G00002

```
2.13.2K    GACATCCAGA TGACCCAGTT TCCATCCTCC CTGTCTGCAT CTGTAGGAGA   50
A30        GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA   50
2.14.3K    ---------- ---------- ----TCCTCC CTGTCTGCAT CTGTAGGAGA   26
2.12.1K    ---------- ---------- ---------- -----TGCAT CTGTAGGAGA   15
4.9.2K     GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA   50
Consensus  GACATCCAGA TGACCCAGTY TCCATCCTCC CTGTCTGCAT CTGTAGGAGA   50
                                                  CDR1

2.13.2K    CAGAGTCACC ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG  100
A30        CAGAGTCACC ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG  100
2.14.3K    CAGAGTCACC TTCACTTGCC GGGCAAGTCA GGACATTAGA CGTGATTTAG   76
2.12.1K    CAGAGTCACC TTCACTTGCC GGGCAAGTCA GGACATTAGA CGTGATTTAG   65
4.9.2K     CAGAGTCACC ATCACTTGCC GGGCAAGTCA GGGCATTAGA AGTGATTTAG  100
Consensus  CAGAGTCACC WTCACTTGCC GGGCAAGTCA GGRCATTAGA MRTGATTTAG  100

2.13.2K    GCTGGTATCA GCAGAAACCA GGGAAAGCCC CTAAGCGCCT GATCTATGCT  150
A30        GCTGGTATCA GCAGAAACCA GGGAAAGCCC CTAAGCGCCT GATCTATGCT  150
2.14.3K    GCTGGTATCA GCAGAAACCA GGGAAAGCTC CTAAGCGCCT GATCTATGCT  126
2.12.1K    GCTGGTATCA GCAGAAACCA GGGAAAGCTC CTAAGCGCCT GATCTATGCT  115
4.9.2K     GCTGGTTTCA GCAGAAACCA GGGAAAGCCC CTAAGCGCCT GATCTATGCT  150
Consensus  GCTGGTWTCA GCAGAAACCA GGGAAAGCYC CTAAGCGCCT GATCTATGCT  150
           CDR2

2.13.2K    GCATCCCGTT TGCACAGAGG GGTCCCATCA AGGTTCAGCG GCAGTGGATC  200
A30        GCATCCAGTT TGCAAAGTGG GGTCCCATCA AGGTTCAGCG GCAGTGGATC  200
2.14.3K    GCATCCCGTT TACAAAGTGG GGTCCCATCA AGGTTCAGCG GCAGTGGATC  176
2.12.1K    GCATCCCGTT TACAAAGTGG GGTCCCATCA AGGTTCAGCG GCAGTGGATC  165
4.9.2K     GCATCCAAAT TACACCGTGG GGTCCCATCA AGGTTCAGCG GCAGTGGATC  200
Consensus  GCATCCMRWT TRCAMMGWGG GGTCCCATCA AGGTTCAGCG GCAGTGGATC  200

2.13.2K    TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT GAAGATTTTG  250
A30        TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT GAAGATTTTG  250
2.14.3K    TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT GAAGATTTTG  226
2.12.1K    TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT GAAGATTTTG  215
4.9.2K     TGGGACAGAA TTCACTCTCA CAATCAGCCG CCTGCAGCCT GAAGATTTTG  250
Consensus  TGGGACAGAA TTCACTCTCA CAATCAGCMG CCTGCAGCCT GAAGATTTTG  250
                                    CDR3

2.13.2K    CAACTTATTA CTGTCTACAA CATAATAGTT ACCCGTGCAG TTTTGGCCAG  300
A30        CAACTTATTA CTGTCTACAG CATAATAGTT ACCC-TCCN- ----------  288
2.14.3K    CAACTTATTA CTGTCTACAG CATAATAATT ATCCTCGGAC GTTCGGCCAA  276
2.12.1K    CAACTTATTA CTGTCTACAG CATAATAATT ATCCTCGGAC GTTCGGCCAA  265
4.9.2K     CAACTTATTA CTGTCTACAG CATAATAGTT ACCCTCTCAC TTTCGGCGGA  300
Consensus  CAACTTATTA CTGTYTACAR CATAATARTT AYCCKYBSNS KTTYGGCSRR  300

2.13.2K    GGGACCAAGC TGGAGATCAA AC----                           322
A30        ---------- ---------- ------                           288
2.14.3K    GGGACCGAGG TGGAAATCAT ACGAAC                           302
2.12.1K    GGGACCGAGG TGGAAATCAT ACGAAC                           291
4.9.2K     GGGACCAAGG TGGAGATCAA AC----                           322
Consensus  GGGACCRAGS TGGARATCAW ACGAAC                           326
```

FIG. 1A

163163

```
4.17.3K     ---------- ---------- ---------- ---------- ----AGGAGA    7
O12         GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA   50
Consensus   GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGYAGGAGA   50
                                                  CDR1
4.17.3K     CAGAGTCACC ATCACTTGCC GGGCAAGTCA GAGCATTAGT ACCTTTTTAA   57
O12         CAGAGTCACC ATCACTTGCC GGGCAAGTCA GAGCATTAGC AGCTATTTAA  100
Consensus   CAGAGTCACC ATCACTTGCC GGGCAAGTCA GAGCATTAGY ASCTWTTTAA  100

4.17.3K     ATTGGTATCA GCAGAAACCA GGGAAAGCCC CTAAACTCCT GATCCATGTT  107
O12         ATTGGTATCA GCAGAAACCA GGGAAAGCCC CTAAGCTCCT GATCTATGCT  150
Consensus   ATTGGTATCA GCAGAAACCA GGGAAAGCCC CTAARCTCCT GATCYATGYT  150
            CDR2
4.17.3K     GCATCCAGTT TACAAGGTGG GGTCCCATCA AGGTTCAGTG GCAGTGGATC  157
O12         GCATCCAGTT TGCAAAGTGG GGTCCCATCA AGGTTCAGTG GCAGTGGATC  200
Consensus   GCATCCAGTT TRCAARGTGG GGTCCCATCA AGGTTCAGTG GCAGTGGATC  200

4.17.3K     TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT GAAGATTTTG  207
O12         TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT GAAGATTTTG  250
Consensus   TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT GAAGATTTTG  250
                                  CDR3
4.17.3K     CAACTTACTA CTGTCAACAG AGTTACAATG CCCCACTCAC TTTCGGCGGA  257
O12         CAACTTACTA CTGTCAACAG AGTTACAGTA CCCC-TCCH- ----------  288
Consensus   CAACTTACTA CTGTCAACAG AGTTACARTR CCCCAYYCHC TTTCGGCGGA  300

4.17.3K     GGGACCAAGG TGGAGATCAA AC                               279
O12         ---------- ---------- --                               288
Consensus   GGGACCAAGG TGGAGATCAA AC                               322
```

FIG. 1B

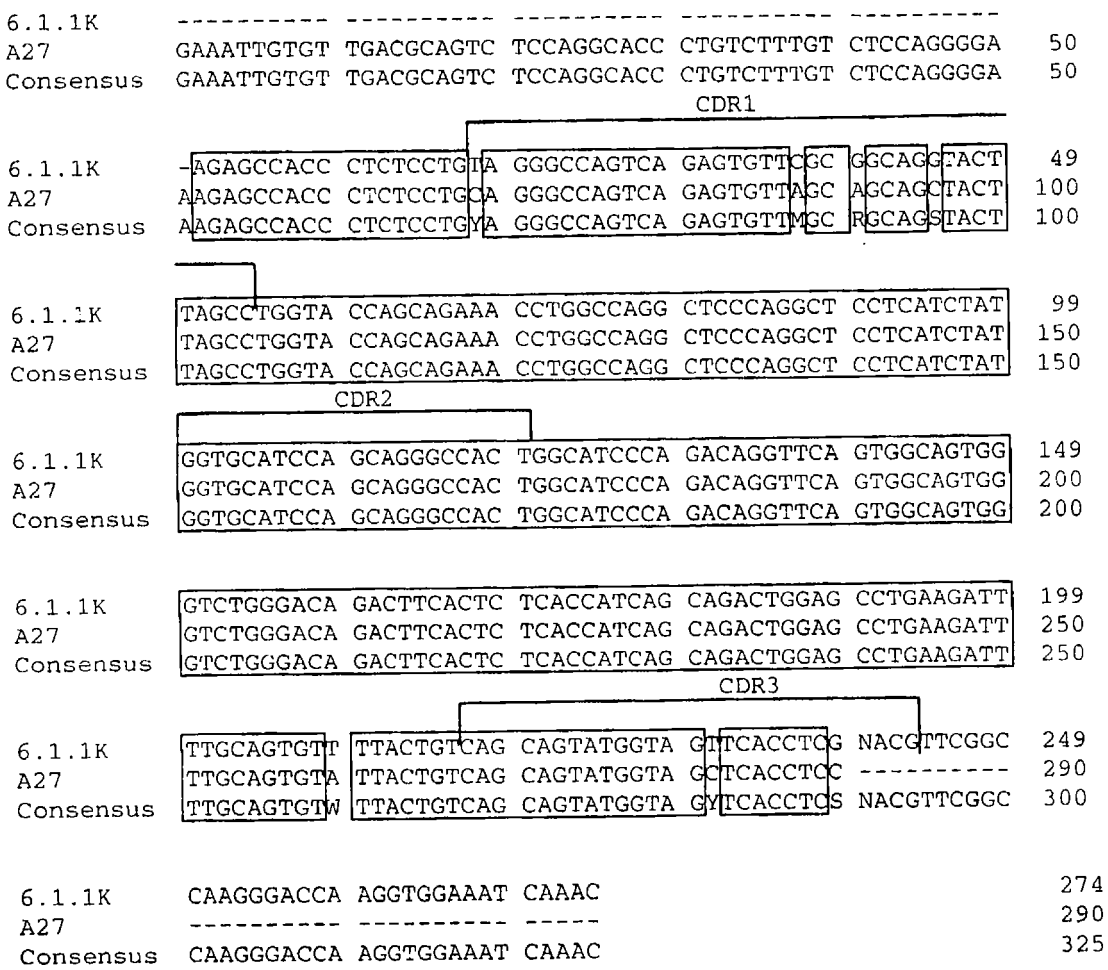

6.1.1K ---------- ---------- ---------- ---------- ----------
A27 GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA 50
Consensus GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA 50
CDR1
6.1.1K -AGAGCCACC CTCTCCTGIA GGGCCAGTCA GAGTGTTCGC GGCAGGTACT 49
A27 AAGAGCCACC CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AGCAGCTACT 100
Consensus AAGAGCCACC CTCTCCTGYA GGGCCAGTCA GAGTGTTMGC RGCAGSTACT 100
6.1.1K TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT 99
A27 TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT 150
Consensus TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT 150
CDR2
6.1.1K GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG 149
A27 GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG 200
Consensus GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG 200
6.1.1K GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT 199
A27 GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT 250
Consensus GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT 250
CDR3
6.1.1K TTGCAGTGTT TTACTGTCAG CAGTATGGTA GTTCACCTCG NACGTTCGGC 249
A27 TTGCAGTGTA TTACTGTCAG CAGTATGGTA GCTCACCTCC ---------- 290
Consensus TTGCAGTGTW TTACTGTCAG CAGTATGGTA GYTCACCTCS NACGTTCGGC 300
6.1.1K CAAGGGACCA AGGTGGAAAT CAAAC 274
A27 ---------- ---------- ----- 290
Consensus CAAGGGACCA AGGTGGAAAT CAAAC 325

FIG. 1C

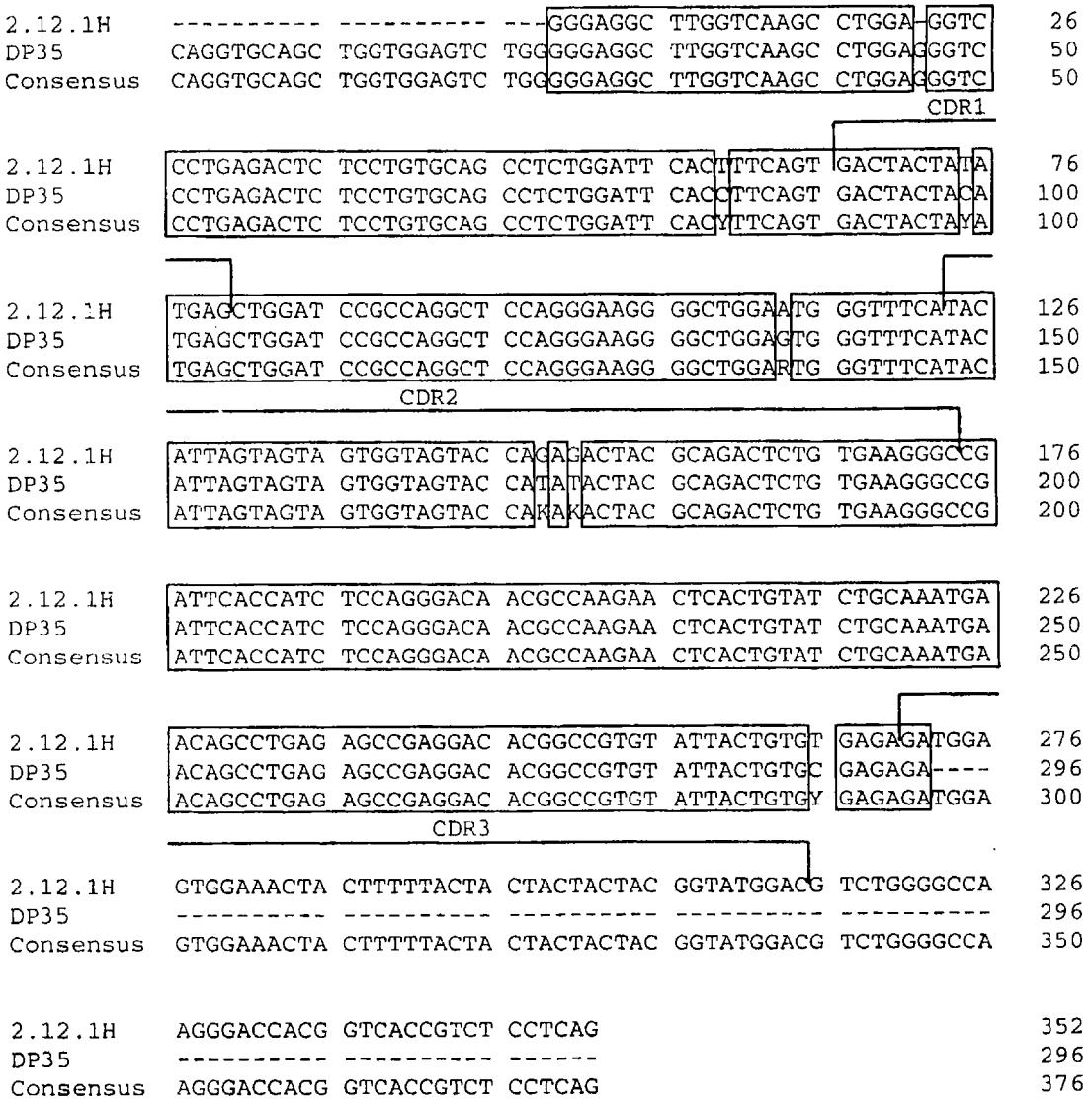

2.12.1H ---------- ---------- ---GGGAGGC TTGGTCAAGC CTGGA-GGTC 26
DP35 CAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGGTCAAGC CTGGAGGGTC 50
Consensus CAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGGTCAAGC CTGGAGGGTC 50
CDR1
2.12.1H CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACTTTCAGT GACTACTATA 76
DP35 CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTCAGT GACTACTACA 100
Consensus CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACYTTCAGT GACTACTAYA 100
2.12.1H TGAGCTGGAT CCGCCAGGCT CCAGGGAAGG GGCTGGAATG GGTTTCATAC 126
DP35 TGAGCTGGAT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTTTCATAC 150
Consensus TGAGCTGGAT CCGCCAGGCT CCAGGGAAGG GGCTGGARTG GGTTTCATAC 150
CDR2
2.12.1H ATTAGTAGTA GTGGTAGTAC CAGAGACTAC GCAGACTCTG TGAAGGGCCG 176
DP35 ATTAGTAGTA GTGGTAGTAC CATATACTAC GCAGACTCTG TGAAGGGCCG 200
Consensus ATTAGTAGTA GTGGTAGTAC CAKAKACTAC GCAGACTCTG TGAAGGGCCG 200
2.12.1H ATTCACCATC TCCAGGGACA ACGCCAAGAA CTCACTGTAT CTGCAAATGA 226
DP35 ATTCACCATC TCCAGGGACA ACGCCAAGAA CTCACTGTAT CTGCAAATGA 250
Consensus ATTCACCATC TCCAGGGACA ACGCCAAGAA CTCACTGTAT CTGCAAATGA 250
2.12.1H ACAGCCTGAG AGCCGAGGAC ACGGCCGTGT ATTACTGTGT GAGAGATGGA 276
DP35 ACAGCCTGAG AGCCGAGGAC ACGGCCGTGT ATTACTGTGC GAGAGA---- 296
Consensus ACAGCCTGAG AGCCGAGGAC ACGGCCGTGT ATTACTGTGY GAGAGATGGA 300
CDR3
2.12.1H GTGGAAACTA CTTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 326
DP35 ---------- ---------- ---------- ---------- ---------- 296
Consensus GTGGAAACTA CTTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350
2.12.1H AGGGACCACG GTCACCGTCT CCTCAG 352
DP35 ---------- ---------- ------ 296
Consensus AGGGACCACG GTCACCGTCT CCTCAG 376

FIG. 2A

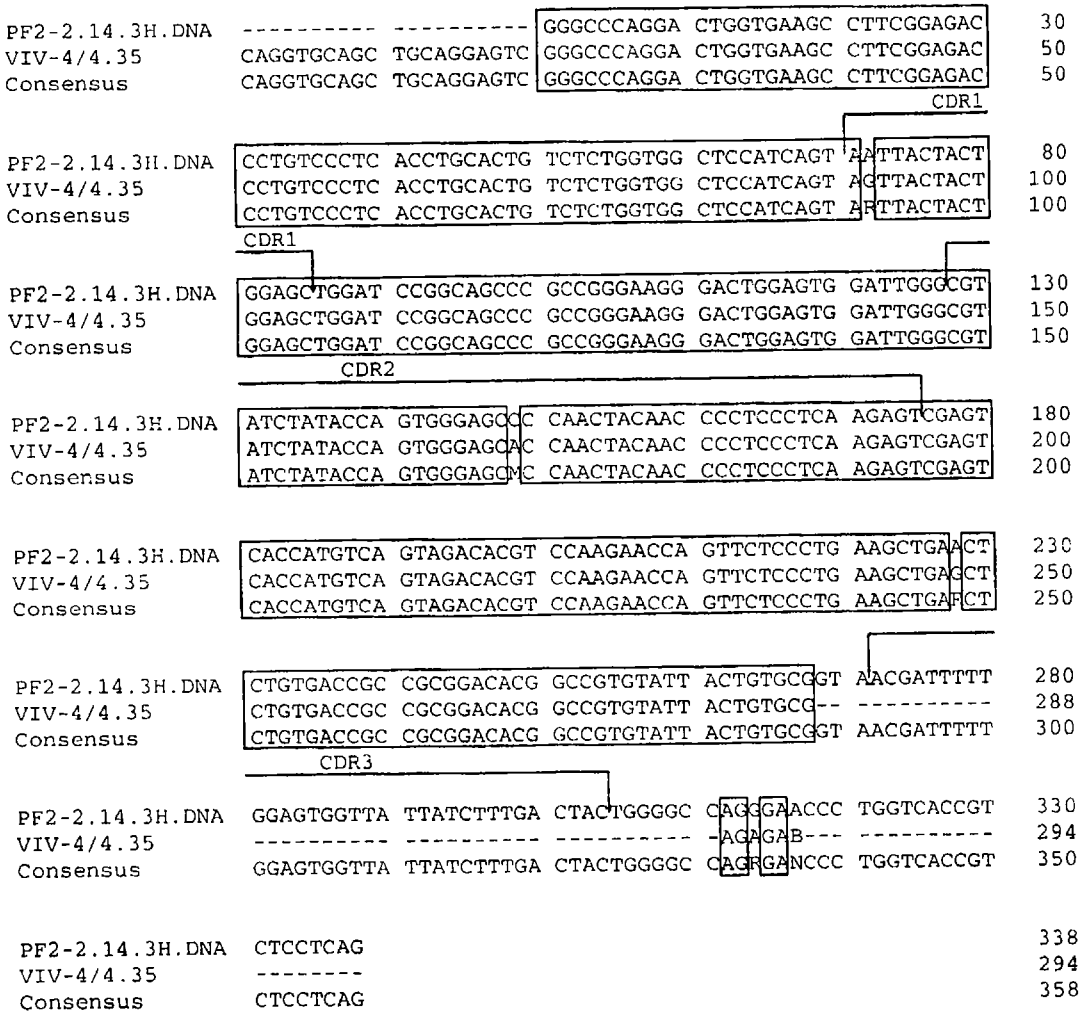

PF2-2.14.3H.DNA ---------- ---------- GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC 30
VIV-4/4.35 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC 50
Consensus CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC 50
CDR1
PF2-2.14.3H.DNA CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AATTACTACT 80
VIV-4/4.35 CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT 100
Consensus CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT ARTTACTACT 100
CDR1
PF2-2.14.3H.DNA GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT 130
VIV-4/4.35 GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT 150
Consensus GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT 150
CDR2
PF2-2.14.3H.DNA ATCTATACCA GTGGGAGCCC CAACTACAAC CCCTCCCTCA AGAGTCGAGT 180
VIV-4/4.35 ATCTATACCA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT 200
Consensus ATCTATACCA GTGGGAGCMC CAACTACAAC CCCTCCCTCA AGAGTCGAGT 200
PF2-2.14.3H.DNA CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAACT 230
VIV-4/4.35 CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGCT 250
Consensus CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGARCT 250
PF2-2.14.3H.DNA CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTTT 280
VIV-4/4.35 CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCG-- ---------- 288
Consensus CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTTT 300
CDR3
PF2-2.14.3H.DNA GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGGGAACCC TGGTCACCGT 330
VIV-4/4.35 ---------- ---------- ---------- -AGAGAB--- ---------- 294
Consensus GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGRGANCCC TGGTCACCGT 350
PF2-2.14.3H.DNA CTCCTCAG 338
VIV-4/4.35 -------- 294
Consensus CTCCTCAG 358

FIG. 2B

```
6.1.1H      GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC  50
4.9.2H      GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC  50
DP47        GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC  50
2.13.2H     GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC  50
Consensus   GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC  50
                                                        CDR1

6.1.1H      CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA  100
4.9.2H      CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA  100
DP47        CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA  100
2.13.2H     CCTGAGACTC TCCTGTACAG CCTCTGGATT CACCTTTAGC AGCTATGCCA  100
Consensus   CCTGAGACTC TCCTGTRCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA  100
            CDR1                                            CDR2

6.1.1H      TGAGCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT  150
4.9.2H      TGAGCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGCT  150
DP47        TGAGCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGCT  150
2.13.2H     TGAACTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGCT  150
Consensus   TGARCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGST  150
                                    CDR2

6.1.1H      ATTACTGGGA GTGGTGGTAG TACATACTAC GCAGACTCCG TGAAGGGCCG  200
4.9.2H      ATTAGTGGTA GTGGTGGTAT CACATACTAC GCAGACTCCG TGAAGGGCCG  200
DP47        ATTAGTGGTA GTGGTGGTAG CACATACTAC GCAGACTCCG TGAAGGGCCG  200
2.13.2H     ATTAGTGGTA GTGGTGGTAC CACATTCTAC GCAGACTCCG TGAAGGGCCG  200
Consensus   ATTASTGGKA GTGGTGGTAB YACATWCTAC GCAGACTCCG TGAAGGGCCG  200

6.1.1H      GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA  250
4.9.2H      GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA  250
DP47        GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA  250
2.13.2H     GTTCACCATC TCCAGAGACA ATTCCAGGAC CACGCTGTAT CTGCAAATGA  250
Consensus   GTTCACCATC TCCAGAGACA ATTCCARGAM CACGCTGTAT CTGCAAATGA  250
                                                        CDR3

6.1.1H      ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATC--  298
4.9.2H      ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG  300
DP47        ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGA----  296
2.13.2H     ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT  300
Consensus   ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK  300
                        CDR3-for 4.9.2 and 2.13.2

6.1.1H      ---------- ---------- ---------- ---------- --------C-  299
4.9.2H      GGCTACGGTG ACTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA  350
DP47        ---------- ---------- ---------- ---------- ----------  296
2.13.2H     GGCTGGTCCG ACTCTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA  350
Consensus   GGCTRSKSYG ACTYTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA  350
                    CDR3-for 6.1.1

6.1.1H      AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC  349
4.9.2H      AGGGACCAC- ---------- ---------- ---------- ----------  359
DP47        ---------- ---------- ---------- ---------- ----------  296
2.13.2H     AGGGACCAC- ---------- ---------- ---------- ----------  359
Consensus   AGGGACYACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC  400
```

FIG. 2C-1

```
6.1.1H      TGGTCACCGT CTCCTCAG                                    367
4.9.2H      -GGTCACCGT CTCCTCAG                                    376
DP47        ---------- --------                                    296
2.13.2H     -GGTCACCGT CTCCTCAG                                    376
Consensus   TGGTCACCGT CTCCTCAG                                    418
```

FIG. 2C-2

```
4.17.3H     ---------- ---------- ---CCCAGGA CTGGTGAAGC CTTCGGAGAC   27
DP71        CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC   50
Consensus   CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC   50
                                                          CDR1

4.17.3H     CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT   77
DP71        CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT  100
Consensus   CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT  100
            CDR1

4.17.3H     GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT  127
DP71        GGAGCTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT  150
Consensus   GGAGYTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT  150
                  CDR2

4.17.3H     ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT  177
DP71        ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT  200
Consensus   ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT  200

4.17.3H     CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGTT  227
DP71        CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGCT  250
Consensus   CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGYT  250
                              CDR3

4.17.3H     CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC  277
DP71        CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGC--- GA--------  289
Consensus   CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC  300

4.17.3H     AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GGACCACGGT  327
DP71        ---------- ---------- ----GA---- ---------- -GA-------  293
Consensus   AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GGACCACGGT  350

4.17.3H     CACCGTCTCC TCAG                                        341
DP71        ---------- ----                                        293
Consensus   CACCGTCTCC TCAG                                        364
```

FIG. 2D

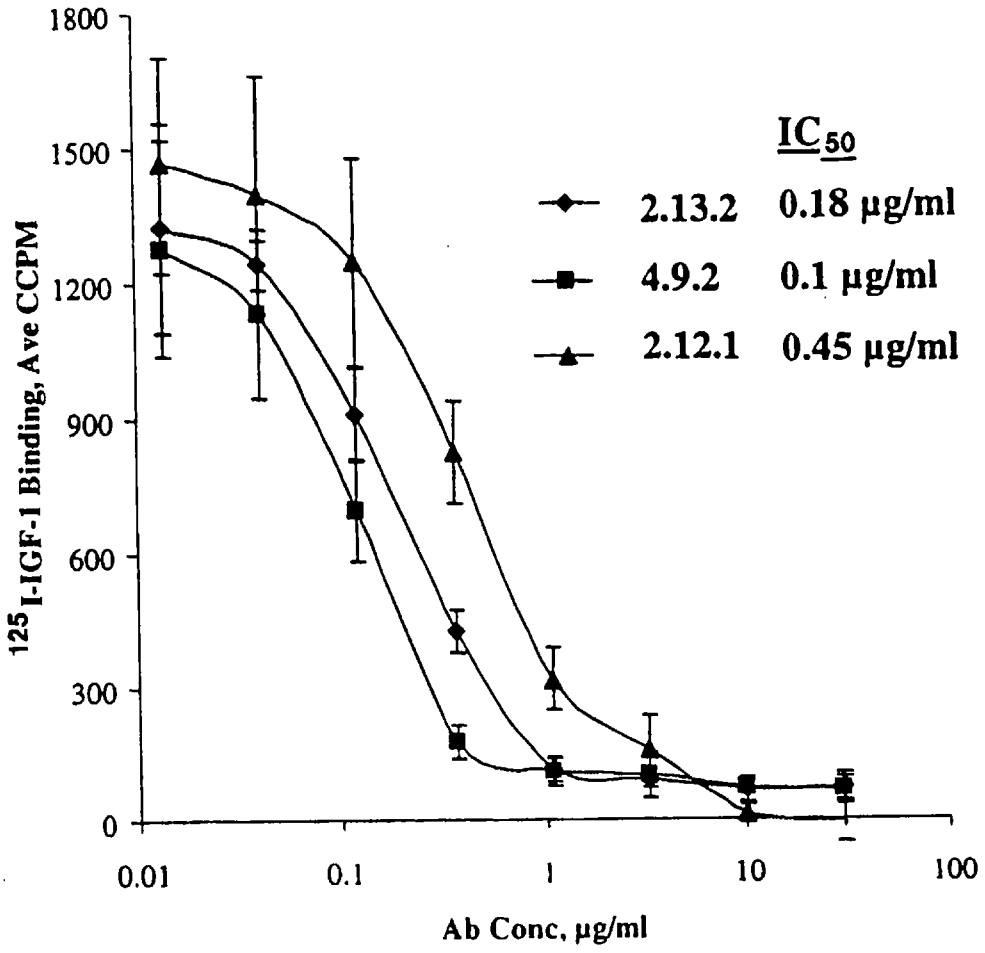

1800
1500
1200
900
600
300
0
0.01
0.1
1
10
100
^{125}I-IGF-1 Binding, Ave CCPM
Ab Conc, µg/ml
IC50
2.13.2 0.18 µg/ml
4.9.2 0.1 µg/ml
2.12.1 0.45 µg/ml

FIG. 3

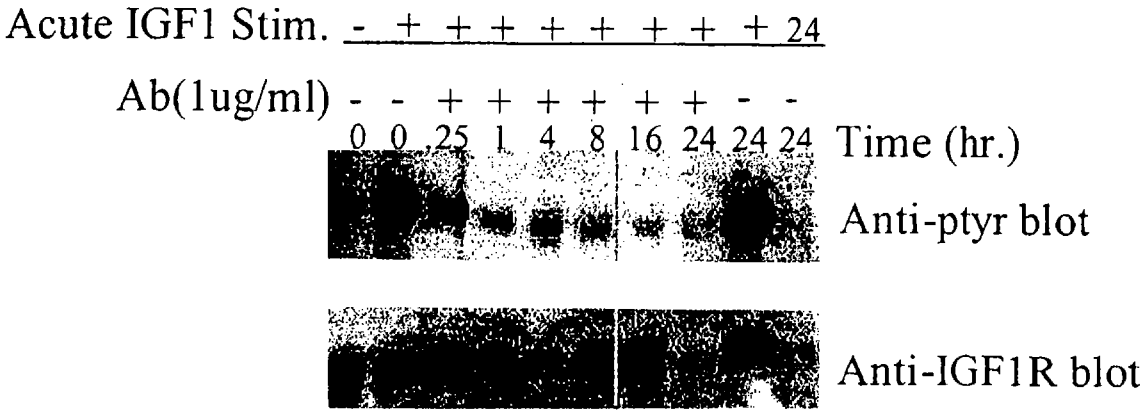

Acute IGF1 Stim. - + + + + + + + + 24
Ab(1ug/ml) - - + + + + + + - -
0 0 .25 1 4 8 16 24 24 24
Time (hr.)
Anti-ptyr blot
Anti-IGF1R blot

FIG. 4

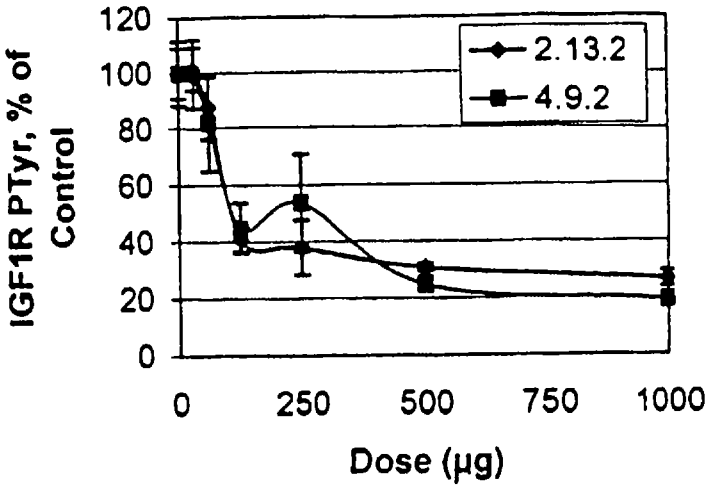

IGF1R PTyr, % of Control
120
100
80
60
40
20
0
0
250
500
750
1000
Dose (µg)
2.13.2
4.9.2

FIG. 5

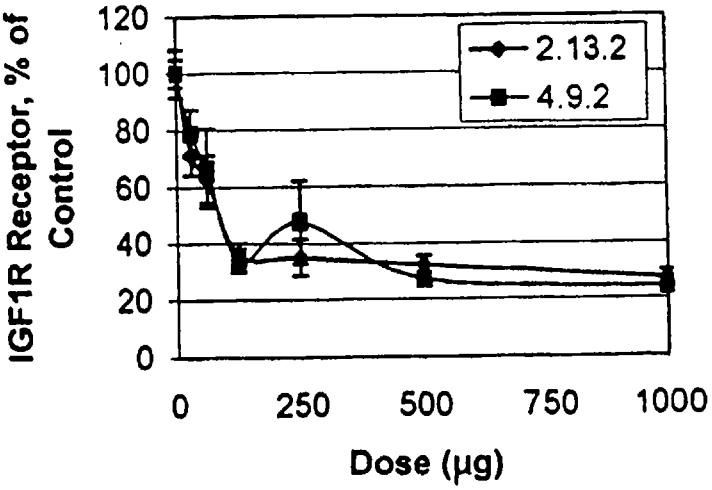

IGF1R Receptor, % of Control
120
100
80
60
40
20
0
0
250
500
750
1000
Dose (µg)
2.13.2
4.9.2

FIG. 6

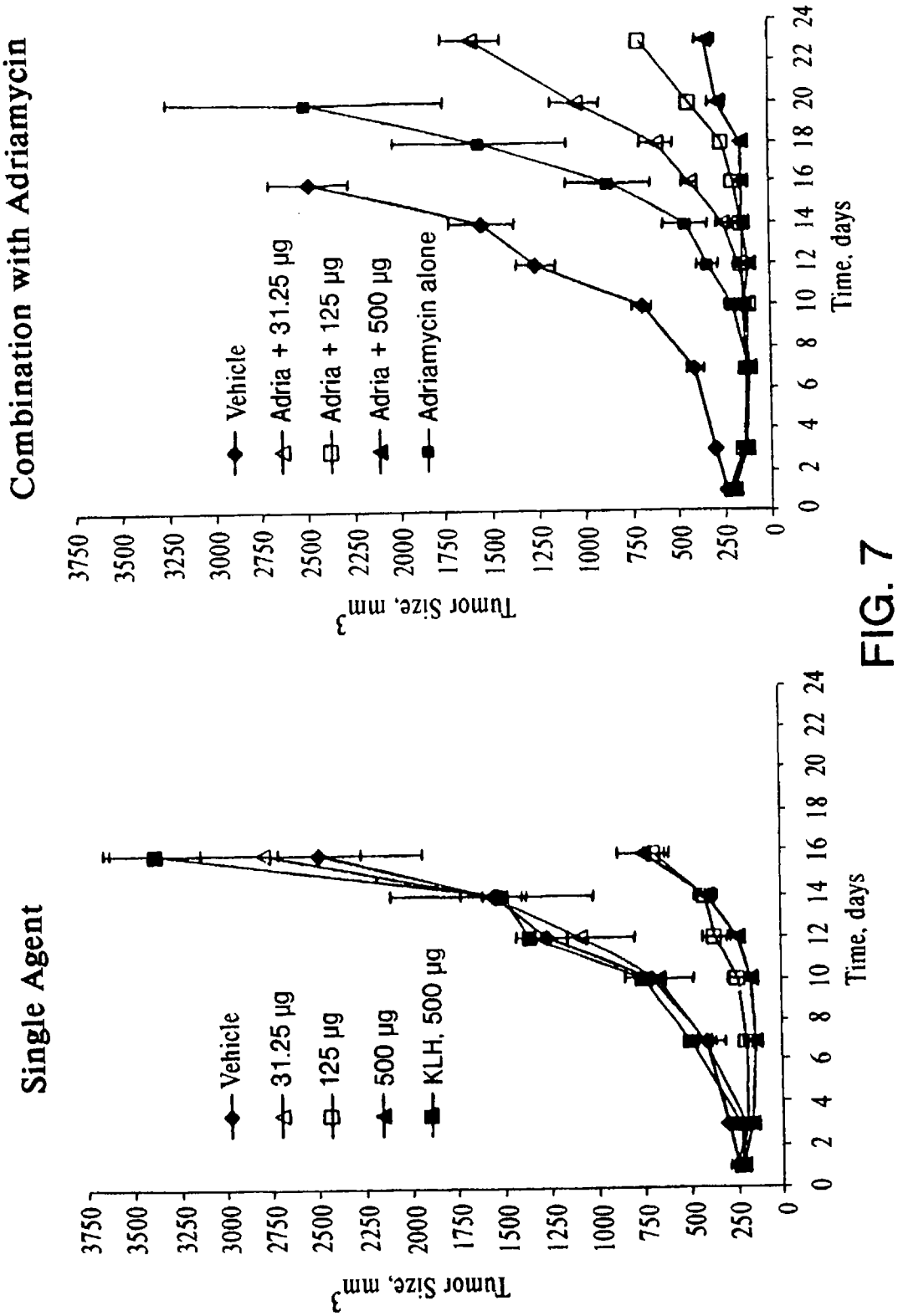

Single Agent
Vehicle
31.25 µg
125 µg
500 µg
KLH, 500 µg
Tumor Size, mm3
Time, days
Combination with Adriamycin
Vehicle
Adria + 31.25 µg
Adria + 125 µg
Adria + 500 µg
Adriamycin alone
Tumor Size, mm3
Time, days

FIG. 7

Treatment: 125 μg dose

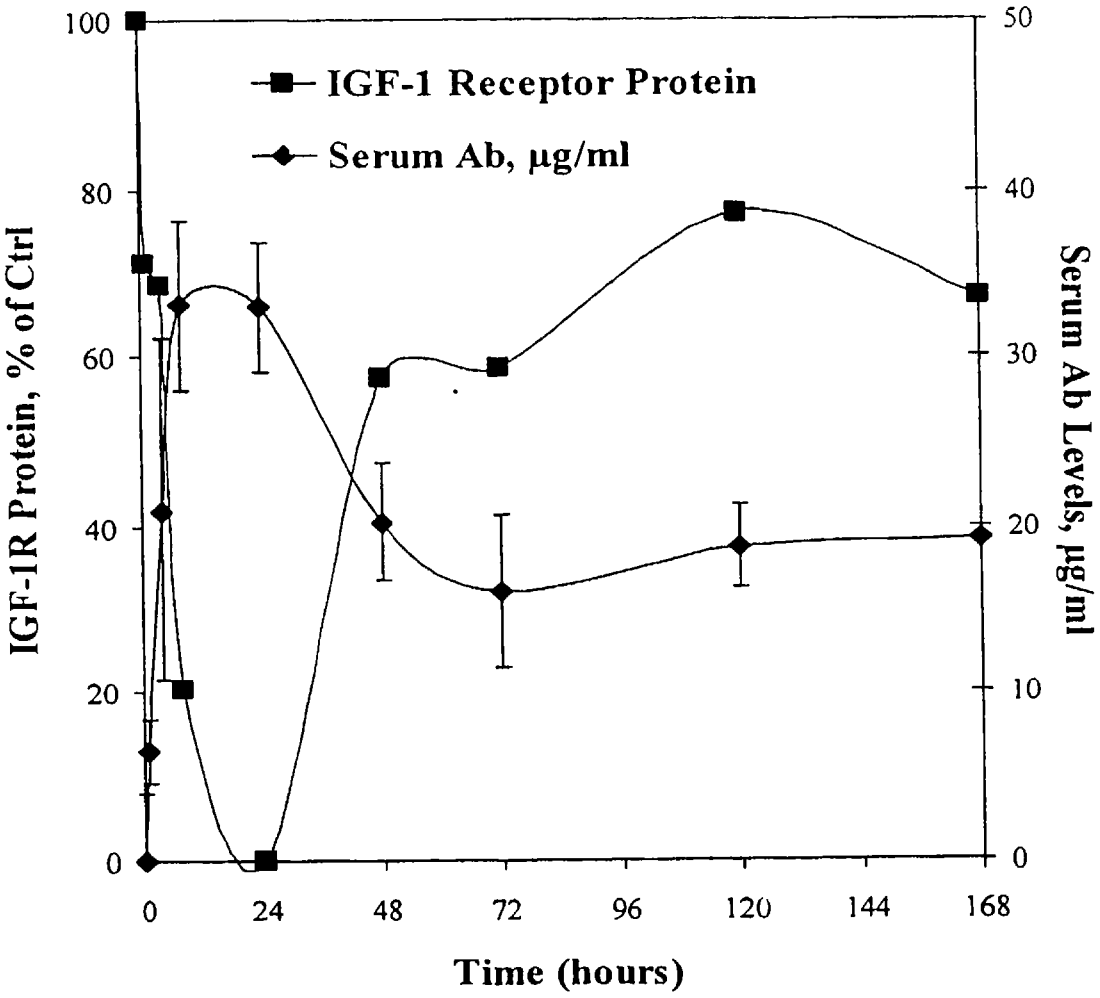


FIG. 8

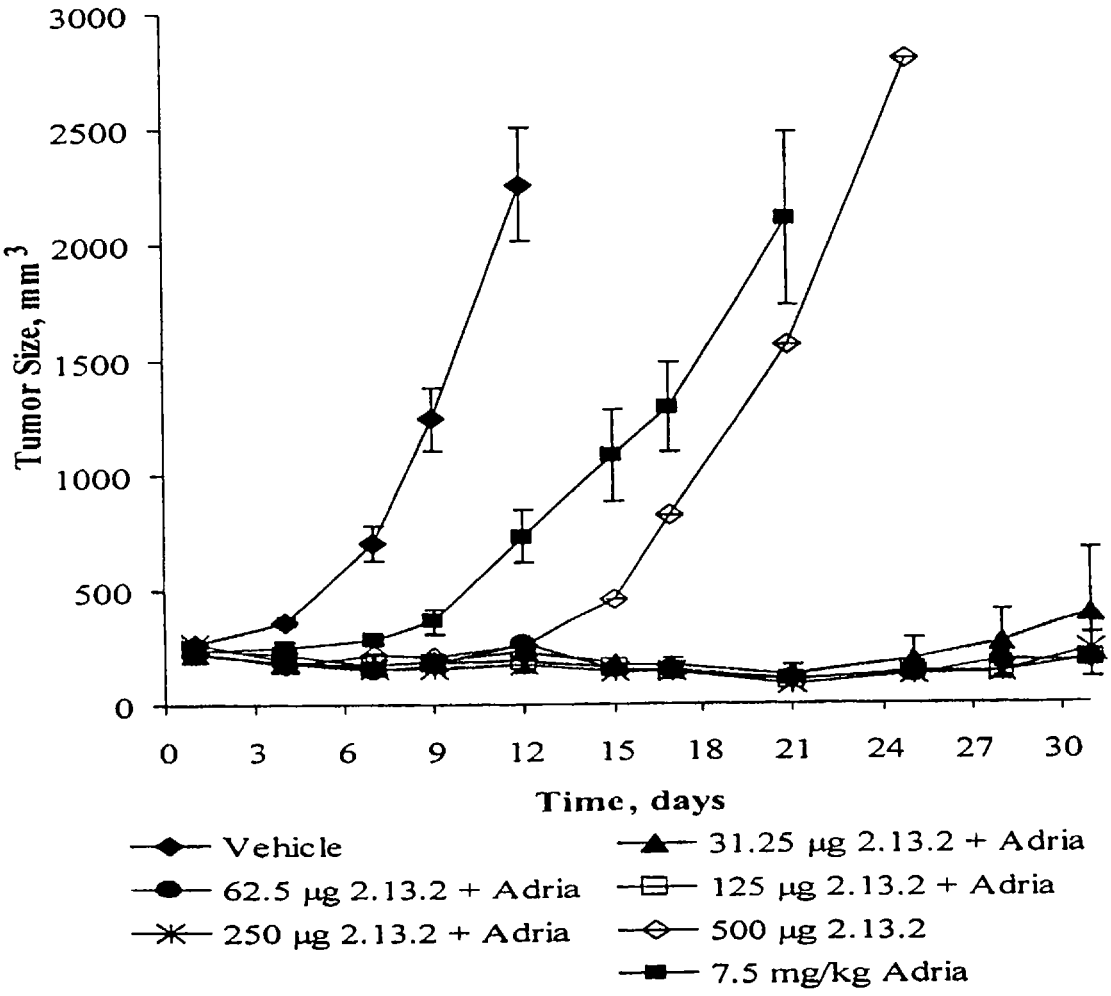

3000
2500
2000
1500
1000
500
0
Tumor Size, mm 3
0
3
6
9
12
15
18
21
24
27
30
Time, days
Vehicle
62.5 µg 2.13.2 + Adria
250 µg 2.13.2 + Adria
31.25 µg 2.13.2 + Adria
125 µg 2.13.2 + Adria
500 µg 2.13.2
7.5 mg/kg Adria

FIG. 9

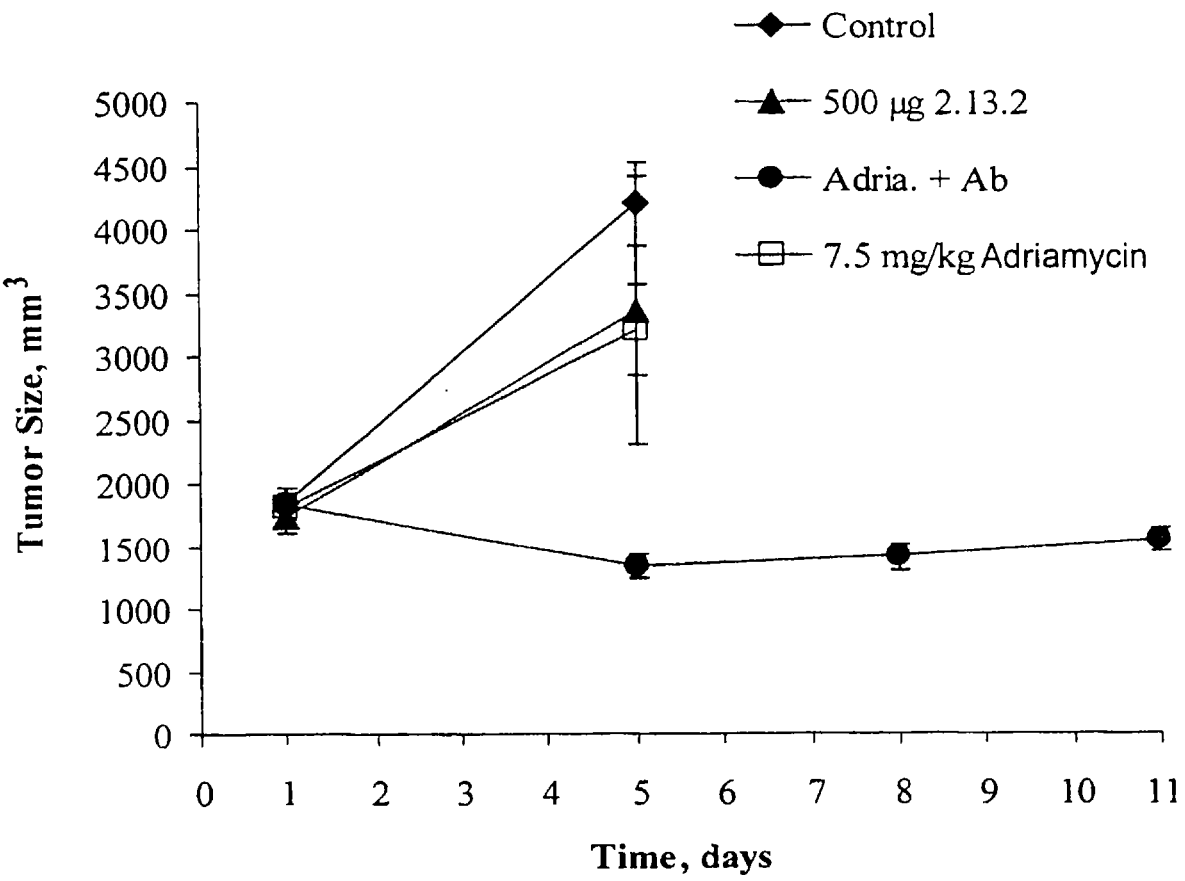

Control
500 µg 2.13.2
Adria. + Ab
7.5 mg/kg Adriamycin
Tumor Size, mm3
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
0 1 2 3 4 5 6 7 8 9 10 11
Time, days

FIG. 10

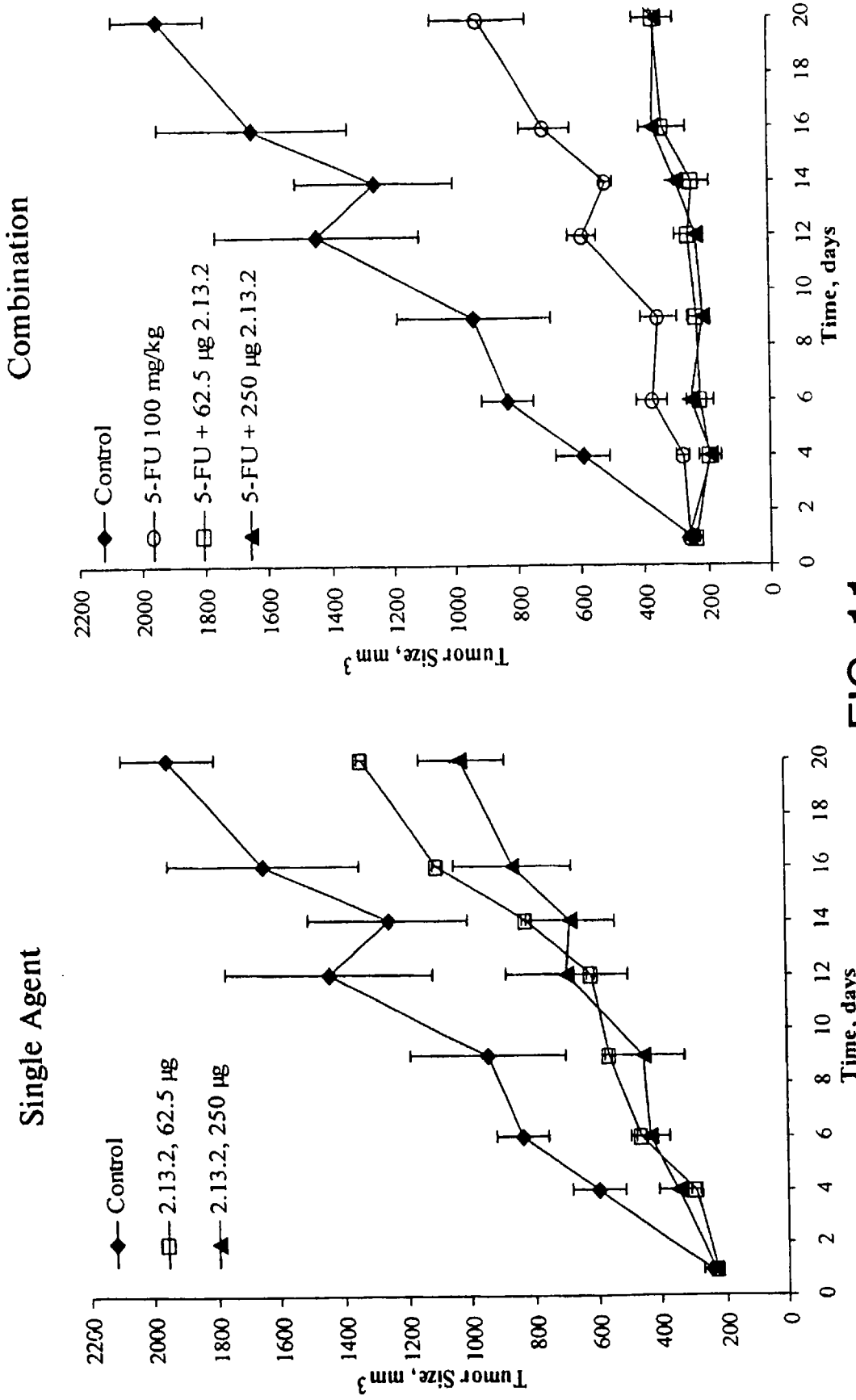

Single Agent
Control
2.13.2, 62.5 µg
2.13.2, 250 µg
Tumor Size, mm3
Time, days
Combination
Control
5-FU 100 mg/kg
5-FU + 62.5 µg 2.13.2
5-FU + 250 µg 2.13.2
Tumor Size, mm3
Time, days

FIG. 11

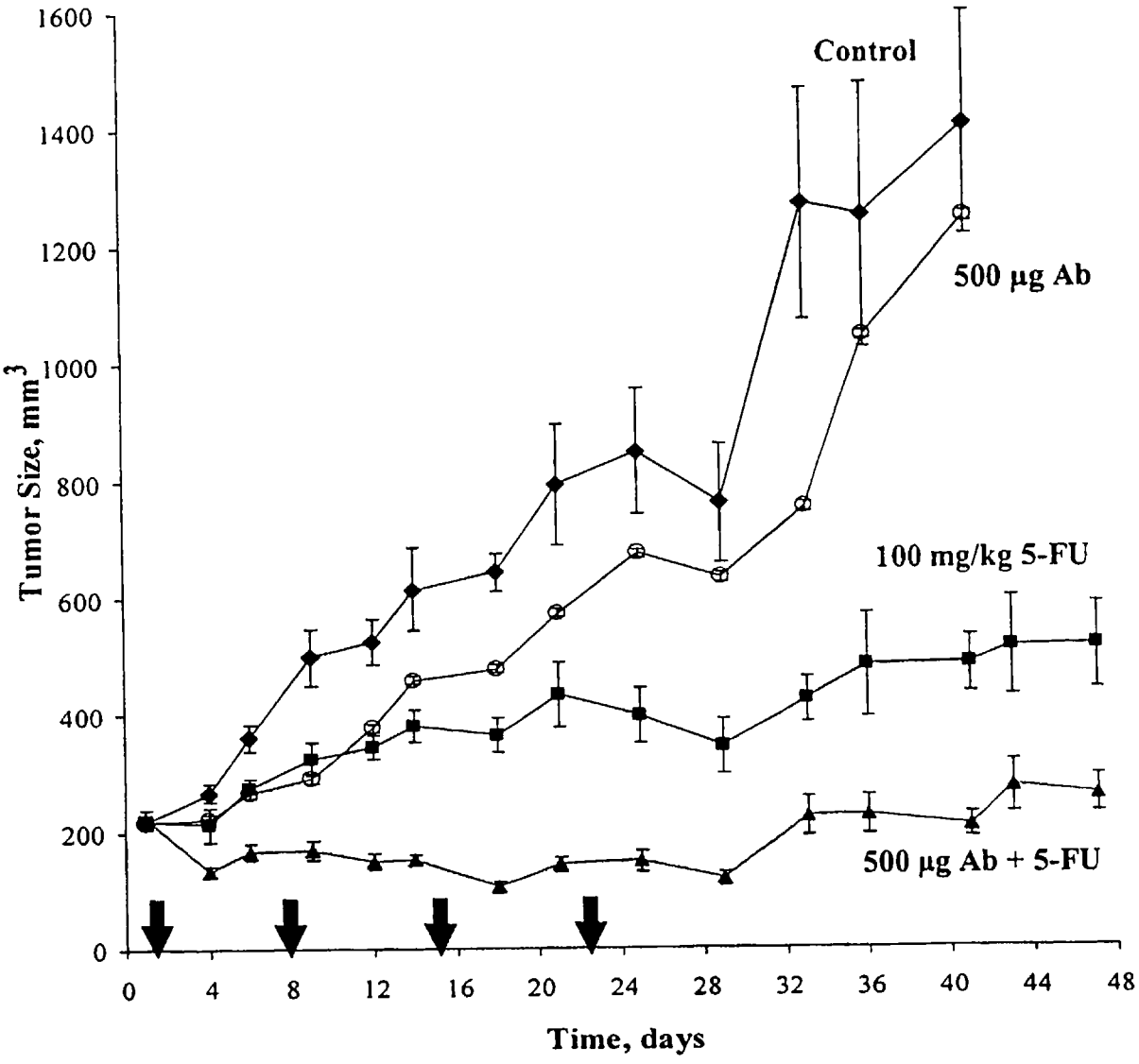

1600
1400
1200
1000
800
600
400
200
0
Tumor Size, mm3
Control
500 µg Ab
100 mg/kg 5-FU
500 µg Ab + 5-FU
0
4
8
12
16
20
24
28
32
36
40
44
48
Time, days

FIG. 12

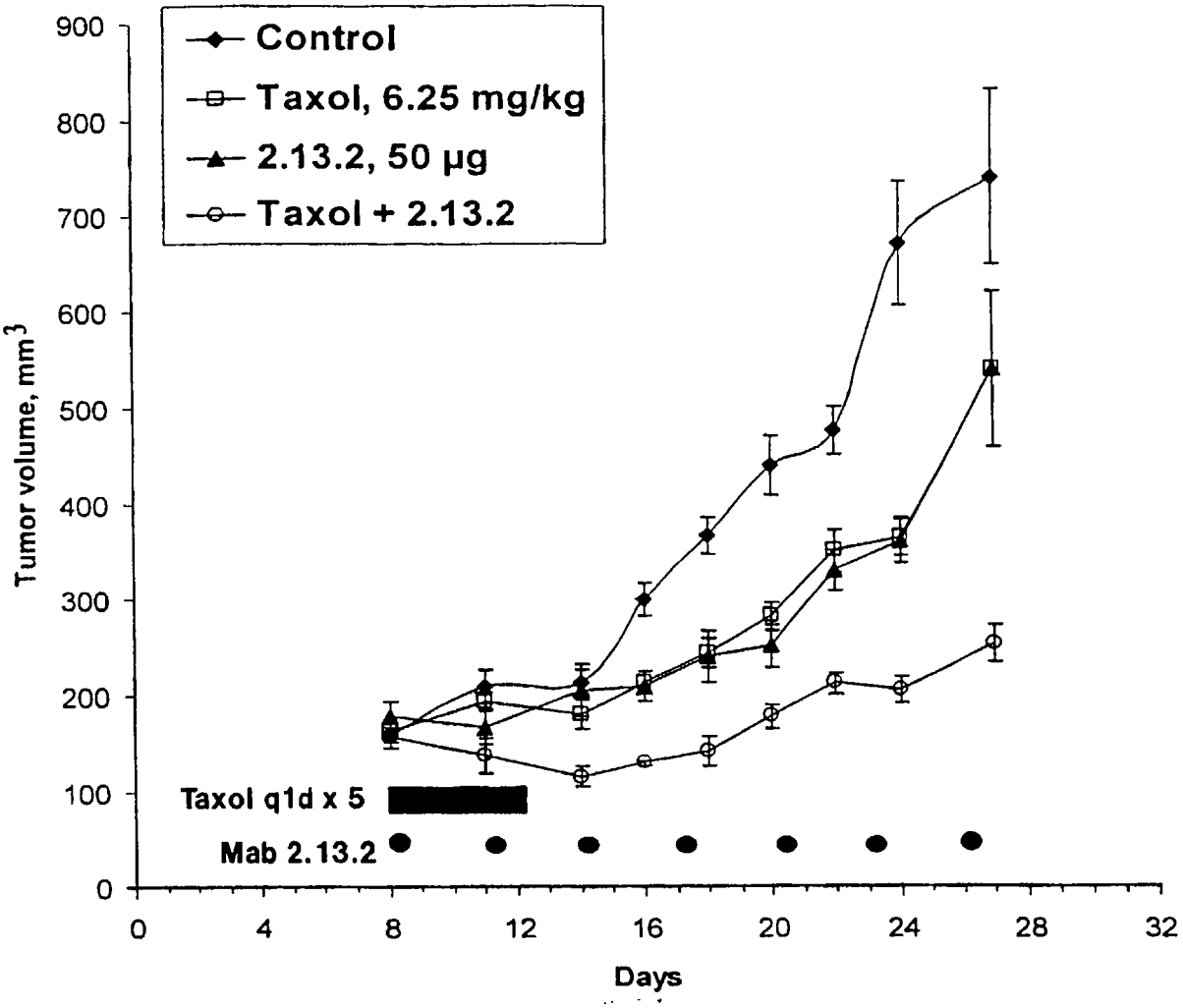

Control
Taxol, 6.25 mg/kg
2.13.2, 50 µg
Taxol + 2.13.2
Tumor volume, mm3
900
800
700
600
500
400
300
200
100
0
Taxol q1d x 5
Mab 2.13.2
0
4
8
12
16
20
24
28
32
Days

FIG. 13

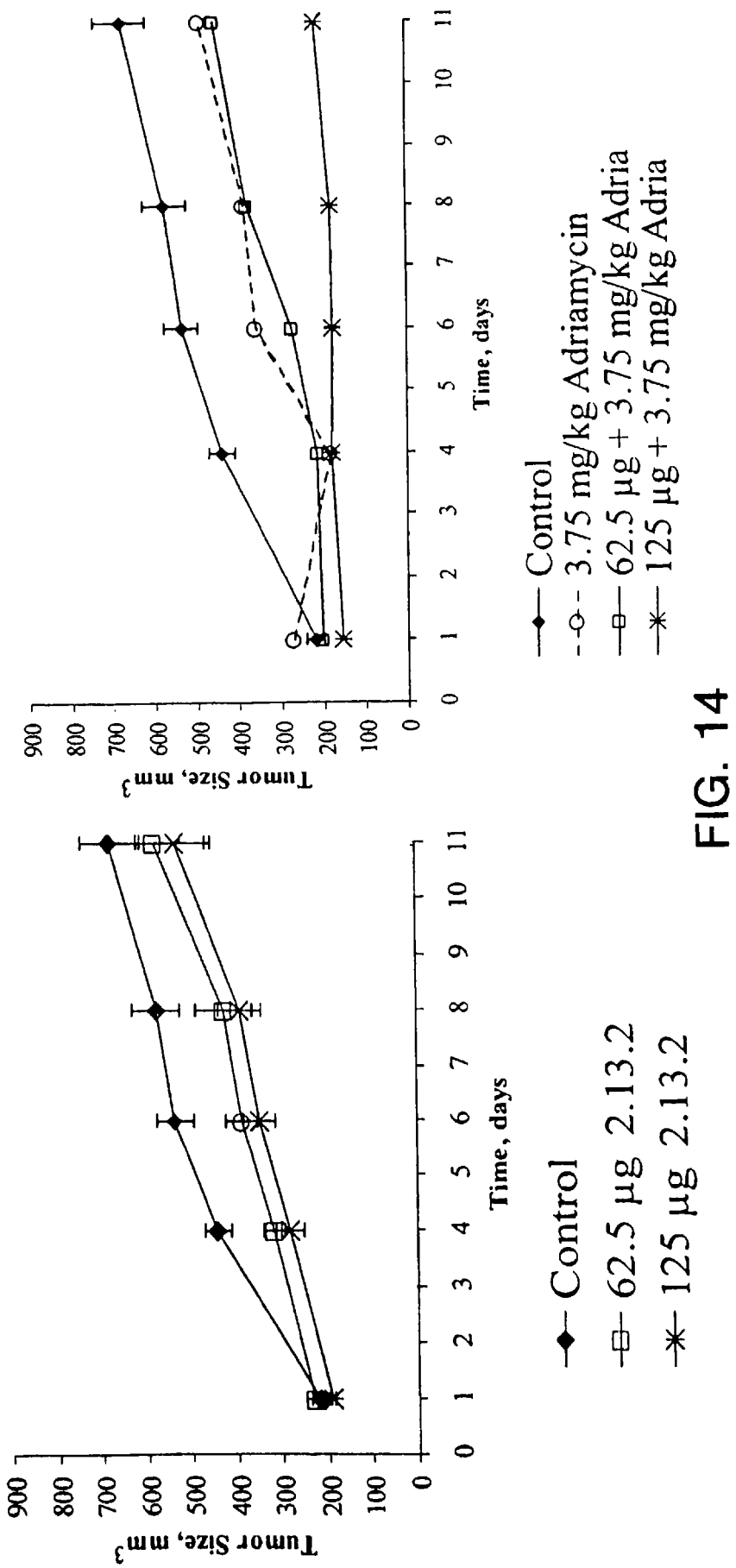

Single Agent
Combination
Tumor Size, mm3
Time, days
0
100
200
300
400
500
600
700
800
900
0 1 2 3 4 5 6 7 8 9 10 11
Control
62.5 µg 2.13.2
125 µg 2.13.2
Control
3.75 mg/kg Adriamycin
62.5 µg + 3.75 mg/kg Adria
125 µg + 3.75 mg/kg Adria

FIG. 14

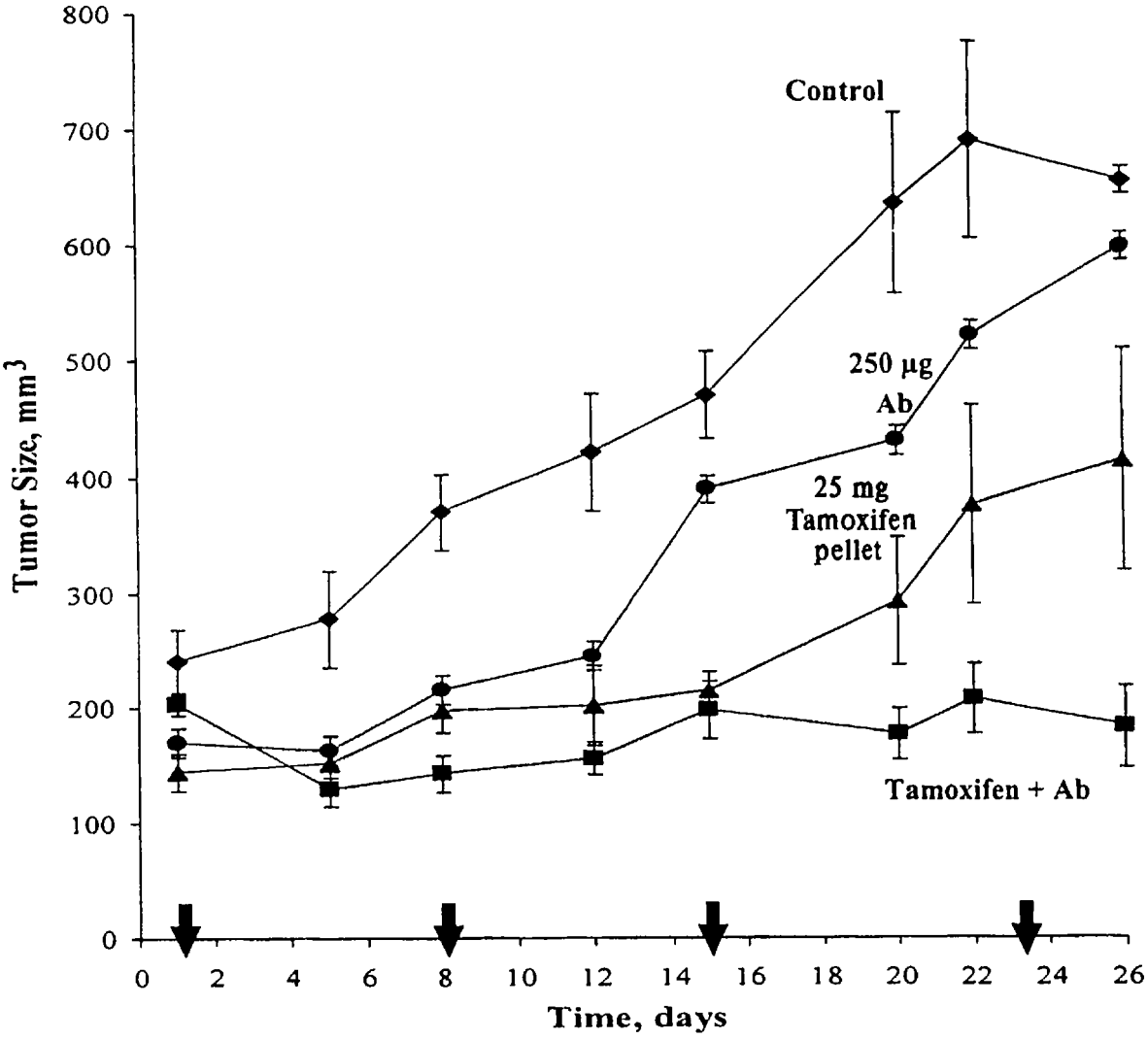

Tumor Size, mm3
800
700
600
500
400
300
200
100
0
Control
250 µg
Ab
25 mg
Tamoxifen
pellet
Tamoxifen + Ab
0
2
4
6
8
10
12
14
16
18
20
22
24
26
Time, days

FIG. 15

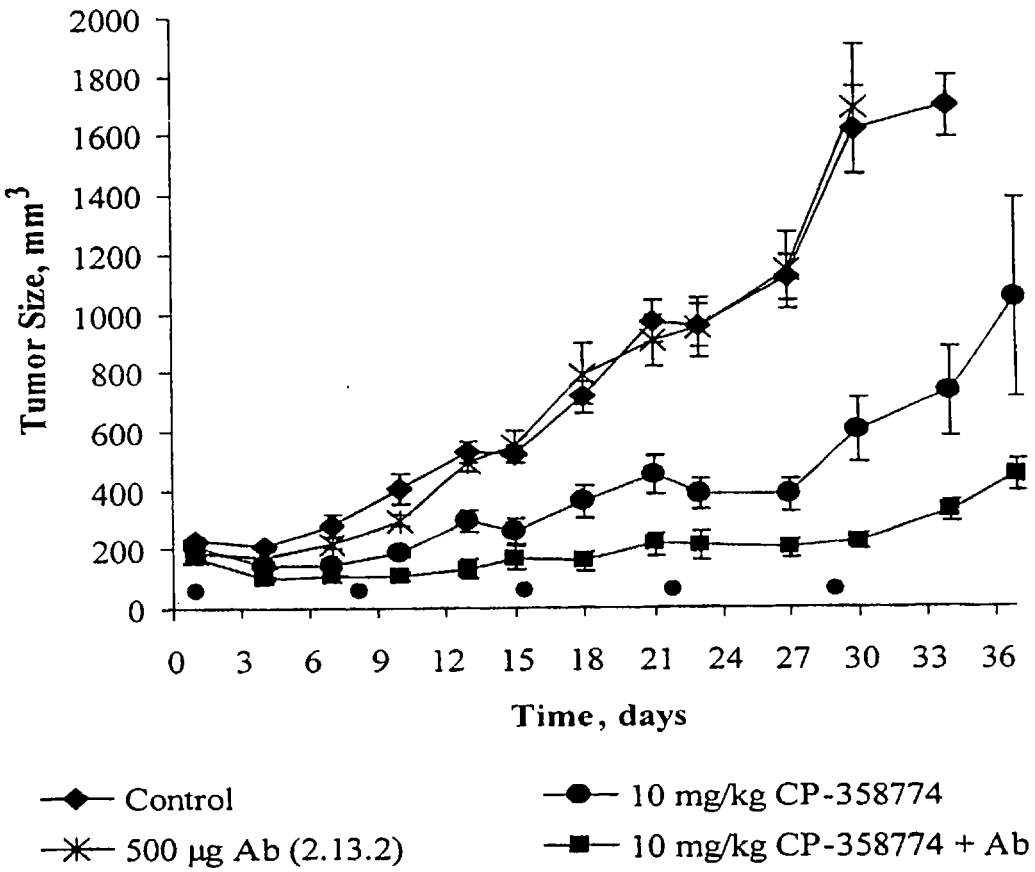

2000
1800
1600
1400
1200
1000
800
600
400
200
0
Tumor Size, mm3
0 3 6 9 12 15 18 21 24 27 30 33 36
Time, days
Control
500 µg Ab (2.13.2)
10 mg/kg CP-358774
10 mg/kg CP-358774 + Ab

FIG. 16

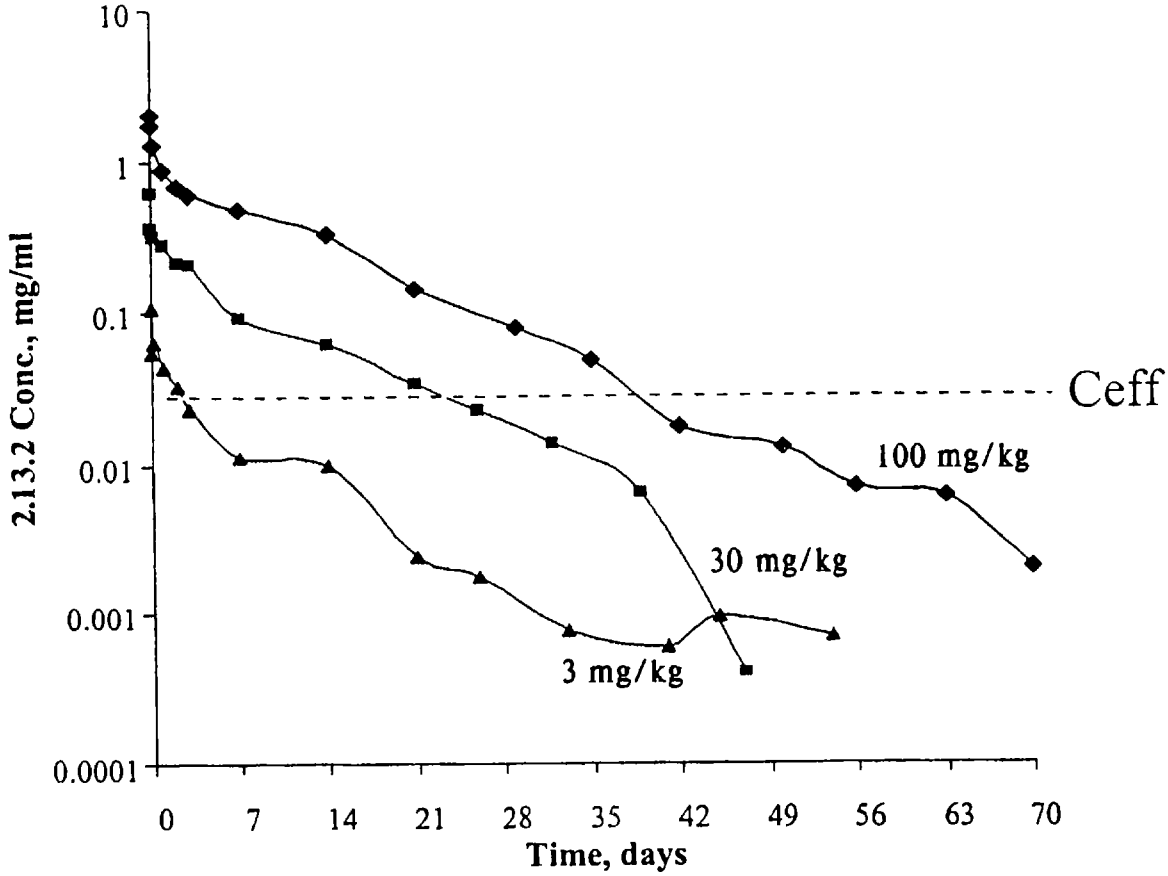

10
1
0.1
0.01
0.001
0.0001
2.13.2 Conc., mg/ml
Ceff
100 mg/kg
30 mg/kg
3 mg/kg
0
7
14
21
28
35
42
49
56
63
70
Time, days

FIG. 17

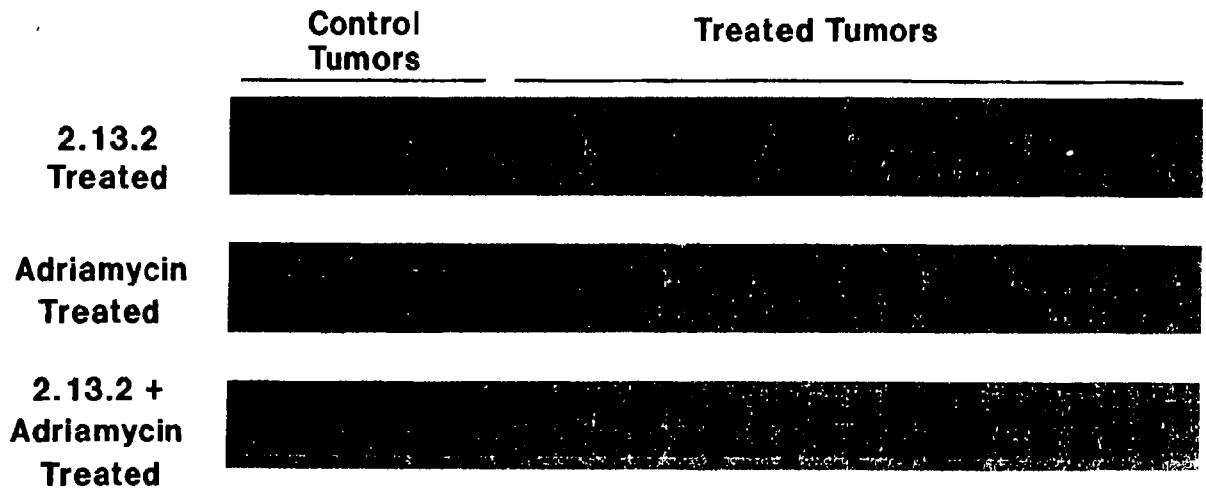

Control Tumors
Treated Tumors
2.13.2 Treated
Adriamycin Treated
2.13.2 + Adriamycin Treated

FIG. 18

Clone	C domain mutations	FR mutation	CDR mutation	Change in Cys	Change in glycosylation
2.13.2 Heavy	0	3	8	0	0
2.13.2 Light	0	1	4	1 (CDR3)	0
2.12.2 Heavy	0	2	8	0	0
2.12.2 Light	0	3	5	0	0

FIG. 19A

```
PF2 2.13.2 Heavy chain (DP-47(3-23)/D6-19/JH6)
                                          +          *                  * *                ++
MEFGLSWLFL VAILKGVQCE VQLLESGGGL VQPGGSLRLS CTASGFTFSS YAMNWVRQAP GKGLEWVSAI SGSGGTTFYA DSVKGRFTIS RDNSRTTLYL
MEFGLSWLFL VAILKGVQCE VQLLESGGGL VQPGGSLRLS CAASGFTFSS YAMSWVRQAP GKGLEWVSAI SGSGGSTYYA DSVKGRFTIS RDNSKNTLYL
                    * *  ***
QMNSLRAEDT AVYYCAK--D LGWSDSYYYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP
QMNSLRAEDT AVYYCAKGYS SGW--YYYYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP

AVLQSSGLYS LSSVVTVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF
AVLQSSGLYS LSSVVTVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF

NWYVDGVEVH NAKTKPREEQ FNSTFRVVSV LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
NWYVDGVEVH NAKTKPREEQ FNSTFRVVSV LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS

DIAVEWESNG QPENNYKTTP PMLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK
DIAVEWESNG QPENNYKTTP PMLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK
```

FIG. 19B

PF2 2.13.2 LC (A30/Jk2)

```
                                +                                                   * *
MDMRVPAQLL GLLLLWFPGA RCDIQMTQFP SSLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAASRLHRGV PSRFSGSGSG TEFTLTISSL
MDMRVPAQLL GLLLLWFPGA RCDIQMTQSP SSLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAASSLQSGV PSRFSGSGSG TEFTLTISSL
                  **
QPEDFATYYC LQHNSYPCSF GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST
QPEDFATYYC LQHNSYPYTF GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST

LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
```

FIG. 19C

PF2 2.12.1 Heavy chain (DP-35(3-11)/D3-3/JH6)

```
                    +                                                          **
MEFGLSWVFL VAIIKGVQCQ AQLVESGGGL VKPGGSLRLS CAASGFTFSD YYMSWIRQAP GKGLEWVSYI SSSGSTRDYA DSVKGRFTIS RDNAKNSLYL
MEFGLSWVFL VAIIKGVQCQ VQLVESGGGL VKPGGSLRLS CAASGFTFSD YYMSWIRQAP GKGLEWVSYI SSSGSTIYYA DSVKGRFTIS RDNAKNSLYL
                  +   *  **  ***
QMNSLRAEDT AVYYCVR--D GVETTF-YYY YYGMDVWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF
QMNSLRAEDT AVYYCARVLR FLEWLLYYYY YYGMDVWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF

PAVLQSSGLY SLSSVVTVPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ
PAVLQSSGLY SLSSVVTVPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ

FNWYVDGVEV HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK TISKTKGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP
FNWYVDGVEV HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK TISKTKGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP

SDIAVEWESN GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLSP GK
SDIAVEWESN GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLSP GK
```

FIG. 19D

PF2.12.1 Light chain (A30/Jk1)

```
                                                +       *   *                       *
MDMRVPAQLL GLLLLWFPGA RCDIQMTQSP SSLSASVGDR VTFTCRASQD IRRDLGWYQQ KPGKAPKRLI YAASRLQSGV PSRFSGSGSG TEFTLTISSL
MDMRVPAQLL GLLLLWFPGA RCDIQMTQSP SSLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAASSLQSGV PSRFSGSGSG TEFTLTISSL
                 *   *       +   +
QPEDFATYYC LQHNNYPRTF GQGTEVEIIR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST
QPEDFATYYC LQHNSYPWTF GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST

LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
```

FIG. 19E

SEQUENCE LISTING

<110> ABGENIX, INC.
PFIZER, INC.

<120> ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

<130> ABX-PF2

<140>
<141>

<150> 60/259,927
<151> 2001-01-05

<160> 60

<170> PatentIn Ver. 2.1

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<211> 291
<212> DNA
<213> Homo sapiens

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tgcatctgta ggagacagag tcaccttcac ttgccgggca agtcaggaca ttagacgtga 60
tttaggctgg tatcagcaga aaccagggaa agctcctaag cgcctgatct atgctgcatc 120
ccgtttacaa agtggggtcc catcaaggtt cagcggcagt ggatctggga cagaattcac 180
tctcacaatc agcagcctgc agcctgaaga ttttgcaact tattactgtc tacagcataa 240
taattatcct cggacgttcg gccaagggac cgaggtggaa atcatacgaa c 291

<210> 2
<211> 136
<212> PRT
<213> Homo sapiens

<400> 2
Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg Ala Ser Gln Asp
1 5 10 15

Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
20 25 30

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
50 55 60

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn
65 70 75 80

Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile Ile Arg
85 90 95

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
100 105 110

```
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
        115                 120                 125

Pro Arg Glu Ala Lys Val Gln Trp
    130                 135
```

<210> 3
<211> 352
<212> DNA
<213> Homo sapiens

<400> 3
gggaggcttg gtcaagcctg gaggtccctg agactctcct gtgcagcctc tggattcact 60
ttcagtgact actatatgag ctggatccgc caggctccag ggaaggggct ggaatgggtt 120
tcatacatta gtagtagtgg tagtaccaga gactacgcag actctgtgaa gggccgattc 180
accatctcca gggacaacgc caagaactca ctgtatctgc aaatgaacag cctgagagcc 240
gaggacacgg ccgtgtatta ctgtgtgaga gatggagtgg aaactacttt ttactactac 300
tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc ag 352

<210> 4
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<213> Homo sapiens

<400> 4

```
Gly Arg Leu Gly Gln Ala Trp Arg Ser Leu Arg Leu Ser Cys Ala Ala
  1               5                  10                  15

Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala
             20                  25                  30

Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser
         35                  40                  45

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

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
 65                  70                  75                  80

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Gly Val Glu Thr Thr
                 85                  90                  95

Phe Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

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

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ser Cys Ala
165 170

<210> 5
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<212> DNA
<213> Homo sapiens

<400> 5
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atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatcccgtt tgcacagagg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtttacaa cataatagtt acccgtgcag ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 6
<211> 107
<212> PRT
<213> Homo sapiens

<400> 6
Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Arg Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Cys
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 7
<211> 375
<212> DNA
<213> Homo sapiens

<400> 7
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cctgtacagc ctctggattc acctttagca gctatgccat gaactgggtc cgccaggctc 120
cagggaaggg gctggagtgg gtctcagcta ttagtggtag tggtggtacc acattctacg 180
cagactccgt gaagggccgg ttcaccatct ccagagacaa ttccaggacc acgctgtatc 240
tgcaaatgaa cagcctgaga gccgaggaca cggccgtata ttactgtgcg aaagatcttg 300
gctggtccga ctcttactac tactactacg gtatggacgt ctggggccaa gggaccacgg 360

tcaccgtctc ctcag 375

<210> 8
<211> 124
<212> PRT
<213> Homo sapiens

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1 5 10 15

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

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

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

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

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

Lys Asp Leu Gly Trp Ser Asp Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 9
<211> 302
<212> DNA
<213> Homo sapiens

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attagacgtg atttaggctg gtatcagcag aaaccaggga aagctcctaa gcgcctgatc 120
tatgctgcat cccgtttaca aagtggggtc ccatcaaggt tcagcggcag tggatctggg 180
acagaattca ctctcacaat cagcagcctg cagcctgaag attttgcaac ttattactgt 240
ctacagcata ataattatcc tcggacgttc ggccaaggga ccgaggtgga aatcatacga 300
ac 302

<210> 10
<211> 100
<212> PRT
<213> Homo sapiens

<400> 10
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg
1 5 10 15

```
Ala Ser Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro
            20                  25                  30

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    50                  55                  60

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
65                  70                  75                  80

Leu Gln His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val
                85                  90                  95

Glu Ile Ile Arg
            100
```

<210> 11
<211> 338
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<213> Homo sapiens

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ctccatcagt aattactact ggagctggat ccggcagccc gccgggaagg gactggagtg 120
gattgggcgt atctatacca gtgggagccc caactacaac ccctccctca agagtcgagt 180
caccatgtca gtagacacgt ccaagaacca gttctccctg aagctgaact ctgtgaccgc 240
cgcggacacg gccgtgtatt actgtgcggt aacgattttt ggagtggtta ttatctttga 300
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Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr
  1               5                  10                  15

Val Ser Gly Gly Ser Ile Ser Asn Tyr Tyr Trp Ser Trp Ile Arg Gln
            20                  25                  30

Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile Tyr Thr Ser Gly
        35                  40                  45

Ser Pro Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Ser Val
    50                  55                  60

Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Asn Ser Val Thr Ala
65                  70                  75                  80

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Val Thr Ile Phe Gly Val Val
                85                  90                  95
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Ile Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 13
<211> 322
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gggaaagccc ctaagcgcct gatctatgct gcatccaaat tacaccgtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagccg cctgcagcct 240
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gggaccaagg tggagatcaa ac 322

<210> 14
<211> 107
<212> PRT
<213> Homo sapiens

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Ser Asp
20 25 30

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

Tyr Ala Ala Ser Lys Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 15
<211> 376
<212> DNA
<213> Homo sapiens

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
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ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtat cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatctg 300
ggctacggtg acttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360

gtcaccgtct cctcag 376

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<211> 125
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<213> Homo sapiens

<400> 16
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Lys Asp Leu Gly Tyr Gly Asp Phe Tyr Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 17
<211> 279
<212> DNA
<213> Homo sapiens

<400> 17
caggagacag agtcaccatc acttgccggg caagtcagag cattagtacc tttttaaatt 60
ggtatcagca gaaaccaggg aaagccccta aactcctgat ccatgttgca tccagtttac 120
aaggtggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc actctcacca 180
tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt tacaatgccc 240
cactcacttt cggcggaggg accaaggtgg agatcaaac 279

<210> 18
<211> 92
<212> PRT
<213> Homo sapiens

<400> 18
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr
1 5 10 15

Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
20 25 30

```
Ile His Val Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser
       35                  40                  45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
     50                  55                  60

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Ala Pro
 65                  70                  75                  80

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                 85                  90
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<210> 19
<211> 341
<212> DNA
<213> Homo sapiens

<400> 19
cccaggactg gtgaagcctt cggagaccct gtccctcacc tgcactgtct ctggtggctc 60
catcagtagt tactactgga gttggatccg gcagccccca gggaagggac tggagtggat 120
tgggtatatc tattacagtg ggagcaccaa ctacaacccc tccctcaaga gtcgagtcac 180
catatcagta gacacgtcca agaaccagtt ctccctgaag ctgagttctg tgaccgctgc 240
ggacacggcc gtgtattact gtgccaggac gtatagcagt tcgttctact actacggtat 300
ggacgtctgg ggccaaggga ccacggtcac cgtctcctca g 341

<210> 20
<211> 113
<212> PRT
<213> Homo sapiens

<400> 20

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Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val
  1               5                  10                  15

Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro
             20                  25                  30

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser
         35                  40                  45

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp
     50                  55                  60

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Ser Ser Ser Phe Tyr
                 85                  90                  95

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
            100                 105                 110

Ser
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<210> 21
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (240)
<223> a, c, t, g, other or unknown

<400> 21
agagccaccc tctcctgtag ggccagtcag agtgttcgcg gcaggtactt agcctggtac 60
cagcagaaac ctggccaggc tcccaggctc ctcatctatg gtgcatccag cagggccact 120
ggcatcccag acaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 180
agactggagc ctgaagattt tgcagtgttt tactgtcagc agtatggtag ttcacctcgn 240
acgttcggcc aagggaccaa ggtggaaatc aaac 274

<210> 22
<211> 91
<212> PRT
<213> Homo sapiens

<400> 22
Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Arg Tyr
1 5 10 15

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
20 25 30

Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
35 40 45

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

Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg
65 70 75 80

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
85 90

<210> 23
<211> 367
<212> DNA
<213> Homo sapiens

<400> 23
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcaggt attactggga gtggtggtag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcca 300
gggactacgg tgattatgag ttggttcgac ccctggggcc agggaaccct ggtcaccgtc 360
tcctcag 367

<210> 24
<211> 122
<212> PRT
<213> Homo sapiens

<400> 24
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Lys Asp Pro Gly Thr Thr Val Ile Met Ser Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 25
<211> 320
<212> DNA
<213> Homo sapiens

<400> 25
gaactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag ttgaaatctg 60
gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc aaagtacagt 120
ggaaggtgga taacgccctc caatcgggta actcccagga gagtgtcaca gagcaggaca 180
gcaaggacag cacctacagc ctcagcagca ccctgacgct gagcaaagca gactacgaga 240
aacacaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc gtcacaaaga 300
gcttcaacag gggagagtgt 320

<210> 26
<211> 106
<212> PRT
<213> Homo sapiens

<400> 26
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

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

```
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
         35                  40                  45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
     50                  55                  60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65                  70                  75                  80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                 85                  90                  95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
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<210> 27
<211> 978
<212> DNA
<213> Homo sapiens

<400> 27
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 60
agcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca 180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc 240
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 300
aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc 360
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc 420
gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc 480
gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt 540
gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 600
aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg 660
cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 720
caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780
gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 840
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 900
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 960
tccctgtctc cgggtaaa 978

<210> 28
<211> 326
<212> PRT
<213> Homo sapiens

<400> 28
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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
  1               5                  10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
             20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
         35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
     50                  55                  60
```

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                 85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

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

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

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320

Ser Leu Ser Pro Gly Lys
                325
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<210> 29
<211> 296
<212> DNA
<213> Homo sapiens

<400> 29
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagaga 296

<210> 30
<211> 98
<212> PRT
<213> Homo sapiens

<400> 30
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

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

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

Ala Arg

<210> 31
<211> 296
<212> DNA
<213> Homo sapiens

<400> 31
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttagc agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga 296

<210> 32
<211> 98
<212> PRT
<213> Homo sapiens

<400> 32
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Lys
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<210> 33
<211> 296
<212> DNA
<213> Homo sapiens

<400> 33
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60
acctgcgctg tctctggtgg ctccatcagc agtagtaact ggtggagttg ggtccgccag 120
cccccaggga aggggctgga gtggattggg gaaatctatc atagtgggag caccaactac 180
aacccgtccc tcaagagtcg agtcaccata tcagtagaca agtccaagaa ccagttctcc 240
ctgaagctga gctctgtgac cgccgcggac acggccgtgt attactgtgc gagaga 296

<210> 34
<211> 98
<212> PRT
<213> Homo sapiens

<400> 34

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

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

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

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

Ala Arg
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<210> 35
<211> 293
<212> DNA
<213> Homo sapiens

<400> 35
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag aga 293

<210> 36
<211> 97
<212> PRT
<213> Homo sapiens

<400> 36
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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

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

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg

<210> 37
<211> 290
<212> DNA
<213> Homo sapiens

<400> 37
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctcc 290

<210> 38
<211> 96
<212> PRT
<213> Homo sapiens

<400> 38
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

<210> 39
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (288)
<223> a, c, t, g, other or unknown

<400> 39
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accctccn 288

<210> 40
<211> 96
<212> PRT
<213> Homo sapiens

<400> 40
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
85 90 95

<210> 41
<211> 288
<212> DNA
<213> Homo sapiens

<400> 41
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcch 288

<210> 42
<211> 96
<212> PRT
<213> Homo sapiens

<400> 42
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

<210> 43
<211> 293
<212> DNA
<213> Homo sapiens

<400> 43
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120
gccgggaagg gactggagtg gattgggcgt atctatacca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc cgcggacacg gccgtgtatt actgtgcgag aga 293

<210> 44
<211> 97

<212> PRT
<213> Homo sapiens

<400> 44
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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

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

Gly Arg Ile Tyr Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg

<210> 45
<211> 470
<212> PRT
<213> Homo sapiens

<400> 45
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Thr Thr Phe Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Asp Leu Gly Trp Ser Asp Ser Tyr Tyr Tyr Tyr
115 120 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
130 135 140

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145                 150                 155                 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
    210                 215                 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
305                 310                 315                 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470


<210> 46
<211> 470
<212> PRT
<213> Homo sapiens

<400> 46
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
  1               5                  10                  15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
             20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
         35                  40                  45

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

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
 65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                 85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Lys Gly Tyr Ser Ser Gly Trp Tyr Tyr Tyr Tyr Tyr
        115                 120                 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140

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

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
    210                 215                 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240
```

```
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
305                 310                 315                 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470


<210> 47
<211> 236
<212> PRT
<213> Homo sapiens

<400> 47
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
  1               5                  10                  15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser
             20                  25                  30
```

```
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
         35                  40                  45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
     50                  55                  60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu His Arg Gly Val
 65                  70                  75                  80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                 85                  90                  95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
            100                 105                 110

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 48
<211> 236
<212> PRT
<213> Homo sapiens

<400> 48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
  1               5                  10                  15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
             20                  25                  30

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

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
     50                  55                  60
```

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                85                  90                  95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
            100                 105                 110

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 49
<211> 470
<212> PRT
<213> Homo sapiens

<400> 49
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
  1               5                  10                  15

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
         35                  40                  45

Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
     50                  55                  60

Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Arg Asp Tyr Ala
 65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95
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```
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Val Arg Asp Gly Val Glu Thr Thr Phe Tyr Tyr Tyr Tyr
        115                 120                 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140

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

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
    210                 215                 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
305                 310                 315                 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
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```
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470


<210> 50
<211> 473
<212> PRT
<213> Homo sapiens

<400> 50
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
  1               5                  10                  15

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
         35                  40                  45

Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
     50                  55                  60

Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala
 65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                 85                  90                  95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Val Leu Arg Phe Leu Glu Trp Leu Leu Tyr Tyr
        115                 120                 125

Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
    130                 135                 140

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

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190
```

```
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
    210                 215                 220

Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
225                 230                 235                 240

Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
    290                 295                 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 51
<211> 236

<212> PRT
<213> Homo sapiens

<400> 51
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
100 105 110

His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile
115 120 125

Ile Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 52
<211> 236
<212> PRT
<213> Homo sapiens

<400> 52
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30

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

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
    50                  55                  60

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                85                  90                  95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
            100                 105                 110

His Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                 120                 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 53
<211> 326
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<220>
<221> modified_base
<222> (289)
<223> a, c, t, g, other or unknown
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<400> 53
gacatccaga tgacccagty tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
wtcacttgcc gggcaagtca ggrcattaga mrtgatttag gctggtwtca gcagaaacca 120
gggaaagcyc ctaagcgcct gatctatgct gcatccmrwt trcammgwgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcmg cctgcagcct 240
gaagattttg caacttatta ctgtytacar cataatartt aycckybsns kttyggcsrr 300
gggaccrags tggaratcaw acgaac 326

<210> 54
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 54
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgyaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagy asctwtttaa attggtatca gcagaaacca 120
gggaaagccc ctaarctcct gatcyatgyt gcatccagtt trcaargtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacartr ccccayychc tttcggcgga 300
gggaccaagg tggagatcaa ac 322

<210> 55
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<220>
<221> modified_base
<222> (291)
<223> a, c, t, g, other or unknown

<400> 55
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgya gggccagtca gagtgttmgc rgcagstact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtw ttactgtcag cagtatggta gytcacctcs nacgttcggc 300
caagggacca aggtggaaat caaac 325

<210> 56
<211> 376
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 56
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt cacyttcagt gactactaya tgagctggat ccgccaggct 120
ccagggaagg ggctggartg ggtttcatac attagtagta gtggtagtac cakakactac 180
gcagactctg tgaagggccc attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgy gagagatgga 300
gtggaaacta ctttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360
gtcaccgtct cctcag 376

<210> 57
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<220>
<221> modified_base
<222> (337)
<223> a, c, t, g, other or unknown

<400> 57
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt arttactact ggagctggat ccggcagccc 120
gccgggaagg gactggagtg gattgggcgt atctatacca gtgggagcmc caactacaac 180
ccctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240
aagctgarct ctgtgaccgc cgcggacacg gccgtgtatt actgtgcggt aacgattttt 300
ggagtggtta ttatctttga ctactggggc cagrganccc tggtcaccgt ctcctcag 358

<210> 58
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 58
caggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
tcctgtrcag cctctggatt caccttttagc agctatgcca tgarctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagst attastggka gtggtggtab yacatwctac 180
gcagactccg tgaagggccc gttcaccatc tccagagaca attccargam cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatctk 300
ggctrsksyg actyttacta ctactactac ggtatggacg tctggggcca agggacyacg 360
gtgattatga gttggttcga cccctggggc cagggaaccc tggtcaccgt ctcctcag 418

<210> 59
<211> 364
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 59
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttactact ggagytggat ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgact caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagyt ctgtgaccgc tgcggacacg gccgtgtatt actgtgccag gacgtatagc 300
agttcgttct actactacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360
tcag 364

<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly-Ser Linker

<400> 60
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Applicants : PFIZER INC., et al.

Filed : 20 December 2001 (20.12.01)

Title : ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

Agent's Ref. : ABX-PF/2 PCT

Indications Relating to the Expert Solution in Respect of Deposited Biological Material Referred to in the Description

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 4.9.2 in the description on

page 75, lines 8-18

The deposit was made in:

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

on December 12, 2000, under Accession Number PTA 2789.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by

the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

Applicants	:	PFIZER INC., et al.
Filed	:	20 December 2001 (20.12.01)
Title	:	ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
Agent's Ref.	:	ABX-PF/2 PCT

Indications Relating to the Expert Solution in Respect of Deposited Biological Material Referred to in the Description

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 4.17.3 in the description on

page 75, lines 8-18

The deposit was made in:

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

on December 12, 2000, under Accession Number PTA 2793.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by

the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

Applicants	:	PFIZER INC., et al.
Filed	:	20 December 2001 (20.12.01)
Title	:	ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
Agent's Ref.	:	ABX-PF/2 PCT

Indications Relating to the Expert Solution in Respect of Deposited Biological Material Referred to in the Description

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 2.12.1 in the description on

page 75, lines 8-18

The deposit was made in:

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

on December 12, 2000, under Accession Number PTA 2792.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by

the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

Applicants	:	PFIZER INC., et al.
Filed	:	20 December 2001 (20.12.01)
Title	:	ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
Agent's Ref.	:	ABX-PF/2 PCT

Indications Relating to the Expert Solution in Respect of Deposited Biological Material Referred to in the Description

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 2.13.2 in the description on

page 75, lines 8-18

The deposit was made in:

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

on December 12, 2000, under Accession Number PTA 2788.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by

the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

Applicants	:	PFIZER INC., et al.
Filed	:	20 December 2001 (20.12.01)
Title	:	ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
Agent's Ref.	:	ABX-PF/2 PCT

Indications Relating to the Expert Solution in Respect of Deposited Biological Material Referred to in the Description

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 2.14.3 in the description on

page 75, lines 8-18

The deposit was made in:

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

on December 12, 2000, under Accession Number PTA 2790.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by

the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

Applicants	:	PFIZER INC., et al.
Filed	:	20 December 2001 (20.12.01)
Title	:	ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
Agent's Ref.	:	ABX-PF/2 PCT

Indications Relating to the Expert Solution in Respect of Deposited Biological Material Referred to in the Description

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 3.1.1 in the description on

page 75, lines 8-18

The deposit was made in:

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

on December 12, 2000, under Accession Number PTA 2791.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by

the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.