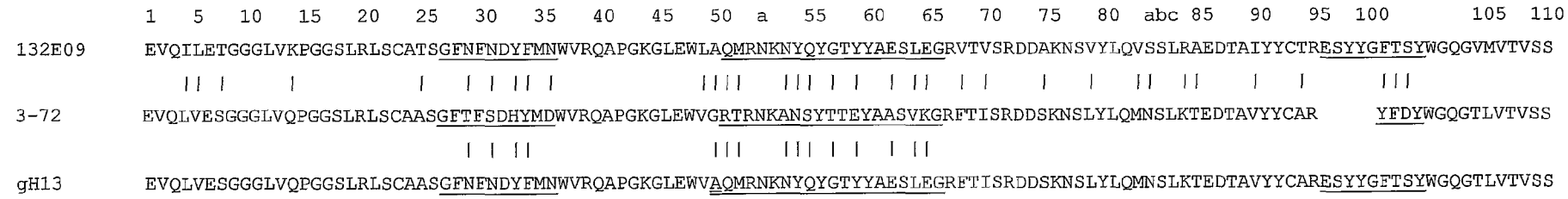
Figure 1

(a)


1 5 10 15 20 25 30 35 40 45 50 a 55 60 65 70 75 80 abc 85 90 95 100 105 110
132E09 EVQILETGGGLVKPGGSLRLSCATSGFNFNDYFMNWVRQAPGKGLEWLAQMRNKNYQYGTYYAESLEGRVTVSRDDAKNSVYLQVSSLRAEDTAIYYCTRESYYGFTSYWGQGVMVTVSS
3-72 EVQLVESGGGLVQPGGSLRLSCAASGFTFSDHYMDWVRQAPGKGLEWVGRTRNKANSYTTEYAASVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR YFDYWGQGTLVTVSS
gH13 EVQLVESGGGLVQPGGSLRLSCAASGFNFNDYFMNWVRQAPGKGLEWVAQMRNKNYQYGTYYAESLEGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARESYYGFTSYWGQGTLVTVSS

(b)

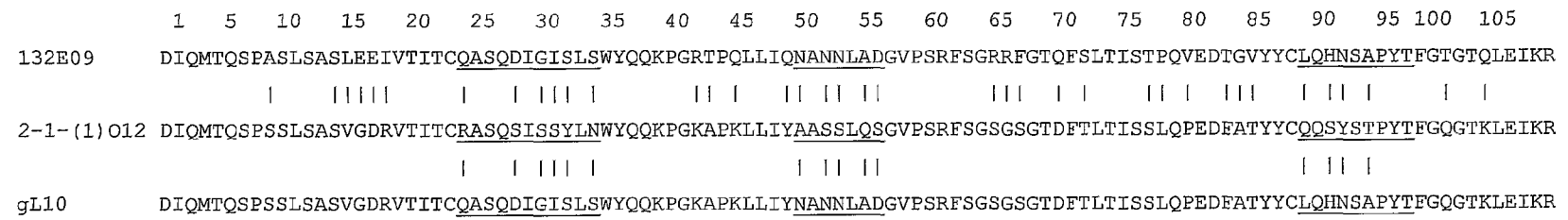

1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105
132E09 DIQMTQSPASLSASLEEIVTITCQASQDIGISLSWYQQKPGRTPQLLIQNANNLADGVPSRFSGRRFGTQFSLTISTPQVEDTGVYYCLQHNSAPYTFGTGTQLEIKR
2-1-(1)012 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYTFGQGTKLEIKR
gL10 DIQMTQSPSSLSASVGDRVTITCQASQDIGISLSWYQQKPGKAPKLLIYNANNLADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSAPYTFGQGTKLEIKR

Figure 2

(a) Translated sequence of 240.g1 heavy chain, showing intron/exon boundaries

```
          10          20          30          40          50
ATG GAG TGG AGC TGG GTG TTT TTG TTC TTC CTG TCC GTG ACC ACA GGC GTG CAC TCT
TAC CTC ACC TCG ACC CAC AAA AAC AAG AAG GAC AGG CAC TGG TGT CCG CAC GTG AGA
 M   E   W   S   W   V   F   L   F   F   L   S   V   T   T   G   V   H   S>

 60          70          80          90          100         110
GAA GTC CAG CTC GTT GAG AGT GGC GGT GGC CTG GTC CAG CCC GGT GGA TCA CTC CGA
CTT CAG GTC GAG CAA CTC TCA CCG CCA CCG GAC CAG GTC GGG CCA CCT AGT GAG GCT
 E   V   Q   L   V   E   S   G   G   G   L   V   Q   P   G   G   S   L   R>

    120         130         140         150         160         170
CTG TCC TGC GCT GCA AGC GGG TTT AAT TTT AAT GAT TAC TTC ATG AAC TGG GTT CGG
GAC AGG ACG CGA CGT TCG CCC AAA TTA AAA TTA CTA ATG AAG TAC TTG ACC CAA GCC
 L   S   C   A   A   S   G   F   N   F   N   D   Y   F   M   N   W   V   R>

        180         190         200         210         220
CAG GCA CCT GGC AAA GGC CTG GAA TGG GTG GCT CAG ATG AGG AAC AAG AAT TAT CAG
GTC CGT GGA CCG TTT CCG GAC CTT ACC CAC CGA GTC TAC TCC TTG TTC TTA ATA GTC
 Q   A   P   G   K   G   L   E   W   V   A   Q   M   R   N   K   N   Y   Q>

230         240         250         260         270         280
TAC GGG ACA TAC TAT GCC GAG AGT CTG GAG GGA AGG TTC ACC ATC TCC AGG GAC GAT
ATG CCC TGT ATG ATA CGG CTC TCA GAC CTC CCT TCC AAG TGG TAG AGG TCC CTG CTA
 Y   G   T   Y   Y   A   E   S   L   E   G   R   F   T   I   S   R   D   D>

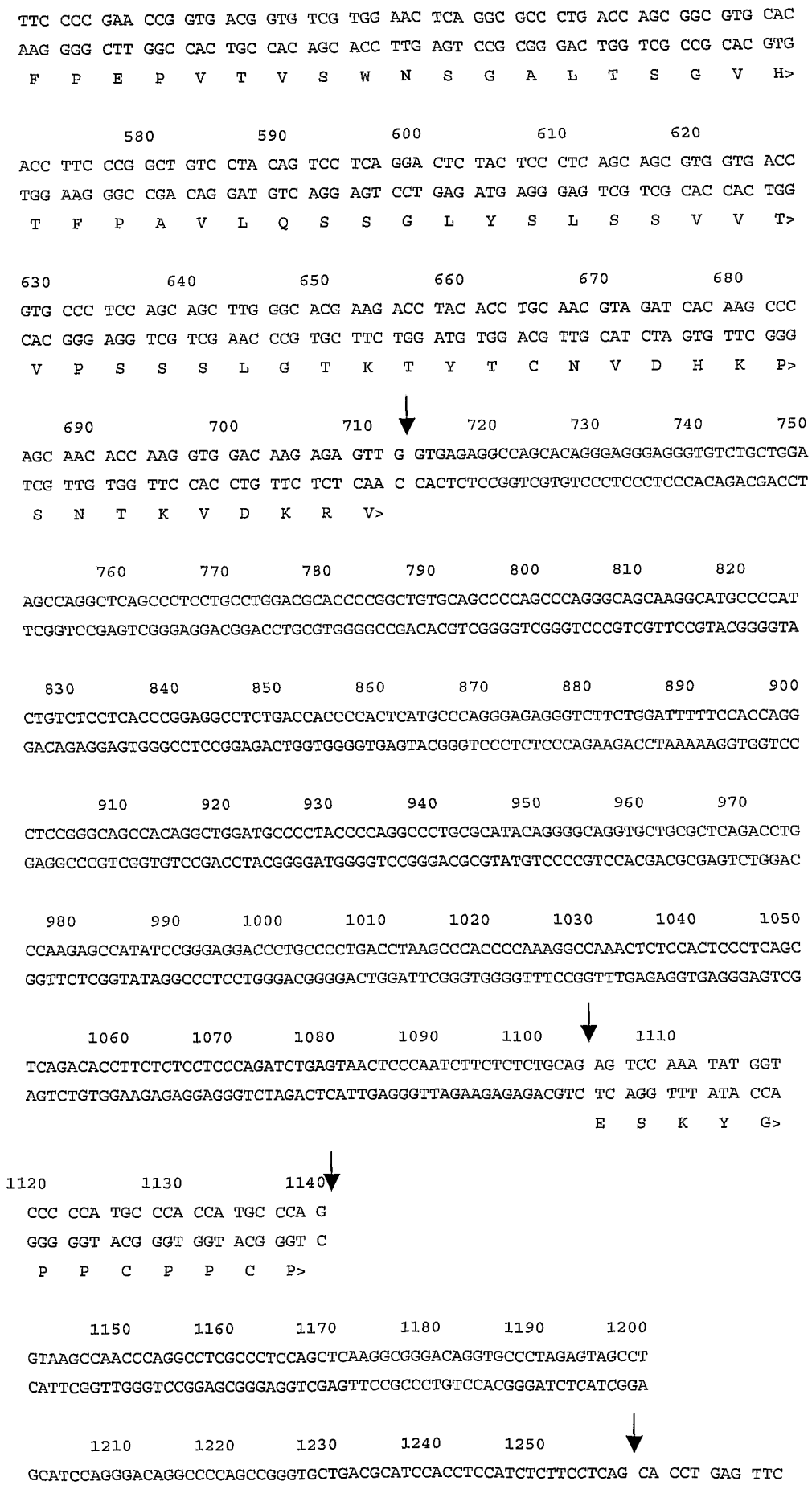
   290         300         310         320         330         340
TCT AAG AAC AGC CTC TAC CTT CAG ATG AAC TCT TTG AAA ACC GAG GAC ACA GCC GTG
AGA TTC TTG TCG GAG ATG GAA GTC TAC TTG AGA AAC TTT TGG CTC CTG TGT CGG CAC
 S   K   N   S   L   Y   L   Q   M   N   S   L   K   T   E   D   T   A   V>

        350         360         370         380         390
TAC TAT TGT GCT AGA GAA AGT TAT TAC GGG TTC ACA TCT TAT TGG GGA CAG GGA ACC
ATG ATA ACA CGA TCT CTT TCA ATA ATG CCC AAG TGT AGA ATA ACC CCT GTC CCT TGG
 Y   Y   C   A   R   E   S   Y   Y   G   F   T   S   Y   W   G   Q   G   T>

400         410         420         430         440         450
CTG GTG ACT GTC TCG AGC GCT TCT ACA AAG GGC CCA TCC GTC TTC CCC CTG GCG CCC
GAC CAC TGA CAG AGC TCG CGA AGA TGT TTC CCG GGT AGG CAG AAG GGG GAC CGC GGG
 L   V   T   V   S   S   A   S   T   K   G   P   S   V   F   P   L   A   P>

  460         470         480         490         500         510
TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC TGC CTG GTC AAG GAC TAC
ACG AGG TCC TCG TGG AGG CTC TCG TGT CGG CGG GAC CCG ACG GAC CAG TTC CTG ATG
 C   S   R   S   T   S   E   S   T   A   A   L   G   C   L   V   K   D   Y>

       520         530         540         550         560         570
```


TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC
AAG GGG CTT GGC CAC TGC CAC AGC ACC TTG AGT CCG CGG GAC TGG TCG CCG CAC GTG
F P E P V T V S W N S G A L T S G V H>
580 590 600 610 620
ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC
TGG AAG GGC CGA CAG GAT GTC AGG AGT CCT GAG ATG AGG GAG TCG TCG CAC CAC TGG
T F P A V L Q S S G L Y S L S S V V T>
630 640 650 660 670 680
GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
CAC GGG AGG TCG TCG AAC CCG TGC TTC TGG ATG TGG ACG TTG CAT CTA GTG TTC GGG
V P S S S L G T K T Y T C N V D H K P>
690 700 710 720 730 740 750
AGC AAC ACC AAG GTG GAC AAG AGA GTT G GTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGA
TCG TTG TGG TTC CAC CTG TTC TCT CAA C CACTCTCCGGTCGTGTCCCTCCCTCCCACAGACGACCT
S N T K V D K R V>
760 770 780 790 800 810 820
AGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCATGCCCCAT
TCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGGGGTCGGGTCCCGTCGTTCCGTACGGGGTA
830 840 850 860 870 880 890 900
CTGTCTCCTCACCCGGAGGCCTCTGACCACCCCACTCATGCCCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGG
GACAGAGGAGTGGGCCTCCGGAGACTGGTGGGGTGAGTACGGGTCCCTCTCCCAGAAGACCTAAAAAGGTGGTCC
910 920 930 940 950 960 970
CTCCGGGCAGCCACAGGCTGGATGCCCCTACCCCAGGCCCTGCGCATACAGGGGCAGGTGCTGCGCTCAGACCTG
GAGGCCCGTCGGTGTCCGACCTACGGGGATGGGGTCCGGGACGCGTATGTCCCCGTCCACGACGCGAGTCTGGAC
980 990 1000 1010 1020 1030 1040 1050
CCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGC
GGTTCTCGGTATAGGCCCTCCTGGGACGGGGACTGGATTCGGGTGGGGTTTCCGGTTTGAGAGGTGAGGGAGTCG
1060 1070 1080 1090 1100 1110
TCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTGCAG AG TCC AAA TAT GGT
AGTCTGTGGAAGAGAGGAGGGTCTAGACTCATTGAGGGTTAGAAGAGAGACGTC TC AGG TTT ATA CCA
E S K Y G>
1120 1130 1140
CCC CCA TGC CCA CCA TGC CCA G
GGG GGT ACG GGT GGT ACG GGT C
P P C P P C P>
1150 1160 1170 1180 1190 1200
GTAAGCCAACCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCT
CATTCGGTTGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGATCTCATCGGA
1210 1220 1230 1240 1250
GCATCCAGGGACAGGCCCCAGCCGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAG CA CCT GAG TTC

```
CGTAGGTCCCTGTCCGGGGTCGGCCCACGACTGCGTAGGTGGAGGTAGAGAAGGAGTC GT GGA CTC AAG
                                                            A   P   E   F>

1270         1280         1290         1300         1310         1320
   CTG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC ATG ATC
   GAC CCC CCT GGT AGT CAG AAG GAC AAG GGG GGT TTT GGG TTC CTG TGA GAG TAC TAG
    L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T   L   M   I>

    1330         1340         1350         1360         1370         1380
   TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG
   AGG GCC TGG GGA CTC CAG TGC ACG CAC CAC CAC CTG CAC TCG GTC CTT CTG GGG CTC
    S   R   T   P   E   V   T   C   V   V   V   D   V   S   Q   E   D   P   E>

         1390         1400         1410         1420         1430         1440
   GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG
   CAG GTC AAG TTG ACC ATG CAC CTA CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC
    V   Q   F   N   W   Y   V   D   G   V   E   V   H   N   A   K   T   K   P>

             1450         1460         1470         1480         1490
   CGG GAG GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC
   GCC CTC CTC GTC AAG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG
    R   E   E   Q   F   N   S   T   Y   R   V   V   S   V   L   T   V   L   H>

  1500         1510         1520         1530         1540         1550
   CAG GAC TGG CTG AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG
   GTC CTG ACC GAC TTG CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CCG GAG GGC
    Q   D   W   L   N   G   K   E   Y   K   C   K   V   S   N   K   G   L   P>

       1560         1570         1580                    ↓
   TCC TCC ATC GAG AAA ACC ATC TCC AAA GCC AAA G
   AGG AGG TAG CTC TTT TGG TAG AGG TTT CGG TTT C
    S   S   I   E   K   T   I   S   K   A   K>

1590       1600       1610       1620       1630       1640       1650
   GTGGGACCCACGGGGTGCGAGGGCCACATGGACAGAGGTCAGCTCGGCCCACCCTCTGCCCT
   CACCCTGGGTGCCCCACGCTCCCGGTGTACCTGTCTCCAGTCGAGCCGGGTGGGAGACGGGA

                                                ↓
         1660       1670       1680            1690         1700         1710
   GGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAG GG CAG CCC CGA GAG CCA CAG GTG TAC ACC
   CCCTCACTGGCGACACGGTTGGAGACAGGGATGTC CC GTC GGG GCT CTC GGT GTC CAC ATG TGG
                                       G   Q   P   R   E   P   Q   V   Y   T>

      1720         1730         1740         1750         1760         1770
   CTG CCC CCA TCC CAG GAG GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC
   GAC GGG GGT AGG GTC CTC CTC TAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG
    L   P   P   S   Q   E   E   M   T   K   N   Q   V   S   L   T   C   L   V>

         1780         1790         1800         1810         1820
   AAA GGC TTC TAC CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG
   TTT CCG AAG ATG GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC
    K   G   F   Y   P   S   D   I   A   V   E   W   E   S   N   G   Q   P   E>
```

```
1830          1840          1850          1860          1870          1880
  AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC
  TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG
   N   N   Y   K   T   T   P   P   V   L   D   S   D   G   S   F   F   L   Y>

    1890          1900          1910          1920          1930          1940
  AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC
  TCG TCC GAT TGG CAC CTG TTC TCG TCC ACC GTC CTC CCC TTA CAG AAG AGT ACG AGG
   S   R   L   T   V   D   K   S   R   W   Q   E   G   N   V   F   S   C   S>

        1950          1960          1970          1980          1990
  GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT CTG
  CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGT GTC TTC TCG GAG AGG GAC AGA GAC
   V   M   H   E   A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   L>

2000
  GGT AAA TGA
  CCA TTT ACT
   G   K   *>
```

(b) Light chain

```
             10            20            30            40            50            60
  ATG AGC GTG CCT ACC CAG GTC CTC GGC CTG TTG CTG CTC TGG CTG ACC GAT GCC CGC TGC GAT
  TAC TCG CAC GGA TGG GTC CAG GAG CCG GAC AAC GAC GAG ACC GAC TGG CTA CGG GCG ACG CTA
   M   S   V   P   T   Q   V   L   G   L   L   L   L   W   L   T   D   A   R   C   D>

         70            80            90           100           110           120
  ATC CAG ATG ACT CAA TCA CCC AGT TCC CTG AGC GCC TCT GTC GGC GAC AGG GTG ACC ATC ACA
  TAG GTC TAC TGA GTT AGT GGG TCA AGG GAC TCG CGG AGA CAG CCG CTG TCC CAC TGG TAG TGT
   I   Q   M   T   Q   S   P   S   S   L   S   A   S   V   G   D   R   V   T   I   T>

    130           140           150           160           170           180
  TGC CAG GCC TCT CAA GAC ATT GGC ATC AGC CTG TCC TGG TAC CAG CAA AAA CCC GGC AAG GCC
  ACG GTC CGG AGA GTT CTG TAA CCG TAG TCG GAC AGG ACC ATG GTC GTT TTT GGG CCG TTC CGG
   C   Q   A   S   Q   D   I   G   I   S   L   S   W   Y   Q   Q   K   P   G   K   A>

190           200           210           220           230           240           250
  CCT AAG CTC CTG ATC TAC AAT GCT AAC AAC CTG GCC GAT GGC GTG CCT AGT AGG TTT AGC GGG
  GGA TTC GAG GAC TAG ATG TTA CGA TTG TTG GAC CGG CTA CCG CAC GGA TCA TCC AAA TCG CCC
   P   K   L   L   I   Y   N   A   N   N   L   A   D   G   V   P   S   R   F   S   G>

         260           270           280           290           300           310
  TCT GGT TCC GGA ACA GAT TTC ACA CTC ACC ATC AGC TCA CTG CAG CCC GAG GAC TTC GCC ACT
  AGA CCA AGG CCT TGT CTA AAG TGT GAG TGG TAG TCG AGT GAC GTC GGG CTC CTG AAG CGG TGA
   S   G   S   G   T   D   F   T   L   T   I   S   S   L   Q   P   E   D   F   A   T>

    320           330           340           350           360           370
  TAC TAT TGC CTG CAG CAC AAC AGC GCC CCC TAC ACC TTC GGA CAA GGC ACT AAA CTG GAG ATC
  ATG ATA ACG GAC GTC GTG TTG TCG CGG GGG ATG TGG AAG CCT GTT CCG TGA TTT GAC CTC TAG
```

```
  Y   Y   C   L   Q   H   N   S   A   P   Y   T   F   G   Q   G   T   K   L   E   I>


380         390         400         410         420         430         440
 AAG CGT ACG GTA GCG GCC CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT
 TTC GCA TGC CAT CGC CGG GGT AGA CAG AAG TAG AAG GGC GGT AGA CTA CTC GTC AAC TTT AGA
  K   R   T   V   A   A   P   S   V   F   I   F   P   P   S   D   E   Q   L   K   S>

        450         460         470         480         490         500
 GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG
 CCT TGA CGG AGA CAA CAC ACG GAC GAC TTA TTG AAG ATA GGG TCT CTC CGG TTT CAT GTC ACC
  G   T   A   S   V   V   C   L   L   N   N   F   Y   P   R   E   A   K   V   Q   W>

    510         520         530         540         550         560
 AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG
 TTC CAC CTA TTG CGG GAG GTT AGC CCA TTG AGG GTC CTC TCA CAG TGT CTC GTC CTG TCG TTC
  K   V   D   N   A   L   Q   S   G   N   S   Q   E   S   V   T   E   Q   D   S   K>

570         580         590         600         610         620         630
 GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA
 CTG TCG TGG ATG TCG GAG TCG TCG TGG GAC TGC GAC TCG TTT CGT CTG ATG CTC TTT GTG TTT
  D   S   T   Y   S   L   S   S   T   L   T   L   S   K   A   D   Y   E   K   H   K>

          640         650         660         670         680         690
 GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG
 CAG ATG CGG ACG CTT CAG TGG GTA GTC CCG GAC TCG AGC GGG CAG TGT TTC TCG AAG TTG TCC
  V   Y   A   C   E   V   T   H   Q   G   L   S   S   P   V   T   K   S   F   N   R>

      700
 GGA GAG TGT TAG
 CCT CTC ACA ATC
  G   E   C   *>
```

Figure 3a

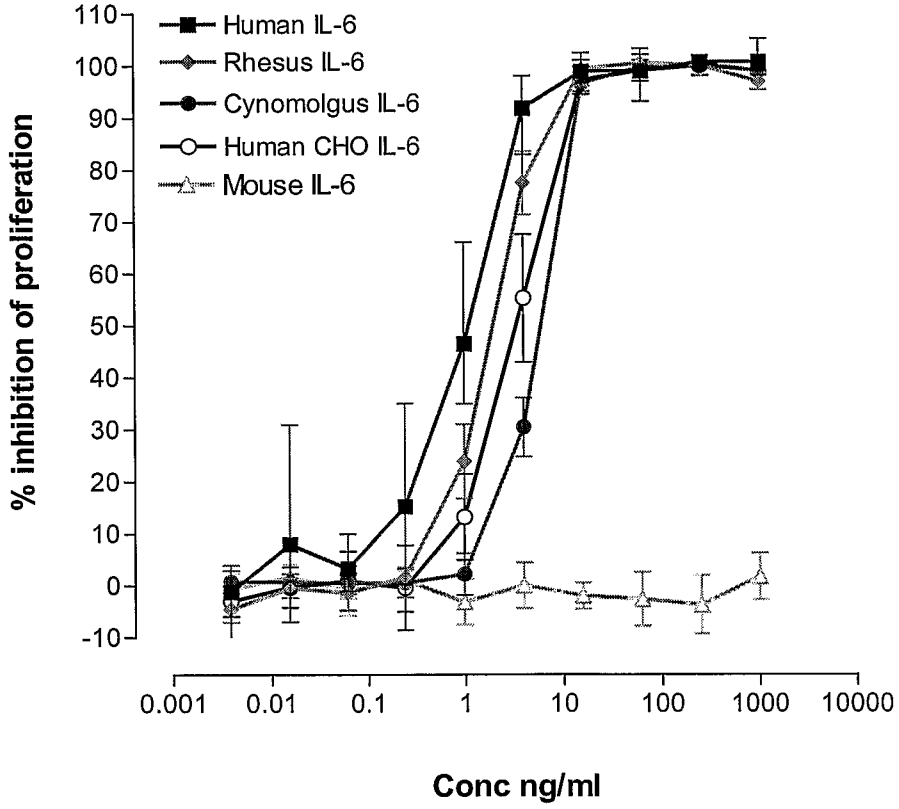

Human IL-6
Rhesus IL-6
Cynomolgus IL-6
Human CHO IL-6
Mouse IL-6
% inhibition of proliferation
110
100
90
80
70
60
50
40
30
20
10
0
-10
0.001
0.01
0.1
1
10
100
1000
10000
Conc ng/ml

Figure 3b

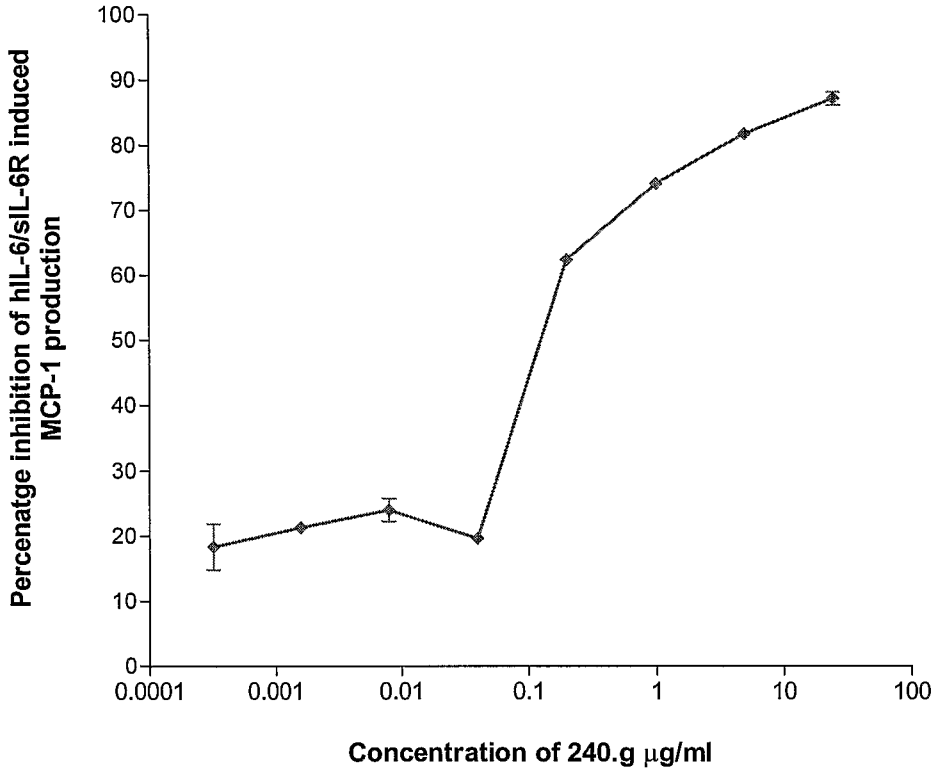

Percenatge inhibition of hIL-6/sIL-6R induced MCP-1 production
100
90
80
70
60
50
40
30
20
10
0
0.0001
0.001
0.01
0.1
1
10
100
Concentration of 240.g μg/ml

Figure 3c

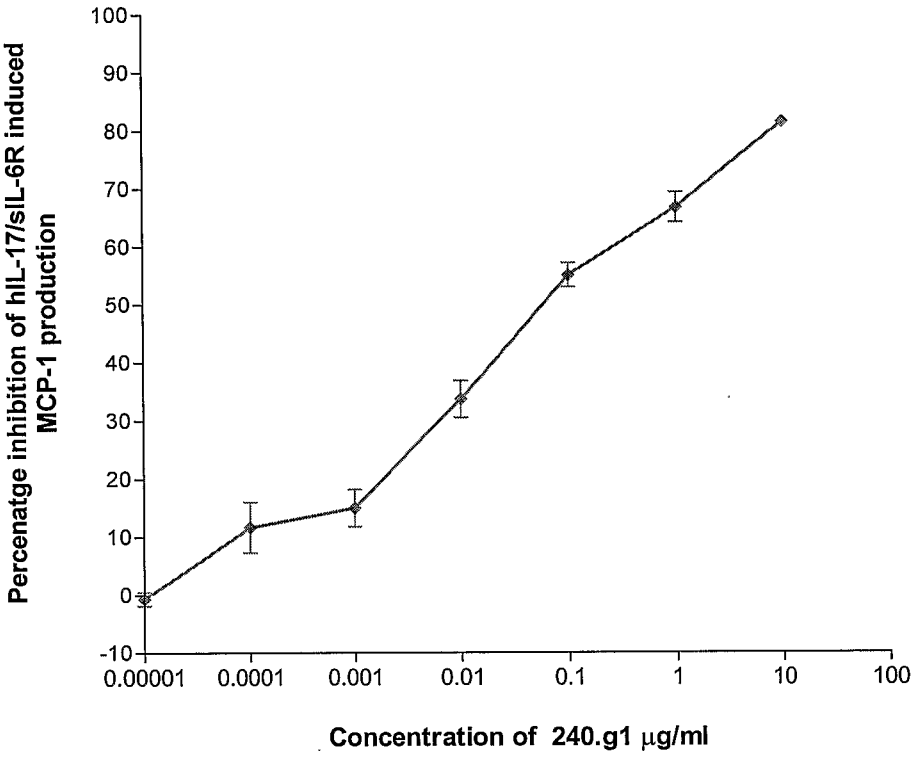
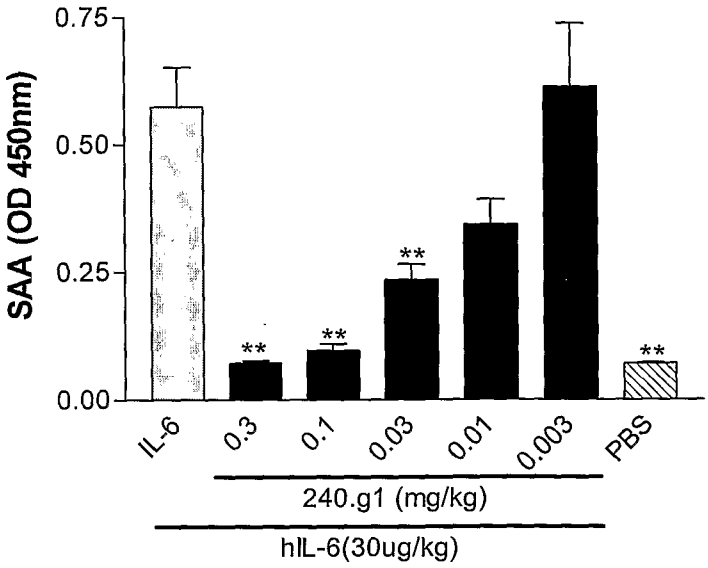

Percenatge inhibition of hIL-17/sIL-6R induced MCP-1 production
100
90
80
70
60
50
40
30
20
10
0
-10
0.00001
0.0001
0.001
0.01
0.1
1
10
100
Concentration of 240.g1 µg/ml

Figure 4


SAA (OD 450nm)
0.75
0.50
0.25
0.00
**
**
**
**
IL-6
0.3
0.1
0.03
0.01
0.003
PBS
240.g1 (mg/kg)
hIL-6(30ug/kg)