC TGAGAAATGC
 601 CTGCATTTGA CCAGAGCAAA GCTGAAAAAT GAATAACTAA CCCCCTTTCC
 651 CTGCTAGAAA TAACAATTAG ATGCCCCAAA GCGATTTTTT TTAACCAAAA
 701 GGAAGATGGG AAGCCAAACT CCATCATGAT GGGTGGATTC CAAATGAACC
 751 CCTGCGTTAG TTACAAAGGA AACCAATGCC ACTTTTGTTT ATAAGACCAG
 801 AAGGTAGACT TTCTAAGCAT AGATATTTAT TGATAACATT TCATTGTAAC
 851 TGGTGTTCTA TACACAGAAA ACAATTTATT TTTTAAATAA TTGTCTTTTT
 901 CCATAAAAAA GATTACTTTC CATTCCTTTA GGGGAAAAAA CCCCTAAATA
 951 GCTTCATGTT TCCATAATCA GTACTTTATA TTTATAAATG TATTTATTAT
1001 TATTATAAGA CTGCATTTTA TTTATATCAT TTTATTAATA TGGATTTATT
1051 TATAGAAACA TCATTCGATA TTGCTACTTG AGTGTAAGGC TAATATTGAT
1101 ATTTATGACA ATAATTATAG AGCTATAACA TGTTTATTTG ACCTCAATAA
1151 ACACTTGGAT ATCCTAAAAA AAAAAAAAAA AAAGCGGCCG C
```

FIG. 5

SEQ ID NO:3

MAVLQKSMSFSLMGTLAASCLLLIALWAQEANALPVNTRCKLEVSNFQQPYI
VNRTFMLAKEASLADNNTDVRLIGEKLFRGVSAKDQCYLMKQVLNFTLEDVL
LPQSDRFQPYMQEVVPFLTKLSNQLSSCHISGDDQNIQKNVRRLKETVKKLG
ESGEIKAIGELDLLFMSLRNACV

SEQ ID NO:4

ATGGCTGTCCTGCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGC
CGCCAGCTGCCTGCTTCTCATTGCCCTGTGGGCCCAGGAGGCAAATGCGC
TGCCCGTCAACACCCGGTGCAAGCTTGAGGTGTCCAACTTCCAGCAGCCG
TACATCGTCAACCGCACCTTTATGCTGGCCAAGGAGGCCAGCCTTGCAGA
TAACAACACAGACGTCCGGCTCATCGGGGAGAAACTGTTCCGAGGAGTCA
GTGCTAAAGATCAGTGCTACCTGATGAAGCAGGTGCTCAACTTCACCCTG
GAAGACGTTCTGCTCCCCCAGTCAGACAGGTTCCAGCCCTACATGCAGGA
GGTGGTACCTTTCCTGACCAAACTCAGCAATCAGCTCAGCTCCTGTCACA
TCAGCGGTGACGACCAGAACATCCAGAAGAATGTCAGAAGGCTGAAGGAG
ACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAGGCGATTGGGGAACT
GGACCTGCTGTTTATGTCTCTGAGAAATGCTTGCGTCTGA

FIG. 6

GIL01

V_H (SEQ ID NO:5) with H1, H2, and H3 underlined (SEQ ID NO:8-10, respectively)

E V Q L V E S G G G L V T P G G S L R L S C A A S G F T F S
D Y Y M S W I R Q A P G R G L E W V S A I S G S G G S T Y Y
A D S V K G R I T I S R D N A K N S L Y L Q M S S L R S E D
T A V Y Y C A R G L W V W D P L D Y W G R G T L V T V S S

V_H (SEQ ID NO:14) with H1, H2, and H3 underlined (SEQ ID NO:17-19, respectively)

GAGGTGCAGTTGGTGGAGTCTGGGGGAGGCTTGGTCACGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGG
GAGGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGATCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGA
GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGCTTTGGGTTTGGGATCCTCTTGACTACTGGGGCAGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:6) with L1, L2, and L3 underlined (SEQ ID NO:11-13, respectively)

D I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H
W L A W Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F
S G S G S G T D F T L T I S S L Q P D D F A T Y Y C Q Q Y S N
Y P L T F G G G T K L E I K R

V_L (SEQ ID NO:15) with L1, L2, and L3 underlined (SEQ ID NO:20-22, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCCTGGTATCAGCAGAAGCCAGG
GAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATG
ATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCGGAGGGACCAAGCTGGAGATCAAACGT

FIG. 7

GIL16

V_H (SEQ ID NO:23) with H1, H2, and H3 underlined (SEQ ID NO:26-28, respectively)

Q V Q L V E S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I
S W V R Q A P G Q G L E W M G W I S A Y T G N T N Y A Q K F Q G R V
T M T T D T S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y
Y D A F D I W G Q G T L V T V S S

V_H (SEQ ID NO:32) with H1, H2, and H3 underlined (SEQ ID NO:35-37, respectively)

CAGGTGCAGCTGGTGGAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTATC
AGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAGAGTC
ACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGTGGATAC
TATGATGCTTTTGATATCTGGGGCCAAGGCACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:24) with L1, L2, and L3 underlined (SEQ ID NO:29-31, respectively)

D I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L A
W Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G S G
T D F T L T I S S L Q P D D F A T Y Y C Q Q Y S N Y P L T F G G G T
K L E I K R

V_L (SEQ ID NO:33) with L1, L2, and L3 underlined (SEQ ID NO:38-40, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCC
TGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCGGAGGGACC
AAGCTGGAGATCAAACGT

FIG. 7(cont.)

GIL45

V_H (SEQ ID NO:41) with H1, H2, and H3 underlined (SEQ ID NO:44-46, respectively)

Q M Q L V Q S G G G V V Q P G R S L R L S C A A S G F T F S N Y G M Y W V R Q
A P G K G L E W V A H I W Y D G S N E K Y A D S V K G R M T V S R D N S R N T
L Y L Q M N S L R A E D T A V Y Y C A T E Q H W I T A F D I W G K G T L V T V
S S

V_H (SEQ ID NO:50) with H1, H2, and H3 underlined (SEQ ID NO:53-55, respectively)

CAGATGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTATGGCATGTACTGGGTCCGCCA
GGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACATATTTGGTATGATGGAAGTAATGAAAAGTATGCAGACTCCGTGAAGGGCCGAATGACCGTCTCCAGAGACAATTCCAGGAACA
CGTTGTATTTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGACAGAGCAACACTGGATTACTGCTTTTGATATCTGGGGCAAAGGCACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:42) with L1, L2, and L3 underlined (SEQ ID NO:47-49, respectively)

Q S V L T Q P A S V S G S P G Q S I T I S C T G T S S D V G G Y N Y V S W Y Q
Q H P G K A P K L M I Y E G S K R P S G V S N R F S G S K S G N T A S L T I S
G L Q A E D E A D Y Y C S S Y T T R S T R V F G G G T K L T V L G

V_L (SEQ ID NO:51) with L1, L2, and L3 underlined (SEQ ID NO:56-58, respectively)

CAGTCTGTGCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCA
ACAACACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCT
CTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAACCAGGAGCACTCGAGTTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 7(cont.)

GIL60

V_H (SEQ ID NO:59) with H1, H2, and H3 underlined (SEQ ID NO:62-64, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N
W V R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I
S R D N A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G S F
Y Y F G Y W G R G T L V T V S S

V_H (SEQ ID NO:68) with H1, H2, and H3 underlined (SEQ ID NO:71-73, respectively)

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAA
CTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGAGGATGGTATAGTGGGAGC
TTCTACTACTTTGGCTACTGGGGCCGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:60) with L1, L2, and L3 underlined (SEQ ID NO:65-67, respectively)

Q A V L T Q P S S V S G S P G Q S I T I S C T G A S G D V G A Y N F V
S W Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S G
N T A S L T I S G L Q A E D E S D Y Y C S S Y T S T F S V V F G G G T
K V T V L G

V_L (SEQ ID NO:69) with L1, L2, and L3 underlined (SEQ ID NO:74-76, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGGTGCTTATAACTTTGT
CTCCTGGTACCAACAACACCCAGGCAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTG
GCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCAGCTCATATACAAGCACCTTCTCTGTGGTATTTGGCGGAGGG
ACCAAGGTCACCGTCCTAGGT

FIG. 7(cont.)

GIL68

V_H (SEQ ID NO:77) with H1, H2, and H3 underlined (SEQ ID NO:80-82, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H W V R Q T P G
Q G F E W M G W V N P D T G G T R Y A Q K F Q G W V T M T R D M S N T T A Y M E L P
R L R D D D T A V Y Y C A R D L T G F D P F D I W G Q G T L V T V S S

V_H (SEQ ID NO:86) with H1, H2, and H3 underlined (SEQ ID NO:89-91, respectively)

GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTGGGTGCGACAGACCCCTGGA
CAAGGGTTTGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTGGGTCACAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGCCC
AGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:78) with L1, L2, and L3 underlined (SEQ ID NO:83-85, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y Q Q R P G Q A
P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S R V E A G D E A D
F Y C Q V W D S S T D R P L F G G G T K L T V L G

V_L (SEQ ID NO:87) with L1, L2, and L3 underlined (SEQ ID NO:92-94, respectively)

CAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCAGCAGAGGCCAGGCCAGG
CCCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGAGGC
CGACTTTTACTGTCAGGTGTGGGATAGTAGTACTGATCGTCCGCTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 7(cont.)

GIL92

V_H (SEQ ID NO:95) with H1, H2, and H3 underlined (SEQ ID NO:98-100, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y
M H W V R Q A P G Q G L E W V G W I N P Y T G G A F Y A Q K F R G
R V T M T R D T S I N T A Y M E L S R L G S D D T A V Y Y C A R E
P E K F D F W G G D N W G R G T M V T V S S

V_H (SEQ ID NO:104) with H1, H2, and H3 underlined (SEQ ID NO:107-109, respectively)

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTA
TATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGG
GCAGGGTCACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTGAGCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGA
GAACCTGAAAAATTCGATTTTTGGGGGGGTGACAACTGGGGCCGGGGGACAATGGTCACCGTCTCCTCA

V_L (SEQ ID NO:96) with L1, L2, and L3 underlined (SEQ ID NO:101-103, respectively)

Q A V L T Q P S S V S G A P G Q R V T I S C T G S S S N I G A G Y
G V H W Y Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G
S K S G T S A S L A I T G L Q A E D E A D Y Y C Q S Y D S S L S G
Y V F G T G T Q L T V L G

V_L (SEQ ID NO:105) with L1, L2, and L3 underlined (SEQ ID NO:110-112, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTA
TGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGT
GGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTCCTAGGT

FIG. 7 (cont.)

097D09

V_H (SEQ ID NO:113) with H1, H2, and H3 underlined (SEQ ID NO:116-118, respectively)

E V Q L V E S G G G L V T P G G S L R L S C A A S G F T F S D Y Y M
S W V R Q A P G R G L E W V S A I S G S G G S T Y Y A D S V K G R I
T I S R D N A K N S L Y L Q M S S L R S E D T A V Y Y C A R G L W V
W D P L D Y W G R G T L V T V S S

V_H (SEQ ID NO:122) with H1, H2, and H3 underlined (SEQ ID NO:125-127, respectively)

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCACGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACATG
AGCTGGGTCCGCCAGGCTCCAGGGAGGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGATC
ACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGCTTTGGGTT
TGGGATCCTCTTGACTACTGGGGCAGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:114) with L1, L2, and L3 underlined (SEQ ID NO:119-121, respectively)

D I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L A
W Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G F G
T D F T L T I S S L Q P D D F A T Y Y C Q Q Y S E F A W T F G G G T
K L E I K R

V_L (SEQ ID NO:123) with L1, L2, and L3 underlined (SEQ ID NO:128-130, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCC
TGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGATTTGGG
ACCGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAATACAGCGAGTTCGCCTGGACCTTCGGCGGAGGGACC
AAGCTGGAGATCAAACGT

FIG. 7(cont.)

062A09

V_H (SEQ ID NO:131) with H1, H2, and H3 underlined (SEQ ID NO:134-136, respectively)

Q V Q L V E S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I
S W V R Q A P G Q G L E W M G W V S A Y T G N T N Y A Q K F Q G R V
T M T T D T S T S T A Y M E L R G L R S D D T A V Y Y C A R D R G Y
Y D A F D I W G Q G T L V T V S S

V_H (SEQ ID NO:84) with H1, H2, and H3 underlined (SEQ ID NO:143-145, respectively)

AGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTATCA
GCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGGTCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAGAGTCA
CCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGAGGGGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGTGGATACT
ATGATGCTTTTGATATCTGGGGCCAAGGCACCCTGGTCACCGTCTCCTCA

L (SEQ ID NO:132) with L1, L2, and L3 underlined (SEQ ID NO:137-139, respectively)

I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L A W
Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G S G T
D F T L T I S S L Q P D D F A T Y Y C Q Q M G E Y N A T I G G G T K
L E I K R

L (SEQ ID NO:141) with L1, L2, and L3 underlined (SEQ ID NO:146-148, respectively)

ACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCCT
GGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGATTTGGGA
CAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAAATGGGCGAGTACAACGCCACCATCGGCGGAGGGACCA
AGCTGGAGATCAAACGT

FIG. 7(cont.)

062G05

V_H (SEQ ID NO:149) with H1, H2, and H3 underlined (SEQ ID NO:152-154, respectively)

Q V Q L V E S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I S
W V R Q A P G Q G L E W M G W I S A Y T G N T N Y A Q K F Q G R V T M
T T D T S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y Y D A
F D I W G Q G T L V T V S S

V_H (SEQ ID NO:158) with H1, H2, and H3 underlined (SEQ ID NO:161-163, respectively)

CAGGTGCAGCTGGTGGAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTATCAGC
TGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAGAGTCACCATG
ACCACAGACACATCCACGAGCACAGCCTACATGGAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGTGGATACTATGATGCT
TTCGATATCTGGGGCCAAGGCACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:150) with L1, L2, and L3 underlined (SEQ ID NO:155-157, respectively)

D I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L A W
Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G S G T D
F T L T I S S L Q P D D F A T Y Y C Q Q M G E W K A A F G G G T K L E
I K R

V_L (SEQ ID NO:159) with L1, L2, and L3 underlined (SEQ ID NO:164-166, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCCTGG
TATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGATTTGGGACAGAT
TTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAAATGGGGGAGTGGAAGGCGGCCTTCGGCGGAGGGACCAAGCTGGAGATCAAACGT

FIG. 7(cont.)

087B03

V_H (SEQ ID NO:167) with H1, H2, and H3 underlined (SEQ ID NO:170-172, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N
W V R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I
S R D N A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G A A
W N M G Y W G R G T L V T V S S

V_H (SEQ ID NO:176) with H1, H2, and H3 underlined (SEQ ID NO:179-181, respectively)

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAAC
TGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCATC
TCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGAGGATGGTATAGTGGGGCCGCG
TGGAACATGGGCTACTGGGGCCGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:168) with L1, L2, and L3 underlined (SEQ ID NO:173-175, respectively)

Q A V L T Q P S S V S G S P G Q S I T I S C T G A S G D V G A Y N F V
S W Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S S
N T A S L T I S G L Q A E D E S D Y Y C S S Y T S T F S V V F G G G T
K V T V L G

V_L (SEQ ID NO:177) with L1, L2, and L3 underlined (SEQ ID NO:182-184, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGGTGCTTATAACTTTGTC
TCCTGGTACCAACAACACGCCAGGCAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTAGC
AACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCAGCTCATATACAAGCACCTTCTCTGTGGTATTTGGCGGAGGGACC
AAGGTCACCGTCCTAGGT

FIG. 7(cont.)

367D04

V_H (SEQ ID NO:185) with H1, H2, and H3 underlined (SEQ ID NO:188-190, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N W V
R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I S R D N
A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G S P W S L G H W
G R G T L V T V S S

V_H (SEQ ID NO:194) with H1, H2, and H3 underlined (SEQ ID NO:197-199, respectively)

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAACTGGGT
CCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACA
ACGCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGAGGATGGTATAGTGGGAGCCCGTGGTCGCTGGGCCAC
TGGGGCCGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:186) with L1, L2, and L3 underlined (SEQ ID NO:191-193, respectively)

Q A V L T Q P S S V S G S P G Q S V T I S C T G A S G D V G A Y N F V S W
Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S G N T A S
L T I S R L Q A E D E S D Y Y C S S Y T S R Y T T E F G G G T K V T V L G

V_L (SEQ ID NO:195) with L1, L2, and L3 underlined (SEQ ID NO:200-202, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCCGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGGTGCTTATAACTTTGTCTCCTG
GTACCAACAACACCCAGGCAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCT
CCCTGACCATCTCTAGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCAGCTCATATACATCGAGGTACACGACCGAGTTTGGCGGAGGGACCAAGGTCACCGTCCTAGGT

FIG. 7(cont.)

368D04

V_H (SEQ ID NO:203) with H1, H2, and H3 underlined (SEQ ID NO:206-208, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N W
V R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I S R
D N A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G A A W N M
G Y W G R G T L V T V S S

V_H (SEQ ID NO:212) with H1, H2, and H3 underlined (SEQ ID NO:215-217, respectively)

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAACTG
GGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCATCTCCA
GAGACAACGCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGAGGATGGTATAGTGGGGCCGCGTGGAAC
ATGGGCTACTGGGGCCGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:204) with L1, L2, and L3 underlined (SEQ ID NO:209-211, respectively)

Q A V L T Q P S S V S G S P G Q S I T I S C T G A S G D V G A Y N F V S
W Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S G N T
A S L T I S G L Q A E D E S D Y Y C A S L V S D F S V V F G G G T K V T
V L G

V_L (SEQ ID NO:213) with L1, L2, and L3 underlined (SEQ ID NO:218-220, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCCGTGTCTGGGTCCCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGGTGCTTATAACTTTGTCTC
CTGGTACCAACAACACCCAGGCAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACA
CGGCCTCCCTGACCATCTCTGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCGCCTCCCTCGTCTCCGACTTCTCTGTGGTATTTGGCGGAGGGACCAAGGTCACCGTCCTAGGT

FIG. 7(cont.)

166B06

V_H (SEQ ID NO:221) with H1, H2, and H3 underlined (SEQ ID NO:224-226, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H W
V R Q T P G Q G F E W M G W V N P D T G G T R Y A Q K F Q G W V T M T R
D M S N T T A Y M E L P R L R D D D T A V Y Y C A R D L T G F D P F D I
W G Q G T L V T V S S

V_H (SEQ ID NO:230) with H1, H2, and H3 underlined (SEQ ID NO:233-235, respectively)

GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTG
GGTGCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTGGGTCACAATGACCA
GGGACATGTCCAACACCACAGCCTACATGGAGCTGCCCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATTTGATCCTTTTGAT
ATCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:222) with L1, L2, and L3 underlined (SEQ ID NO:227-229, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y Q
Q R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L
T I S R V E A G D E A D F Y C Q V W D L F N D N G V F G G G T K L T V L
G

V_L (SEQ ID NO:231) with L1, L2, and L3 underlined (SEQ ID NO:236-238, respectively)

CAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCA
GCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATTATGACTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCC
TGACCATCAGCAGGGTCGAGGCCGGGGATGAGGCCGACTTTTACTGTCAGGTGTGGGATCTCTTCAACGACAACGGCGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

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FIG. 7(cont.)

166G05

V_H (SEQ ID NO:239) with H1, H2, and H3 underlined (SEQ ID NO:242-244, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H W V
R Q T P G Q G F E W M G W V N P D T G G T R Y A Q K F Q G W V T M T R D M
S N T T A Y M E L P R L R D D D T A V Y Y C A R D L T G F D P F D I W G Q
G T L V T V S S

V_H (SEQ ID NO:248) with H1, H2, and H3 underlined (SEQ ID NO:251-253, respectively)

GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTGGGT
GCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTGGGTCACAATGACCAGGGACA
TGTCCAACACCACAGCCTACATGGAGCTGCCCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATTTGATCCTTTTGATATCTGGGGC
CAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:240) with L1, L2, and L3 underlined (SEQ ID NO:245-247, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y Q Q
R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I
S R V E A G D E A D F Y C Q V W D F L T D S G S F G G G T K L T V L G

V_L (SEQ ID NO:249) with L1, L2, and L3 underlined (SEQ ID NO:254-256, respectively)

CAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCACAATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCAGCA
GAGGCCAGGCCAGGCGCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCCTGACCA
TCAGCAGGGTCGAGGCCGGGGATGAGGCCGACTTTTACTGTCAGGTGTGGGATTTCCTCACCGACTCGGGGTCGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

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FIG. 7(cont.)

375G06

V_H (SEQ ID NO:257) with H1, H2, and H3 underlined (SEQ ID NO:260-262, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H W
V R Q T P G Q G F E W M G W V N P D T G G T R Y A Q K F Q G W V T M T R
D M S N T T A Y M E L P R L R D D D T A V Y Y C A R D L T G Y D Y Y D R
W G Q G T L V T V S S

V_H (SEQ ID NO:266) with H1, H2, and H3 underlined (SEQ ID NO:269-271, respectively)

GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTG
GGTGCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTGGGTCACAATGACCA
GGGACATGTCCAACACCACAGCCTACATGGAGCTGCCCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATACGACTACTACGAC
CGGTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:258) with L1, L2, and L3 underlined (SEQ ID NO:263-265, respectively)

Q S V L T Q P P S M S V A P G K T A T I T C G G N N F R N K R V H W Y Q
Q R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L
T I S R V E A G D E A D F Y C Q V W D F L A D E A M F G G G T K L T V L

V_L (SEQ ID NO:267) with L1, L2, and L3 underlined (SEQ ID NO:272-274, respectively)

CAGTCTGTGCTGACTCAGCCGCCCTCAATGTCAGTGGCCCCAGGAAAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCA
GCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCC
TGACCATCAGCAGGGTCGAGGCCGGGGATGAGGCCGACTTTTACTGTCAGGTGTGGGATTTCCTCGCCGACGAGGCGATGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 7(cont.)

376B10

V_H (SEQ ID NO:275) with H1, H2, and H3 underlined (SEQ ID NO:278-280, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H
W V R Q T P G Q G F E W M G W V N P D T G G T R Y A Q K F Q G W V T M
T R D M S N T T A Y M E L P G L R D D D T A V Y Y C A R D L T G Y D Q
Y T A W G Q G T L V T V S S

V_H (SEQ ID NO:284) with H1, H2, and H3 underlined (SEQ ID NO:287-289, respectively)

GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATATTCA
CTGGGTGCGACAGACCCCAGGACAAGGGTTTGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACGAGATACGCGCAGAAGTTTCAGGGCTGGGTCACAA
TGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGCCCGGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGGTACGAC
CAGTACACGGCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:276) with L1, L2, and L3 underlined (SEQ ID NO:281-283, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y
Q Q R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A
T L T I S R V E A G D E A D F Y C S T F D P F T D R P L F G G G T K L
T V L G

V_L (SEQ ID NO:285) with L1, L2, and L3 underlined (SEQ ID NO:290-292, respectively)

CAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTA
TCAGCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGG
CCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGAGGCCGACTTTTACTGTAGCACCTTCGACCCCTTCACTGATCGTCCGCTGTTCGGCGGAGGGACCAAG
CTGACCGTCCTAGGT

FIG. 7(cont.)

354A08

V_H (SEQ ID NO:293) with H1, H2, and H3 underlined (SEQ ID NO:296-298, respectively)

QVQLVQSGAEKKPGASVKVSCKASGYTFTDYYMHWVRQAPGQGLEWVGWINPYTGGAFYAQKFRGRVTMTRDTSINTAYMELSRLGSDDTAVYYCAREPERFGGSTG
QVWGRGTMVTVSS

V_H (SEQ ID NO:302) with H1, H2, and H3 underlined (SEQ ID NO:305-307, respectively)

CAGGTCCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATATGCACTG
GGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAGGGTCACAATGACCA
GGGACACGTCCATCAACACAGCCTACATGGAGCTAAGCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAGATTCGGCGACTCCACG
GGGCAGGTCTGGGGCCGGGGGACAATGGTCACCGTCTCGAGT

V_L (SEQ ID NO:294) with L1, L2, and L3 underlined (SEQ ID NO:299-301, respectively)

QAVLTQPSSVSGAPRQRVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCYHWDKEQSGYVFGTGTQLTVLSA

V_L (SEQ ID NO:303) with L1, L2, and L3 underlined (SEQ ID NO:308-310, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCCCCAAGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTACA
CTGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCT
CAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCTACCACTGGGACAAGGAGCAGAGTGGTTATGTCTTCGGAACTGGGACCCAG
CTCACCGTTTTAAGTGCG

FIG. 7(cont.)

355B06

V_H (SEQ ID NO:311) with H1, H2, and H3 underlined (SEQ ID NO:314-316, respectively)

EVQLVQSGAEVKKPGASVKVSCQASGYTFTDYYMHWVRQAPGQGLEWVGWINPYTGSAFYAQKFRGRATMTRNTSINTAYMELSRLGSDDTAVYYCAREPEKFGES
SGQLWGRGTMVTISS

V_H (SEQ ID NO:320) with H1, H2, and H3 underlined (SEQ ID NO:323-325, respectively)

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCACCGACTACTATATGCACT
GGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGGTGGATCAACCCTTATACTGGTAGCGCATTCTATGCACAGAAGTTTCGGGGCAGGGCCACAATGAC
CAGGAACACGTCCATCAACACAGCCTACATGGAGCTGAGCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAAATTCGGCGAGTCC
AGCGGCCAGTTGTGGGGCCGGGGGACAATGGTCACCATCTCGAGT

V_L (SEQ ID NO:312) with L1, L2, and L3 underlined (SEQ ID NO:317-319, respectively)

QAVLTQPSSVSGAPGQRVTISCTGSSSNIGPGYGVHWYQQLPGTAPKLLIYGDSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSGLSGYVFGTGTQLTVLSA

V_L (SEQ ID NO:321) with L1, L2, and L3 underlined (SEQ ID NO:326-328, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTAC
ACTGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCAC
CTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCCGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCGGCCTGAGTGGTTATGTCTTCGGAACTGGGACC
CAGCTCACCGTTTTAAGTGCG

FIG. 7(cont.)

355E04

V_H (SEQ ID NO:329) with H1, H2, and H3 underlined (SEQ ID NO:332-334, respectively)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTHYYMHWVRQAPGQGLEWVGWINPYTGGAFYAQKFQGRVTMTRDTSINTAYMELSRLGSDDTAVYYCAREPEKFDSPN
AEIWGRGTMVTISS

V_H (SEQ ID NO:338) with H1, H2, and H3 underlined (SEQ ID NO:341-343, respectively)

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAAAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCCACTACTATATGCACTG
GGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCAGGGCAGGGTCACAATGACCA
GGGACACGTCCATCAACACAGCCTACATGGAGCTGAGCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAAATTCGACTCGCCGAAC
GCCGAGATCTGGGGCCGGGGGACAATGGTCACCATCTCGAGT

V_L (SEQ ID NO:330) with L1, L2, and L3 underlined (SEQ ID NO:335-337, respectively)

QAVLTQPSSVSGAPGQRVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGYVFGTGTQLTVLSA

V_L (SEQ ID NO:339) with L1, L2, and L3 underlined (SEQ ID NO:344-346, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTACA
CTGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCT
CAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTTATGTCTTCGGAACCGGGACCCAG
CTCACCGTTTTAAGTGCG

FIG. 7(cont.)

356A11

V_H (SEQ ID NO:347) with H1, H2, and H3 underlined (SEQ ID NO:350-352, respectively)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWVGWINPYTGSAFYAQKFRGRVTMTRDTSINTAYMELSRLGSDDTAVYYCAREPE
KFDSDDSDVWGRGTMVTVSG

V_H (SEQ ID NO:356) with H1, H2, and H3 underlined (SEQ ID NO:359-361, respectively)

CAGGTTCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAACTACTATAT
GCACTGGGTGCGACAGGCCCCTGGACAGGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTAGCGCATTCTATGCACAGAAGTTTCGGGGCAGGG
TTACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTGAGCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAA
AAATTCGACTCCGACGACTCCGACGTCTGGGGCCGCGGGACAATGGTCACCGTCTCGGGT

V_L (SEQ ID NO:348) with L1, L2, and L3 underlined (SEQ ID NO:353-355, respectively)

QAVLTPPSVSGAPGQRVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLIIYGDSSRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDNSLSGYVFGTGTQLTVLSA

V_L (SEQ ID NO:357) with L1, L2, and L3 underlined (SEQ ID NO:362-364, respectively)

CAGGCTGTGCTGACTCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGG
TGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCATCATCTATGGTGACAGCAGTCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAACAGCCTGAGCGGTTATGTC
TTCGGAACTGGGACCCAGCTCACCGTTTTAAGTGCG

FIG. 7(cont.)

GIL01

V_H (SEQ ID NO:365) with H1, H2, and H3 underlined (SEQ ID NO:368-370, respectively)

Q V Q L V E S G G G L V K P G G S L R L S C A A S G F T F S D Y Y M S W I R Q
A P G K G L E W V S A I S G S G G S T Y Y A D S V K G R I T I S R D N A K N S
L Y L Q M N S L R A E D T A V Y Y C A R G L W V W D P L D Y W G R G T L V T V
S S

V_H (SEQ ID NO:374) with H1, H2, and H3 underlined (SEQ ID NO:377-379, respectively)

CAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCCA
GGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGATCACCATCTCCAGAGACAACGCCAAGAACT
CACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGCTTTGGGTTTGGGATCCTCTTGACTACTGGGGCAGAGGAACCCTGGTCACCGTCTCTTCA

V_L (SEQ ID NO:366) with L1, L2, and L3 underlined (SEQ ID NO:371-373, respectively)

D I Q M T Q S P S T L S A S V G D R V T I T C R A S E G I Y H W L A W Y Q Q K
P G K A P K L L I Y K A S S L A S G V P S R F S G S G S G T E F T L T I S S L
Q P D D F A T Y Y C Q Q Y S N Y P L T F G G G T K V E I K R

V_L (SEQ ID NO:375) with L1, L2, and L3 underlined (SEQ ID NO:380-382, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCCTGGTATCAGCAGAA
GCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCC
TGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGT

FIG. 8

GIL16

V_H (SEQ ID NO:383) with H1, H2, and H3 underlined (SEQ ID NO:386-388, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I S W V
R Q A P G Q G L E W M G W I S A Y T G N T N Y A Q K F Q G R V T M T T D T
S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y Y D A F D I W G Q
G T L V T V S S

V_H (SEQ ID NO:392) with H1, H2, and H3 underlined (SEQ ID NO:395-397, respectively)

CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTATCAGCTGGGT
GCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCACAGACA
CATCCACGAGCACAGCCTACATGGAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGTGGATACTATGATGCTTTTGATATCTGGGGC
CAAGGCACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:384) with L1, L2, and L3 underlined (SEQ ID NO:389-391, respectively)

D I Q M T Q S P S T L S A S V G D R V T I T C R A S E G I Y H W L A W Y Q
Q K P G K A P K L L I Y K A S S L A S G V P S R F S G S G S G T E F T L T
I S S L Q P D D F A T Y Y C Q Q Y S N Y P L T F G G G T K V E I K R

V_L (SEQ ID NO:393) with L1, L2, and L3 underlined (SEQ ID NO:398-400, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCCTGGTATCA
GCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCA
CCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGT

FIG. 8(cont.)

GIL45

V_H (SEQ ID NO:401) with H1, H2, and H3 underlined (SEQ ID NO:404-406, respectively)

Q M Q L V E S G G G V V Q P G R S L R L S C A A S G F T F S N Y G M
Y W V R Q A P G K G L E W V A H I W Y D G S N E K Y A D S V K G R M
T V S R D N S K N T L Y L Q M N S L R A E D T A V Y Y C A T E Q H W
I T A F D I W G K G T L V T V S S

V_H (SEQ ID NO:410) with H1, H2, and H3 underlined (SEQ ID NO:413-415, respectively)

CAGATGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTATGGCAT
GTACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACATATTTGGTATGATGGAAGTAATGAAAAGTATGCAGACTCCGTGAAGGGCCGAA
TGACCGTCTCCAGAGACAATTCCAAGAACACGTTGTATTTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGACAGAGCAACAC
TGGATTACTGCTTTTGATATCTGGGGCAAAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:402) with L1, L2, and L3 underlined (SEQ ID NO:407-409, respectively)

Q S A L T Q P A S V S G S P G Q S I T I S C T G T S S D V G G Y N Y
V S W Y Q Q H P G K A P K L M I Y E G S K R P S G V S N R F S G S K
S G N T A S L T I S G L Q A E D E A D Y Y C S S Y T T R S T R V F G
G G T K L T V L G

V_L (SEQ ID NO:411) with L1, L2, and L3 underlined (SEQ ID NO:416-418, respectively)

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTA
TGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCA
AGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTACTACTGCAGCTCATATACAACCAGGAGCACTCGAGTTTTC
GGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 8(cont.)

GIL60

V_H (SEQ ID NO:419) with H1, H2, and H3 underlined (SEQ ID NO:422-424, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N W V
R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I S R D N
A K N S L Y L Q M N S L R A E D T A L Y H C A R G W Y S G S F Y Y F G Y W
G R G T L V T V S S

V_H (SEQ ID NO:428) with H1, H2, and H3 underlined (SEQ ID NO:431-433, respectively)

GAGGTGCAGCTGGTGGAGAGcGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAACTGGGTC
CGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAC
GCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATCACTGTGCGAGAGGATGGTATAGTGGGAGCTTCTACTACTTTGGCTACTGG
GGCCGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:420) with L1, L2, and L3 underlined (SEQ ID NO:425-427, respectively)

Q A A L T Q P A S V S G S P G Q S I T I S C T G A S G D V G A Y N F V S W
Y Q Q H P G K A P K L I I Y D V N K R P S G V S N R F S G S K S G N T A S
L T I S G L Q A E D E A D Y Y C S S Y T S T F S V V F G G G T K L T V L G

V_L (SEQ ID NO:429) with L1, L2, and L3 underlined (SEQ ID NO:434-436, respectively)

CAGGCTGCGCTGACTCAGCCGGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGGTGCTTATAACTTTGTCTCCTGG
TACCAACAACACCCAGGCAAAGCCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCC
CTGACCATCTCTGGGCTCCAGGCCGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCACCTTCTCTGTGGTATTTGGCGGAGGGACCAAGCTGACCGTCCTAGGT

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FIG. 8(cont.)

GIL68

V_H (SEQ ID NO:437) with H1, H2, and H3 underlined (SEQ ID NO:440-442, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F S D Y Y I H W V R Q
A P G Q G L E W M G W V N P D T G G T R Y A Q K F Q G R V T M T R D M S I S T
A Y M E L S R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q G T L V T V
S S

V_H (SEQ ID NO:446) with H1, H2, and H3 underlined (SEQ ID NO:449-451, respectively)

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTGGGTGCGACA
GGCCCCTGGACAAGGGTTGGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCCGGGTCACAATGACCAGGGACATGTCCATCTCCA
CAGCCTACATGGAGCTGTCCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:438) with L1, L2, and L3 underlined (SEQ ID NO:443-445, respectively)

S S V L T Q P P S V S V A P G K T A R I T C G G N N F R N K R V H W Y Q Q K P
G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S R V E
A G D E A D Y Y C Q V W D S S T D R P L F G G G T K L T V L G

V_L (SEQ ID NO:447) with L1, L2, and L3 underlined (SEQ ID NO:452-454, respectively)

TCGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCCGCATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCAGCAGAAGCC
AGGCCAGGCCCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCG
AGGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTACTGATCGTCCGCTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 8(cont.)

GIL92

V_H (SEQ ID NO:455) with H1, H2, and H3 underlined (SEQ ID NO:458-460, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y M H W V R
Q A P G Q G L E W V G W I N P Y T G G A F Y A Q K F R G R V T M T R D T S I
S T A Y M E L S R L R S D D T A V Y Y C A R E P E K F D F W G G D N W G R G
T L V T V S S

V_H (SEQ ID NO:464) with H1, H2, and H3 underlined (SEQ ID NO:467-469, respectively)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATATGCACTGGGTGCG
ACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAGGGTCACAATGACCAGGGACACGTCCA
TCAGCACAGCCTACATGGAGCTGAGCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAAATTCGATTTTTGGGGGGGTGACAACTGGGGCCGG
GGGACATTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:456) with L1, L2, and L3 underlined (SEQ ID NO:461-463, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H W Y
Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G S K S G T S A S L A
I T G L Q A E D E A D Y Y C Q S Y D S S L S G Y V F G G G T Q L T V L G

V_L (SEQ ID NO:465) with L1, L2, and L3 underlined (SEQ ID NO:470-472, respectively)

CAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTACACTGGTA
CCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 8(cont.)

062A09

V_H (SEQ ID NO:473) with H1, H2, and H3 underlined (SEQ ID NO:476-478, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I S W
V R Q A P G Q G L E W M G W V S A Y T G N T N Y A Q K F Q G R V T M T T
D T S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y Y D A F D I
W G Q G T L V T V S S

V_H (SEQ ID NO:482) with H1, H2, and H3 underlined (SEQ ID NO:485-487, respectively)

CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTATCAGCTG
GGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGGTCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCA
CAGACACATCCACGAGCACAGCCTACATGGAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGTGGATACTATGATGCTTTTGAT
ATCTGGGGCCAAGGCACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:474) with L1, L2, and L3 underlined (SEQ ID NO:479-481, respectively)

D I Q M T Q S P S T L S A S V G D R V T I T C R A S E G I Y H W L A W Y
Q Q K P G K A P K L L I Y K A S S L A S G V P S R F S G S G S G T E F T
L T I S S L Q P D D F A T Y Y C Q Q M G E Y N A T F G G G T K V E I K R

V_L (SEQ ID NO:483) with L1, L2, and L3 underlined (SEQ ID NO:488-490, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTTGGCCTGGTA
TCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCA
CTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAAATGGGCGAGTACAACGCCACCTTCGGCGGAGGGACCAAGGTGGAGATCAAACGT

FIG. 8(cont.)

087B03

V_H (SEQ ID NO:491) with H1, H2, and H3 underlined (SEQ ID NO:494-496, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N W V
R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I S R D N
A K N S L Y L Q M N S L R A E D T A L Y H C A R G W Y S G A A W N M G Y W
G R G T L V T V S S

V_H (SEQ ID NO:500) with H1, H2, and H3 underlined (SEQ ID NO:503-505, respectively)

GAGGTGCAGCTGGTGGAGAGCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAACTGGGTC
CGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAC
GCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATCACTGTGCGAGAGGATGGTATAGTGGGGCCGCGTGGAACATGGGCTACTGG
GGCCGAGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:492) with L1, L2, and L3 underlined (SEQ ID NO:497-499, respectively)

Q A A L T Q P A S V S G S P G Q S I T I S C T G A S G D V G A Y N F V S W
Y Q Q H P G K A P K L I I Y D V N K R P S G V S N R F S G S K S G N T A S
L T I S G L Q A E D E A D Y Y C S S Y T S T F S V V F G G G T K L T V L G

V_L (SEQ ID NO:501) with L1, L2, and L3 underlined (SEQ ID NO:506-508, respectively)

CAGGCTGCGCTGACTCAGCCGGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGGTGCTTATAACTTTGTCTCCTGG
TACCAACAACACCCAGGCAAAGCCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCC
CTGACCATCTCTGGGCTCCAGGCCGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCACCTTCTCTGTGGTATTTGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 8(cont.)

166B06

V_H (SEQ ID NO:509) with H1, H2, and H3 underlined (SEQ ID NO:512-514, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F S D Y Y I H W V
R Q A P G Q G L E W M G W V N P D T G G T R Y A Q K F Q G R V T M T R D M
S I S T A Y M E L S R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q
G T L V T V S S

V_H (SEQ ID NO:518) with H1, H2, and H3 underlined (SEQ ID NO:521-523, respectively)

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTGGGT
GCGACAGGCCCCTGGACAAGGGTTGGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCCGGGTCACAATGACCAGGGACA
TGTCCATCTCCACAGCCTACATGGAGCTGTCCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATTTGATCCTTTTGATATCTGGGGC
CAGGGAACCCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:510) with L1, L2, and L3 underlined (SEQ ID NO:515-517, respectively)

S S V L T Q P P S V S V A P G K T A R I T C G G N N F R N K V H W Y Q Q K
P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S
R V E A G D E A D Y Y C Q V W D L F N D N G V F G G G T K L T V L G

V_L (SEQ ID NO:519) with L1, L2, and L3 underlined (SEQ ID NO:524-526, respectively)

TCGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCCGCATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCAGCA
GAAGCCAGGCCAGGCCCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCCTGACCA
TCAGCAGGGTCGAGGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATCTCTTCAACGACAACGGCGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

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FIG. 8(cont.)

166G05

V_H (SEQ ID NO:527) with H1, H2, and H3 underlined (SEQ ID NO:530-532, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F S D Y Y I H W V R
Q A P G Q G L E W M G W V N P D T G G T R Y A Q K F Q G R V T M T R D M S I
S T A Y M E L S R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q G T L
V T V S S

V_H (SEQ ID NO:536) with H1, H2, and H3 underlined (SEQ ID NO:539-541, respectively)

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACTGGGTGCG
ACAGGCCCCTGGACAAGGGTTGGAGTGGATGGGATGGGTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCCGGGTCACAATGACCAGGGACATGTCCA
TCTCCACAGCCTACATGGAGCTGTCCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTAACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACC
CTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:528) with L1, L2, and L3 underlined (SEQ ID NO:533-535, respectively)

S S V L T Q P P S V S V A P G K T A R I T C G G N N F R N K R V H W Y Q Q K
P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S R
V E A G D E A D Y Y C Q V W D F L T D S G S F G G G T K L T V L G

V_L (SEQ ID NO:537) with L1, L2, and L3 underlined (SEQ ID NO:542-544, respectively)

TCGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAAAGACGGCCCGCATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGTATCAGCAGAA
GCCAGGCCAGGCCCCTGTCCTGGTCATCTATTATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGCCACCCTGACCATCAGCA
GGGTCGAGGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATTTCCTCACCGACTCGGGGTCGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 8(cont.)

354A08

V_H (SEQ ID NO:545) with H1, H2, and H3 underlined (SEQ ID NO:548-550, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y M H W V R
Q A P G Q G L E W V G W I N P Y T G G A F Y A Q K F R G R V T M T R D T S I
S T A Y M E L S R L R S D D T A V Y Y C A R E P E R F G D S T G Q V W G R G
T L V T V S S

V_H (SEQ ID NO:554) with H1, H2, and H3 underlined (SEQ ID NO:557-559, respectively)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATATGCACTGGGTGCG
ACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAGGGTCACAATGACCAGGGACACGTCCA
TCAGCACAGCCTACATGGAGCTGAGCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAGATTCGGCGACTCCACGGGGCAGGTCTGGGGCCGG
GGGACATTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:546) with L1, L2, and L3 underlined (SEQ ID NO:551-553, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H W Y
Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G S K S G T S A S L A
I T G L Q A E D E A D Y Y C Y H W D K E Q S G Y V F G G G T Q L T V L G

V_L (SEQ ID NO:555) with L1, L2, and L3 underlined (SEQ ID NO:560-562, respectively)

CAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTACACTGGTA
CCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCTACCACTGGGACAAGGAGCAGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 8(cont.)

355B06

V_H (SEQ ID NO:563) with H1, H2, and H3 underlined (SEQ ID NO:566-568, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y M H W V
R Q A P G Q G L E W V G W I N P Y T G S A F Y A Q K F R G R V T M T R D T
S I S T A Y M E L S R L R S D D T A V Y Y C A R E P E K F G E S S G Q L W
G R G T L V T V S S

V_H (SEQ ID NO:572) with H1, H2, and H3 underlined (SEQ ID NO:575-577, respectively)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATATGCACTGGGTG
CGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTAGCGCTTTCTATGCACAGAAGTTTCGGGGCAGGGTCACAATGACCAGGGACACG
TCCATCAGCACAGCCTACATGGAGCTGAGCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAAATTCGGCGAGTCCAGCGGCCAGTTGTGG
GGCCGGGGGACATTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:564) with L1, L2, and L3 underlined (SEQ ID NO:569-571, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H W
Y Q Q L P G T A P K L L I Y G D S N R P S G V P D R F S G S K S G T S A S
L A I T G L Q A E D E A D Y Y C Q S Y D S G L S G Y V F G G G T Q L T V L
G

V_L (SEQ ID NO:573) with L1, L2, and L3 underlined (SEQ ID NO:578-580, respectively)

CAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTACACTGG
TACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCC
CTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCGGCCTGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 8(cont.)

355E04

V_H (SEQ ID NO:581) with H1, H2, and H3 underlined (SEQ ID NO:584-586, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T H Y Y
M H W V R Q A P G Q G L E W V G W I N P Y T G G A F Y A Q K F Q G
R V T M T R D T S I S T A Y M E L S R L R S D D T A V Y Y C A R E
P E K F D S P N A E I W G R G T L V T V S S

V_H (SEQ ID NO:590) with H1, H2, and H3 underlined (SEQ ID NO:593-595, respectively)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCCACTACTAT
ATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCAGGGC
AGGGTCACAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGAGCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAA
CCTGAAAAATTCGACTCGCCGAACGCCGAGATCTGGGGCCGGGGGACATTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:582) with L1, L2, and L3 underlined (SEQ ID NO:587-589, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y
G V H W Y Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G
S K S G T S A S L A I T G L Q A E D E A D Y Y C Q S Y D S S L S G
Y V F G G G T Q L T V L G

V_L (SEQ ID NO:591) with L1, L2, and L3 underlined (SEQ ID NO:596-598, respectively)

CAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTAT
GGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC
TCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGT
TATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 8(cont.)

356A11

V_H (SEQ ID NO:599) with H1, H2, and H3 underlined (SEQ ID NO:602-604, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T N Y Y M H W
V R Q A P G Q G L E W V G W I N P Y T G S A F Y A Q K F R G R V T M T R
D T S I S T A Y M E L S R L R S D D T A V Y Y C A R E P E K F D S D D S
D V W G R G T L V T V S S

V_H (SEQ ID NO:608) with H1, H2, and H3 underlined (SEQ ID NO:611-613, respectively)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAACTACTATATGCACTGG
GTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGGATCAACCCTTATACTGGTAGCGCATTCTATGCACAGAAGTTTCGGGGCAGGGTCACAATGACCAGG
GACACGTCCATCAGCACAGCCTACATGGAGCTGAGCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAAAATTCGACTCCGACGACTCC
GACGTCTGGGGCCGCGGGACATTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:600) with L1, L2, and L3 underlined (SEQ ID NO:605-607, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H
W Y Q Q L P G T A P K L L I Y G D S N R P S G V P D R F S G S K S G T S
A S L A I T G L Q A E D E A D Y Y C Q S Y D N S L S G Y V F G G G T Q L
T V L G

V_L (SEQ ID NO:609) with L1, L2, and L3 underlined (SEQ ID NO:614-616, respectively)

CAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGGTGTACAC
TGGTACCAACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCA
GCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAACAGCCTGAGCGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

48/84

FIG. 8(cont.)

368D04

V_H (SEQ ID NO:617) with H1, H2, and H3 underlined (SEQ ID NO:620-622, respectively)

EVQLVESGGG VVRPGGSLRL SCAASGFTFD DYGMNWVRQA PGKGLEWVSG

VNWNGGTRDY AASVKGRFTI SRDNAKNSLY LQMNSLRAED TALYHCARGW

YSGAAWNMGY WGRGTLVTVS S

V_H (SEQ ID NO:626) with H1, H2, and H3 underlined (SEQ ID NO:629-631, respectively)

GAGGTGCAGCTGGTGGAGAGCGGCGGAGGCGTGGTGAGACCAGGCGGCAGCCTGAGACTGAGCTGCGCCGCCAGCGGCTTCACCTTCGACGACTACGGCATGAA
CTGGGTGAGGCAGGCCCCAGGCAAGGGCCTGGAGTGGGTGTCCGGCGTGAACTGGAACGGCGGCACCAGAGACTACGCCGCCTCTGTGAAGGGCAGATTCACCA
TCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCCTGTACCACTGCGCCAGAGGCTGGTACAGCGGAGCC
GCCTGGAACATGGGCTACTGGGGCAGAGGCACCCTGGTGACCGTGTCCAGC

V_L (SEQ ID NO:618) with L1, L2, and L3 underlined (SEQ ID NO:623-625, respectively)

QAALTQPASV SGSPGQSITI SCTGASGDVG AYNFVSWYQQ HPGKAPKLII

YDVNKRPSGV SNRFSGSKSG NTASLTISGL QAEDEADYYC ASLVSDFSVV

FGGGTKLTVL

V_L (SEQ ID NO:627) with L1, L2, and L3 underlined (SEQ ID NO:632-634, respectively)

CAGGCCGCCCTGACCCAGCCCGCCAGCGTGTCTGGCAGCCCAGGCCAGAGCATCACCATCAGCTGCACCGGCGCCAGCGGCGATGTGGGCGCCTACAACTTCGT
GTCCTGGTATCAGCAGCACCCCGGCAAGGCCCCCAAGCTGATCATCTACGACGTGAACAAGAGACCCAGCGGCGTGTCCAACAGATTCAGCGGCAGCAAGAGCG
GCAACACCGCCAGCCTGACCATCAGCGGACTGCAGGCCGAGGACGAGGCCGACTACTACTGCGCCAGCCTGGTGTCCGACTTCAGCGTGGTGTTCGGCGGAGGC
ACCAAGCTGACCGTGCTG

FIG. 8(cont.)

GIL01

SEQ ID NO:7

E V Q L V E S G G G L V T P G G S L R L S C A A S G F T F
S D Y Y M S W I R Q A P G R G L E W V S A I S G S G G S T
Y Y A D S V K G R I T I S R D N A K N S L Y L Q M S S L R
S E D T A V Y Y C A R G L W V W D P L D Y W G R G T L V T
V S S G G G G S G G G G S G G G G S D I Q M T Q S P S T L
S A S I G D R V T I T C R A S E G I Y H W L A W Y Q Q K P
G K A P K L L I Y K A S S L A S G A P S R F S G S G S G T
D F T L T I S S L Q P D D F A T Y Y C Q Q Y S N Y P L T F
G G G T K L E I K R A A A

SEQ ID NO:16

GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCACGCCTGGAGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTA
CATGAGCTGGATCCGCCAGGCTCCAGGGAGGGGGCTGGAGTGGGTCTCA
GCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGG
GCCGGATCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCA
AATGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA
GGGCTTTGGGTTTGGGATCCTCTTGACTACTGGGGCAGAGGAACCCTGG
TCACCGTCTCTTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGG
TGGCGGATCGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCA
TCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTT
ATCACTGGTTGGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACT
CCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTC
AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
AGCCTGATGATTTTGCAACTTATTACTGCCAACAATATAGTAATTATCC
GCTCACTTTCGGCGGAGGGACCAAGCTGGAGATCAAACGTGCGGCCGCA

FIG. 9

GIL16

SEQ ID NO:25

Q	V	Q	L	V	E	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F
T	S	Y	G	I	S	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	W	I	S	A	Y	T	G	N	T
N	Y	A	Q	K	F	Q	G	R	V	T	M	T	T	D	T	S	T	S	T	A	Y	M	E	L	R	S	L	R
S	D	D	T	A	V	Y	Y	C	A	R	D	R	G	Y	Y	D	A	F	D	I	W	G	Q	G	T	L	V	T
V	S	S	G	G	G	G	S	G	G	G	G	S	G	G	G	G	S	D	I	Q	M	T	Q	S	P	S	T	L
S	A	S	I	G	D	R	V	T	I	T	C	R	A	S	E	G	I	Y	H	W	L	A	W	Y	Q	Q	K	P
G	K	A	P	K	L	L	I	Y	K	A	S	S	L	A	S	G	A	P	S	R	F	S	G	S	G	S	G	T
D	F	T	L	T	I	S	S	L	Q	P	D	D	F	A	T	Y	Y	C	Q	Q	Y	S	N	Y	P	L	T	F
G	G	G	T	K	L	E	I	K	R	A	A	A																

SEQ ID NO:34

CAGGTGCAGCTGGTGGAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
ATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAG
AGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTTGATATCTGGGGCCAAGGCACCCTGGTCACCGT
CTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCG
GAGGGACCAAGCTGGAGATCAAACGTGCGGCCGCA

FIG. 9(cont.)

GIL45

SEQ ID NO:43

Q M Q L V Q S G G G V V Q P G R S L R L S C A A S G F T F S
N Y G M Y W V R Q A P G K G L E W V A H I W Y D G S N E K Y
A D S V K G R M T V S R D N S R N T L Y L Q M N S L R A E D
T A V Y Y C A T E Q H W I T A F D I W G K G T L V T V S S G
G G G S G A G G S G G G G S Q S V L T Q P A S V S G S P G Q
S I T I S C T G T S S D V G G Y N Y V S W Y Q Q H P G K A P
K L M I Y E G S K R P S G V S N R F S G S K S G N T A S L T
I S G L Q A E D E A D Y Y C S S Y T T R S T R V F G G G T K
L T V L G A A A H

SEQ ID NO:52

CAGATGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTATGG
CATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA
CATATTTGGTATGATGGAAGTAATGAAAAGTATGCAGACTCCGTGAAGG
GCCGAATGACCGTCTCCAGAGACAATTCCAGGAACACGTTGTATTTGCA
AATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGACA
GAGCAACACTGGATTACTGCTTTTGATATCTGGGGCAAAGGCACCCTGG
TCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGCAGGTGGCAGCGGCGG
TGGCGGATCGCAGTCTGTGCTGACTCAGCCTGCCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTG
GTGGTTATAACTATGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCC
CAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAAT
CGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTG
GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAC
CAGGAGCACTCGAGTTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
GCGGCCGCA

FIG. 9(cont.)

GIL60

SEQ ID NO:61

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D
D Y G M N W V R Q A P G K G L E W V S G V N G N G G T R D Y
A A S V K G R F T I S R D N A K N S L Y L Q M N S L R A E D
T A L Y Y C A R G W Y S G S F Y Y F G Y W G R G T L V T V S
S G G G G S G G G G S G G G G S A Q A V L T Q P S S V S G S
P G Q S I T I S C T G A S G D V G A Y N F V S W Y Q Q H P G
K T P K L I I Y D V N K R P S G V S N R F S G S K S G N T A
S L T I S G L Q A E D E S D Y Y C S S Y T S T F S V V F G G
G T K V T V L G A A

SEQ ID NO:70

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGG
CATGAACTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCT
GGTGTTAATGGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGG
GCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCA
AATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGA
GGATGGTATAGTGGGAGCTTCTACTACTTTGGCTACTGGGGCCGAGGAA
CCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTC
TGGCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCCGTG
TCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCG
GTGACGTTGGTGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGG
CAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGG
GTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CCATCTCTGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCAGCTC
ATATACAAGCACCTTCTCTGTGGTATTTGGCGGAGGGACCAAGGTCACC
GTCCTAGGTGCGGCC

FIG. 9(cont.)

GIL68

SEQ ID NO:79

E	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	Q	A	S	G	Y	T	F	S	D
Y	Y	I	H	W	V	R	Q	T	P	G	Q	G	F	E	W	M	G	W	V	N	P	D	T	G	G	T	R	Y	A	Q
K	F	Q	G	W	V	T	M	T	R	D	M	S	N	T	T	A	Y	M	E	L	P	R	L	R	D	D	D	T	A	V
Y	Y	C	A	R	D	L	T	G	F	D	P	F	D	I	W	G	Q	G	T	L	V	T	V	S	S	G	G	G	G	S
G	G	G	G	S	G	G	G	G	S	A	Q	S	V	L	T	Q	P	P	S	V	S	V	A	P	G	K	T	A	T	I
T	C	G	G	N	N	F	R	N	K	R	V	H	W	Y	Q	Q	R	P	G	Q	A	P	V	L	V	I	Y	Y	D	S
D	R	P	S	G	I	P	E	R	F	S	G	S	R	S	G	N	T	A	T	L	T	I	S	R	V	E	A	G	D	E
A	D	F	Y	C	Q	V	W	D	S	S	T	D	R	P	L	F	G	G	G	T	K	L	T	V	L	G	A	A	A	

SEQ ID NO:88

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTG
GGTCACCATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTTTTACTGTCAGGTGTGGGATAGTAGTACTGATCGTCCGCTGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCCGCA

FIG. 9(cont.)

GIL92

SEQ ID NO:97

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Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y
M H W V R Q A P G Q G L E W V G W I N P Y T G G A F Y A Q K F R G
R V T M T R D T S I N T A Y M E L S R L G S D D T A V Y Y C A R E
P E K F D F W G G D N W G R G T M V T V S S G G G G S G G G G S G
G G G S A Q A V L T Q P S S V S G A P G Q R V T I S C T G S S S N
I G A G Y G V H W Y Q Q L P G T A P K L L I Y G N S N R P S G V P
D R F S G S K S G T S A S L A I T G L Q A E D E A D Y Y C Q S Y D
S S L S G Y V F G T G T Q L T V L S A A A
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SEQ ID NO:106

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CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGTCACCATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGATTTTTGGGGGGGTGACAACTGGGGCCGGGGGACAATGGT
CACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTG
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC
TGAGTGGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTTTTAAGTGCG
GCCGCA
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FIG. 9(cont.)

097D09

SEQ ID NO:115

EVQLVESGGGLVTPGGSLRLSCAASGFTFSDYYMSWVRQAPGRGLEWVSAIS
GSGGSTYYADSVKGRITISRDNAKNSLYLQMSSLRSEDTAVYYCARGLWVWD
PLDYWGRGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTIT
CRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSRFSGSGFGTDFTLT
ISSLQPDDFATYYCQQYSEFAWTFGGGTKLEIKRAAAH

SEQ ID NO:124

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCACGCCTGGAGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTA
CATGAGCTGGGTCCGCCAGGCTCCAGGGAGGGGGCTGGAGTGGGTCTCA
GCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGG
GCCGGATCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCA
AATGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA
GGGCTTTGGGTTTGGGATCCTCTTGACTACTGGGGCAGAGGAACCCTGG
TCACCGTCTCTTCAGGTGGGGGCGGTTCAGGCGGAGGTGGCAGCGGCGG
TGGCGGATCGGACATCCAGATGACCCAGTCCCCTTCCACCCTGTCTGCA
TCTATTGGAGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTT
ATCACTGGTTGGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACT
CCTGATCTATAAGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTC
AGCGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
AGCCTGATGATTTTGCAACTTATTACTGCCAACAATACAGCGAGTTCGC
CTGGACCTTCGGCGGAGGGACCAAGCTGGAGATCAAACGTGCGGCCGCA
CAT

FIG. 9(cont.)

062A09

SEQ ID NO:133

QVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWV
SAYTGNTNYAQKFQGRVTMTTDTSTSTAYMELRGLRSDDTAVYYCARDRGY
YDAYDIWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRV
TITCRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSRFSGSGFGTD
FTLTISSLQPDDFATYYCQQMGEYNATIGGGTKLEIKRAAAH

SEQ ID NO:142

CAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
GTCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAG
AGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGGGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTATGATATCTGGGGCCAAGGCACCCTGGTCACCGT
CTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGA
TTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAAATGGGCGAGTACAACGCCACCATCGGCG
GAGGGACCAAGCTGGAGATCAAACGTGCGGCCGCACAT

FIG. 9(cont.)

062G05

SEQ ID NO:151

QVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI
SAYTGNTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDRGY
YDAFDIWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRV
TITCRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSRFSGSGFGTD
FTLTISSLQPDDFATYYCQQMGEWKAAFGGGTKLEIKRAAAH

SEQ ID NO:160

CAGGTGCAGCTGGTGGAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
ATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAG
AGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTCGATATCTGGGGCCAAGGCACCCTGGTCACCGT
CTCCTCAGGTGGGGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGCCCCATCAAGGTTCAGCGGCAGTGGA
TTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAAATGGGGGAGTGGAAGGCGGCCTTCGGCG
GAGGGACCAAGCTGGAGATCAAACGTGCGGCCGCACAT

FIG. 9(cont.)

087B03

SEQ ID NO:169

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLEWVSGV
NWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARGWYS
GAAWNMGYWGRGTLVTVSSGGGGSGGGGSGGGGSAQAVLTQPSSVSGSPGQ
SITISCTGASGDVGAYNFVSWYQQHPGKTPKLIIYDVNKRPSGVSNRFSGS
KSSNTASLTISGLQAEDESDYYCSSYTSTFSVVFGGGTKVTVLGAAAH

SEQ ID NO:178

CGAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTG
AGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCATGAACTGGG
TCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTGTTAATTGGAATGG
TGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAC
AACGCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGG
CCTTGTATTACTGTGCGAGAGGATGGTATAGTGGGGCCGCGTGGAACATGGGCTA
CTGGGGCCGAGGAACCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGA
GGTGGCTCTGGCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCCG
TGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGA
CGTTGGTGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAACCCCC
AAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCT
CTGGCTCCAAGTCTAGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCCGA
GGACGAGTCTGATTATTACTGCAGCTCATATACAAGCACCTTCTCTGTGGTATTT
GGCGGAGGGACCAAGGTCACCGTCCTAGGTGCGGCCGCACAT

FIG. 9(cont.)

367D04

SEQ ID NO:187

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLEWVSG
VNWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARGW
YSGSPWSLGHWGRGTLVTVSSGGGGSGGGGSGGSGGGSGGSGGGSSGGGS
GGGGSAQAVLTQPSSVSGSPGQSVTISCTGASGDVGAYNFVSWYQQHPGK
TPKLIIYDVNKRPSGVSNRFSGSKSGNTASLTISRLQAEDESDYYCSSYT
SRYTTEFGGGTKVTVLGAAAH

SEQ ID NO:196

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGG
CATGAACTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCT
GGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGG
GCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCA
AATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGA
GGATGGTATAGTGGGAGCCCGTGGTCGCTGGGCCACTGGGGCCGAGGAA
CCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTC
TGGCGGTAGCGGAGGTGGCTCTGGCGGTAGCGGAGGTGGCTCTAGCGGA
GGTGGCTCTGGCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCCGT
CCTCCGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGG
AGCCAGCGGTGACGTTGGTGCTTATAACTTTGTCTCCTGGTACCAACAA
CACCCAGGCAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGC
CCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGC
CTCCCTGACCATCTCTAGGCTCCAGGCCGAGGACGAGTCTGATTATTAC
TGCAGCTCATATACATCGAGGTACACGACCGAGTTTGGCGGAGGGACCA
AGGTCACCGTCCTAGGTGCGGCCGCACAT

FIG. 9(cont.)

368D04

SEQ ID NO:205

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLEWVSG
VNWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARGW
YSGAAWNMGYWGRGTLVTVSSGGGGSGGGGSGGSGGGSGGGGGGSGGGGS
AQAVLTQPSSVSGSPGQSITISCTGASGDVGAYNFVSWYQQHPGKTPKLI
IYDVNKRPSGVSNRFSGSKSGNTASLTISGLQAEDESDYYCASLVSDFSV
VFGGGTKVTVLGAAAH

SEQ ID NO:214

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGG
CATGAACTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCT
GGTGTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGG
GCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCA
AATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGA
GGATGGTATAGTGGGGCCGCGTGGAACATGGGCTACTGGGGCCGAGGAA
CCCTGGTCACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTC
TGGTGGTAGCGGAGGTGGCTCTGGCGGTGGCGGAGGTGGCTCTGGCGGT
GGCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCCGTGTCTGGGT
CCCCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGT
TGGTGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAACC
CCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTA
ATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTC
TGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCGCCTCCCTCGTC
TCCGACTTCTCTGTGGTATTTGGCGGAGGGACCAAGGTCACCGTCCTAG
GTGCGGCCGCACAT

FIG. 9(cont.)

166B06

SEQ ID NO:223

EVQLVQSGAEVKKPGASVKVSCQASGYTFSDYYIHWVRQTPGQGFEWMGWV
NPDTGGTRYAQKFQGWVTMTRDMSNTTAYMELPRLRDDDTAVYYCARDLTG
FDPFDIWGQGTLVTVSSGGGSSGGGGSGGGGSAQSVLTQPPSVSVAPGKTA
TITCGGNNFRNKRVHWYQQRPGQAPVLVIYYDSDRPSGIPERFSGSRSGNT
ATLTISRVEAGDEADFYCQVWDLFNDNGVFGGGTKLTVLGAAAH

SEQ ID NO:232

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTG
GGTCACAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGTGGAGGCGGCAGTTCAGGTGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTTTTACTGTCAGGTGTGGGATCTCTTCAACGACAACGGCGTGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCCGCACAT

FIG. 9(cont.)

166G05

SEQ ID NO:241

EVQLVQSGAEVKKPGASVKVSCQASGYTFSDYYIHWVRQTPGQGFEWMGWV
NPDTGGTRYAQKFQGWVTMTRDMSNTTAYMELPRLRDDDTAVYYCARDLTG
FDPFDIWGQGTLVTVSSGGGGSGGGGSGGGGSAQSVLTQPPSVSVAPGKTA
TITCGGNNFRNKRVHWYQQRPGQAPVLVIYYDSDRPSGIPERFSGSRSGNT
ATLTISRVEAGDEADFYCQVWDFLTDSGSFGGGTKLTVLGAAAH

SEQ ID NO:250

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTG
GGTCACAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCACAATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGGCGCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTTTTACTGTCAGGTGTGGGATTTCCTCACCGACTCGGGGTCGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCCGCACAT

FIG. 9(cont.)

375G06

SEQ ID NO:259

EVQLVQSGAEVKKPGASVKVSCQASGYTFSDYYIHWVRQTPGQGFEWMGW
VNPDTGGTRYAQKFQGWVTMTRDMSNTTAYMELPRLRDDDTAVYYCARDL
TGYDYYDRWGQGTLVTVSSGGGGSGGGGSGGGGGGSGGGGGGSGGGGSAQ
SVLTQPPSMSVAPGKTATITCGGNNFRNKRVHWYQQRPGQAPVLVIYYDS
DRPSGIPERFSGSRSGNTATLTISRVEAGDEADFYCQVWDFLADEAMFGG
GTKLTVLGAAAH

SEQ ID NO:268

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGACCCCTGGACAAGGGTTTGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCTG
GGTCACAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATACGACTACTACGACCGGTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGTGGAG
GTGGCTCTGGCGGTGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACAG
TCTGTGCTGACTCAGCCGCCCTCAATGTCAGTGGCCCCAGGAAAGACGGC
CACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGTACACTGGT
ATCAGCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATTATGATTCA
GACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAA
CACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGAGGCCGACT
TTTACTGTCAGGTGTGGGATTTCCTCGCCGACGAGGCGATGTTCGGCGGA
GGGACCAAGCTGACCGTCCTAGGTGCGGCCGCACAT

FIG. 9(cont.)

376B10

SEQ ID NO:277

EVQLVQSGAEVKKPGASVKVSCQASGYTFSDYYIHWVRQTPGQGFEWMGW
VNPDTGGTRYAQKFQGWVTMTRDMSNTTAYMELPGLRDDDTAVYYCARDL
TGYDQYTAWGQGTLVTVSSGGGGSGGGGSGGGGSAQSVLTQPPSVSVAPG
KTATITCGGNNFRNKRVHWYQQRPGQAPVLVIYYDSDRPSGIPERFSGSR
SGNTATLTISRVEAGDEADFYCSTFDPFTDRPLFGGGTKLTVLGAAAH

SEQ ID NO:286

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGACCCCAGGACAAGGGTTTGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACGAGATACGCGCAGAAGTTTCAGGGCTG
GGTCACAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCGGGCTGAGAGACGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGGTACGACCAGTACACGGCCTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCACGATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGGCCCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTTTTACTGTAGCACCTTCGACCCCTTCACTGATCGTCCGCTGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCGGCCGCACAT

FIG. 9(cont.)

354A08

SEQ ID NO:295

QVQLVQSGAEKKPGASVKVSCKASGYTFTDYYMHWVRQAPGQGLEWVGWIN
PYTGGAFYAQKFRGRVTMTRDTSINTAYMELSRLGSDDTAVYYCAREPERF
GDSTGQVWGRGTMVTVSSGGGGSGGGGSGGSRSAQAVLTQPSSVSGAPRQR
VTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSK
SGTSASLAITGLQAEDEADYYCYHWDKEQSGYVFGTGTQLTVLSA

SEQ ID NO:304

CAGGTCCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTAA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAGATTCGGCGACTCCACGGGGCAGGTCTGGGGCCGGGGGACAATGGT
CACCGTCTCGAGTGGGGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCAGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCC
CCAAGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCTACCACTGGGACAAGGAGC
AGAGTGGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTTTTAAGTGCG

FIG. 9(cont.)

355B06

SEQ ID NO:313

EVQLVQSGAEVKKPGASVKVSCQASGYTFTDYYMHWVRQAPGQGLEWVGWI
NPYTGSAFYAQKFRGRATMTRNTSINTAYMELSRLGSDDTAVYYCAREPEK
FGESSGQLWGRGTMVTISSGGGGSGGGGSGGSGSAQAVLTQPSSVSGAPGQ
RVTISCTGSSSNIGPGYGVHWYQQLPGTAPKLLIYGDSNRPSGVPDRFSGS
KSGTSASLAITGLQAEDEADYYCQSYDSGLSGYVFGTGTQLTVLSA

SEQ ID NO:322

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTCAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGGTGG
ATCAACCCTTATACTGGTAGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGCCACAATGACCAGGAACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGGCGAGTCCAGCGGCCAGTTGTGGGGCCGGGGGACAATGGT
CACCATCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCCGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCGGCC
TGAGTGGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTTTTAAGTGCG

FIG. 9(cont.)

355E04

SEQ ID NO:331

QVQLVQSGAEVKKPGASVKVSCKASGYTFTHYYMHWVRQAPGQGLEWVGWI
NPYTGGAFYAQKFQGRVTMTRDTSINTAYMELSRLGSDDTAVYYCAREPEK
FDSPNAEIWGRGTMVTISSEGGGSGGGGSGGSGSAQAVLTQPSSVSGAPGQ
RVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGS
KSGTSASLAITGLQAEDEADYYCQSYDSSLSGYVFGTGTQLTVLSA

SEQ ID NO:340

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAAAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCCACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCAGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGACTCGCCGAACGCCGAGATCTGGGGCCGGGGGACAATGGT
CACCATCTCGAGTGAAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC
TGAGTGGTTATGTCTTCGGAACCGGGACCCAGCTCACCGTTTTAAGTGCG

FIG. 9(cont.)

356A11

SEQ ID NO:349

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWVGWI
NPYTGSAFYAQKFRGRVTMTRDTSINTAYMELSRLGSDDTAVYYCAREPEK
FDSDDSDVWGRGTMVTVSGGGGSSGGGGSGGSGSAQAVLTPPSVSGAPGQR
VTISCTGSSSNIGAGYGVHWYQQLPGTAPKLIIYGDSSRPSGVPDRFSGSK
SGTSASLAITGLQAEDEADYYCQSYDNSLSGYVFGTGTQLTVLSA

SEQ ID NO:358

CAGGTTCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAGGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTAGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGTTACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGACTCCGACGACTCCGACGTCTGGGGCCGCGGGACAATGGT
CACCGTCTCGGGTGGAGGCGGCAGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCCCTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCATCATCTATGGTGACAGCAGTCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAACAGCC
TGAGCGGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTTTTAAGTGCG

FIG. 9(cont.)

GIL01

SEQ ID NO:367

QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSAIS
GSGGSTYYADSVKGRITISRDNAKNSLYLQMNSLRAEDTAVYYCARGLWVWD
PLDYWGRGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVTIT
CRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGVPSRFSGSGSGTDFTLT
ISSLQPDDFATYYCQQYSNYPLTFGGGTKVEIKRA

SEQ ID NO:376

CAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACA
TGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCG
GATCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGA
ACAGCCTGAGAGCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGCTT
TGGGTTTGGGATCCTCTTGACTACTGGGGCAGAGGAACCCTGGTCACCGT
CTCTTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAACGTGCG

FIG. 10

GIL16

SEQ ID NO:385

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI
SAYTGNTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDRGY
YDAFDIWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRV
TITCRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGVPSRFSGSGSGTE
FTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKVEIKRA

SEQ ID NO:394

CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
ATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAG
AGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTTGATATCTGGGGCCAAGGCACCCTGGTCACCGT
CTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAACGTGCG

FIG. 10(cont.)

GIL45

SEQ ID NO:403

QMQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMYWVRQAPGKGLEWVAHI
WYDGSNEKYADSVKGRMTVSRDNSKNTLYLQMNSLRAEDTAVYYCATEQHW
ITAFDIWGKGTLVTVSSGGGGSGAGGSGGGGSQSALTQPASVSGSPGQSIT
ISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKRPSGVSNRFSGSKSG
NTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVLGA

SEQ ID NO:412

CAGATGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTATGG
CATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA
CATATTTGGTATGATGGAAGTAATGAAAAGTATGCAGACTCCGTGAAGG
GCCGAATGACCGTCTCCAGAGACAATTCCAAGAACACGTTGTATTTGCA
AATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGACA
GAGCAACACTGGATTACTGCTTTTGATATCTGGGGCAAAGGCACCCTGG
TCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGCAGGTGGCAGCGGCGG
TGGCGGATCACAGTCTGCGCTGACTCAGCCTGCCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTG
GTGGTTATAACTATGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCC
CAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAAT
CGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTG
GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAC
CAGGAGCACTCGAGTTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
GCG

FIG. 10(cont.)

GIL60

SEQ ID NO:421

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLEWVSG
VNWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYHCARGW
YSGSFYYFGYWGRGTLVTVSSGGGGSGGGGSGGGGSAQAALTQPASVSGS
PGQSITISCTGASGDVGAYNFVSWYQQHPGKAPKLIIYDVNKRPSGVSNR
FSGSKSGNTASLTISGLQAEDEADYYCSSYTSTFSVVFGGGTKLTVLGA

SEQ ID NO:430

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCA
TGAACTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGT
GTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCG
ATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAATGA
ACAGTCTGAGAGCCGAGGACACGGCCTTGTATCACTGTGCGAGAGGATGG
TATAGTGGGAGCTTCTACTACTTTGGCTACTGGGGCCGAGGAACCCTGGT
CACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTG
GCGGAAGTGCACAGGCTGCGCTGACTCAGCCGGCCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGG
TGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCCA
AACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGC
TTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCT
CCAGGCCGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCACCT
TCTCTGTGGTATTTGGCGGAGGGACCAAGCTCACCGTCCTAGGTGCG

FIG. 10(cont.)

GIL68

SEQ ID NO: 439

QVQLVQSGAEVKKPGASVKVSCKASGYTFSDYYIHWVRQAPGQGLEWMGWV
NPDTGGTRYAQKFQGRVTMTRDMSISTAYMELSRLRSDDTAVYYCARDLTG
FDPFDIWGQGTLVTVSSGGGGSGGGGSGGGGSASSVLTQPPSVSVAPGKTA
RITCGGNNFRNKRVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSRSGNT
ATLTISRVEAGDEADYYCQVWDSSTDRPLFGGGTKLTVLGA

SEQ ID NO:448

CAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGGCCCCTGGACAAGGGTTGGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCCG
GGTCACAATGACCAGGGACATGTCCATCTCCACAGCCTACATGGAGCTGT
CCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCATCGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCCGCATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAAGCCAGGCCAGGCCCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTATTACTGTCAGGTGTGGGATAGTAGTACTGATCGTCCGCTGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTGCG

FIG. 10(cont.)

GIL92

SEQ ID NO:457

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYYMHWVRQAPGQGLEWVGWI
NPYTGGAFYAQKFRGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREPEK
FDFWGGDNWGRGTLVTVSSGGGGSGGGGSGGGGSAQAVLTQPPSVSGAPGQ
RVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGS
KSGTSASLAITGLQAEDEADYYCQSYDSSLSGYVFGGGTQLTVLSA

SEQ ID NO:466

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGATTTTTGGGGGGGTGACAACTGGGGCCGGGGGACATTGGT
CACCGTCTCGAGTGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTG
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC
TGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTTTTAAGTGCG

FIG. 10(cont.)

062A09

SEQ ID NO:475

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T
F T S Y G I S W V R Q A P G Q G L E W M G W V S A Y T G
N T N Y A Q K F Q G R V T M T T D T S T S T A Y M E L R
S L R S D D T A V Y Y C A R D R G Y Y D A F D I W G Q G
T L V T V S S G G G G S G G G G S G G G G S D I Q M T Q
S P S T L S A S V G D R V T I T C R A S E G I Y H W L A
W Y Q Q K P G K A P K L L I Y K A S S L A S G V P S R F
S G S G S G T E F T L T I S S L Q P D D F A T Y Y C Q Q
M G E Y N A T F G G G T K V E I K R

SEQ ID NO:484

CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
GTCAGCGCTTACACTGGTAACACAAACTATGCACAGAAGTTCCAGGGCAG
AGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTTGATATCTGGGGCCAAGGCACCCTGGTCACCGT
CTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAAATGGGCGAGTACAACGCCACCTTCGGCG
GAGGGACCAAGGTGGAGATCAAACGT

FIG. 10(cont.)

087B03

SEQ ID NO:493

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D
D Y G M N W V R Q A P G K G L E W V S G V N W N G G T R D Y
A A S V K G R F T I S R D N A K N S L Y L Q M N S L R A E D
T A L Y H C A R G W Y S G A A W N M G Y W G R G T L V T V S
S G G G G S G G G G S G G G G S A Q A A L T Q P A S V S G S
P G Q S I T I S C T G A S G D V G A Y N F V S W Y Q Q H P G
K A P K L I I Y D V N K R P S G V S N R F S G S K S G N T A
S L T I S G L Q A E D E A D Y Y C S S Y T S T F S V V F G G
G T K L T V L G

SEQ ID NO:502

GAGGTGCAGCTGGTGGAGAGCGGGGGAGGTGTGGTACGGCCTGGGGGGTC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGATTATGGCA
TGAACTGGGTCCGCCAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGT
GTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCG
ATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAATGA
ACAGTCTGAGAGCCGAGGACACGGCCTTGTATCACTGTGCGAGAGGATGG
TATAGTGGGGCCGCGTGGAACATGGGCTACTGGGGCCGAGGAACCCTGGT
CACCGTCTCCTCAGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTG
GCGGAAGTGCACAGGCTGCGCTGACTCAGCCGGCCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGGTGACGTTGG
TGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCCA
AACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGC
TTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCT
CCAGGCCGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCACCT
TCTCTGTGGTATTTGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 10(cont.)

166B06

SEQ ID NO:511

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T
F S D Y Y I H W V R Q A P G Q G L E W M G W V N P D T G
G T R Y A Q K F Q G R V T M T R D M S I S T A Y M E L S
R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q G
T L V T V S S G G G S S G G G G S G G G G S A S S V L T
Q P P S V S V A P G K T A R I T C G G N N F R N K R V H
W Y Q Q K P G Q A P V L V I Y Y D S D R P S G I P E R F
S G S R S G N T A T L T I S R V E A G D E A D Y Y C Q V
W D L F N D N G V F G G G T K L T V L G

SEQ ID NO:520

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGGCCCCTGGACAAGGGTTGGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCCG
GGTCACAATGACCAGGGACATGTCCATCTCCACAGCCTACATGGAGCTGT
CCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGT
CTCCTCAGGAGGCGGCAGTTCAGGTGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCATCGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCCGCATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAAGCCAGGCCAGGCCCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTATTACTGTCAGGTGTGGGATCTCTTCAACGACAACGGCGTGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 10(cont.)

166G05

SEQ ID NO:529

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T
F S D Y Y I H W V R Q A P G Q G L E W M G W V N P D T G
G T R Y A Q K F Q G R V T M T R D M S I S T A Y M E L S
R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q G
T L V T V S S G G G G S G G G G S G G G G S A S S V L T
Q P P S V S V A P G K T A R I T C G G N N F R N K R V H
W Y Q Q K P G Q A P V L V I Y Y D S D R P S G I P E R F
S G S R S G N T A T L T I S R V E A G D E A D Y Y C Q V
W D F L T D S G S F G G G T K L T V L G

SEQ ID NO:538

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGGCCCCTGGACAAGGGTTGGAGTGGATGGGATGG
GTCAACCCTGACACTGGTGGCACAAGATACGCGCAGAAGTTTCAGGGCCG
GGTCACAATGACCAGGGACATGTCCATCTCCACAGCCTACATGGAGCTGT
CCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTTGATCCTTTTGATATCTGGGGCCAGGGAACCCTGGTCACCGT
CTCCTCAGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCATCGTCTGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCCGCATTACCTGTGGGGGAAACAACTTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAAGCCAGGCCAGGCCCCTGTCCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGGATGA
GGCCGACTATTACTGTCAGGTGTGGGATTTCCTCACCGACTCGGGGTCGT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

FIG. 10(cont.)

354A08

SEQ ID NO:547

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T
D Y Y M H W V R Q A P G Q G L E W V G W I N P Y T G G A F Y
A Q K F R G R V T M T R D T S I S T A Y M E L S R L R S D D
T A V Y Y C A R E P E R F G D S T G Q V W G R G T L V T V S
S G G G G S G G G G S G G S R S A Q A V L T Q P P S V S G A
P G Q R V T I S C T G S S S N I G A G Y G V H W Y Q Q L P G
T A P K L L I Y G N S N R P S G V P D R F S G S K S G T S A
S L A I T G L Q A E D E A D Y Y C Y H W D K E Q S G Y V F G
G G T Q L T V L G

SEQ ID NO:556

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAGATTCGGCGACTCCACGGGGCAGGTCTGGGGCCGGGGGACATTGGT
CACCGTCTCCTCAGGGGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCAGAAGTGCACAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCTACCACTGGGACAAGGAGC
AGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 10(cont.)

355B06

SEQ ID NO:565

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T
F T D Y Y M H W V R Q A P G Q G L E W V G W I N P Y T G
S A F Y A Q K F R G R V T M T R D T S I S T A Y M E L S
R L R S D D T A V Y Y C A R E P E K F G E S S G Q L W G
R G T L V T V S S G G G G S G G G G S G G S G S A Q A V
L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A
G Y G V H W Y Q Q L P G T A P K L L I Y G D S N R P S G
V P D R F S G S K S G T S A S L A I T G L Q A E D E A D
Y Y C Q S Y D S G L S G Y V F G G G T Q L T V L G

SEQ ID NO:574

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTAGCGCTTTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGGCGAGTCCAGCGGCCAGTTGTGGGGCCGGGGGACATTGGT
CACCGTCTCCTCAGGAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCGGCC
TGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 10(cont.)

355E04

SEQ ID NO:583

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T
F T H Y Y M H W V R Q A P G Q G L E W V G W I N P Y T G
G A F Y A Q K F Q G R V T M T R D T S I S T A Y M E L S
R L R S D D T A V Y Y C A R E P E K F D S P N A E I W G
R G T L V T V S S E G G G S G G G G S G G S G S A Q A V
L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A
G Y G V H W Y Q Q L P G T A P K L L I Y G N S N R P S G
V P D R F S G S K S G T S A S L A I T G L Q A E D E A D
Y Y C Q S Y D S S L S G Y V F G G G T Q L T V L G

SEQ ID NO:592

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCCACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTGGCGCATTCTATGCACAGAAGTTTCAGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGACTCGCCGAACGCCGAGATCTGGGGCCGGGGGACATTGGT
CACCGTCTCCTCAGAAGGCGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC
TGAGTGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 10(cont.)

356A11

SEQ ID NO:601

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T
F T N Y Y M H W V R Q A P G Q G L E W V G W I N P Y T G
S A F Y A Q K F R G R V T M T R D T S I S T A Y M E L S
R L R S D D T A V Y Y C A R E P E K F D S D D S D V W G
R G T L V T V S S G G G S S G G G G S G G S G S A Q A V
L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A
G Y G V H W Y Q Q L P G T A P K L L I Y G D S N R P S G
V P D R F S G S K S G T S A S L A I T G L Q A E D E A D
Y Y C Q S Y D N S L S G Y V F G G G T Q L T V L G

SEQ ID NO:610

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAACTACTATA
TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACTGGTAGCGCATTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGACTCCGACGACTCCGACGTCTGGGGCCGCGGGACATTGGT
CACCGTCTCCTCAGGAGGCGGCAGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAACAGCC
TGAGCGGTTATGTCTTCGGAGGTGGGACCCAGCTCACCGTCCTAGGT

FIG. 10(cont.)

368D04

SEQ ID NO:619

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLEWVSGV
NWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYHCARGWYS
GAAWNMGYWGRGTLVTVSSGGGGSGGGGSGGSGGGSGGGGGGSGGGGSAQA
ALTQPASVSGSPGQSITISCTGASGDVGAYNFVSWYQQHPGKAPKLIIYDV
NKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCASLVSDFSVVFGGG
TKLTVL

SEQ ID NO:628

GAGGTGCAGCTGGTGGAGAGCGGCGGAGGCGTGGTGAGACCAGGCGGCA
GCCTGAGACTGAGCTGCGCCGCCAGCGGCTTCACCTTCGACGACTACGG
CATGAACTGGGTGAGGCAGGCCCCAGGCAAGGGCCTGGAGTGGGTGTCC
GGCGTGAACTGGAACGGCGGCACCAGAGACTACGCCGCCTCTGTGAAGG
GCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCA
GATGAACAGCCTGAGAGCCGAGGACACCGCCCTGTACCACTGCGCCAGA
GGCTGGTACAGCGGAGCCGCCTGGAACATGGGCTACTGGGGCAGAGGCA
CCCTGGTGACCGTGTCCAGCGGAGGCGGCGGTTCAGGCGGAGGTGGCTC
TGGTGGTAGCGGAGGTGGCTCTGGCGGTGGCGGAGGTGGCTCTGGCGGT
GGCGGAAGTGCACAGGCCGCCCTGACCCAGCCCGCCAGCGTGTCTGGCA
GCCCAGGCCAGAGCATCACCATCAGCTGCACCGGCGCCAGCGGCGATGT
GGGCGCCTACAACTTCGTGTCCTGGTATCAGCAGCACCCCGGCAAGGCC
CCCAAGCTGATCATCTACGACGTGAACAAGAGACCCAGCGGCGTGTCCA
ACAGATTCAGCGGCAGCAAGAGCGGCAACACCGCCAGCCTGACCATCAG
CGGACTGCAGGCCGAGGACGAGGCCGACTACTACTGCGCCAGCCTGGTG
TCCGACTTCAGCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG

FIG. 10(cont.)