FIGURE 1


```
        10         20         30         40         50
CAACTCAGTCCCACGTTTCGCGCGTTTCGGTGATGACGGTGAAAACCTCT

        60         70         80         90        100
GACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCC

       110        120        130        140        150
GGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCG

       160        170        180        190        200
GGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACC

       210        220        230        240        250
ATAATCCTTTTCATGGAGATTGTATTATATGTGAGAATCGTTTACCCATA

       260        270        280        290        300
AAGGGTAAAATTATTAATTTTTTTTTTTTTTCAAATTTTAACGTTAAAGC

       310        320        330        340        350
-------GCAAATACCTTAATATCTGGATTTTTAATTTTTTTTGTAATTTA

       360        370        380        390        400
AAAAATGATAATTAAAGTAATAATAAAAAATAAAAAAACAATTAAAAAAA

       410        420        430        440        450
AAACCAATAGCCTATTGGTTTTATTTTTTTTTTTTTTAAGGTCGGATAAAG

       460        470        480        490        500
ATCAACAACCATTAAAAAAAAAGTAATTAAATTTTATTATACATTTAAAT

       510        520        530        540        550
ATTATTATTGTTATATTATTATTATTATTTTTATGTGAAGCACTTTCATC

       560        570        580        590        600
ATGATTTAGAAACATTTTCTGTGGACAATTGATGGACCAGATTCATCATA

       610        620        630        640        650
TTCTTCTTTTTGAGATCCACATTTGTTGGAAAGTTGAGAGTGAAGCTAAAA

       660        670        680        690        700
TAGATCCACCAATCCAGACAGAGTATTTACGTTCTGGTGGAGCAATGATT

       710        720        730        740        750
TTAATTTTCATGGTTGATGGTGCTAAAGCAGTTAATTCTTTGTTCATACG

       760        770        780        790        800
ATCAGCAATACCTGGGAACATAGTTGTACCACCTGATAAGACGACATTAC

       810        820        830        840        850
CGTATAAATCTTTACGGATGATCCCTGTAATCCGGGCAGCGCAACGGAAC

       860        870        880        890        900
ATTCATCAGTGTAAAAATGGAATCAATAAAGCCCTGCGCAGCGCGCAGGG

       910        920        930        940        950
TCAGCCTGAATACGCGTTTAATGACCAGCACAGTCGTGATGGCAAGGTCA
```

FIGURE 1

960 970 980 990 1000
GAATAGCGCTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCA

1010 1020 1030 1040 1050
GGCCTGAATCGCCCCATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGA

1060 1070 1080 1090 1100
TGAGAGCTTTGTTGTAGGTGGACCAGTTGGTGATTTTGAACTTTTGCTTT

1110 1120 1130 1140 1150
GCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTGATCTGATCCTTCAA

1160 1170 1180 1190 1200
CTCAGCAAAAGTTCGATTTATTCAACAAAGCCGCCGTCCCGTCAAGTCAG

1210 1220 1230 1240 1250
CGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATTAGAAAA

1260 1270 1280 1290 1300
ACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCA

1310 1320 1330 1340 1350
ATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACC

1360 1370 1380 1390 1400
GAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGA

1410 1420 1430 1440 1450
CTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGG

1460 1470 1480 1490 1500
TTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGG

1510 1520 1530 1540 1550
CAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTAC

1560 1570 1580 1590 1600
GCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGAT

1610 1620 1630 1640 1650
TGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACA

1660 1670 1680 1690 1700
AACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAA

1710 1720 1730 1740 1750
TATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTC

1760 1770 1780 1790 1800
CCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAA

1810 1820 1830 1840 1850
ATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGA

1860 1870 1880 1890 1900
CCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGA

1910 1920 1930 1940 1950
AACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACC

1960 1970 1980 1990 2000
TGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCAT

2010 2020 2030 2040 2050
CCATGTTGGAATTTAATCGCGGCCTTGTTTTAAGAAATAAGAAAAAAAAA

2060 2070 2080 2090 2100
AAAAAAAAATCTTTTTATGCAATCTGAAAAAAAAAAAAAAAAAAAAAAA

2110 2120 2130 2140 2150
AAAAAAAAAAAAAAAAAAAAAATTTTTGAATCCCATTTTTTTT..TTAAT

2160 2170 2180 2190 2200
TTGGGTTTTAAAATTTTCAAATAATAATTAACCAACCCAAGTTTTTTTAA

2210 2220 2230 2240 2250
ACCATTTTTTTTTTTAAAGATTTGATGGGATTAATTAATTTGTAATCTAT

2260 2270 2280 2290 2300
TTAATTCAAAATAAATAAAAATAAATAAAAATTTTTTTTTATCGATCTCGA

2310 2320 2330 2340 2350
GACTAGAGAGGTTTATTTTTAAAAATTACAAAAACTAAAAAGAAAAATAA

2360 2370 2380 2390 2400
AAAGGAAAAATCTTATTAATCTGAAAATTACAGATTTGCCCCAATTTAAA

2410 2420 2430 2440 2450
GAAAAATTATCCAAAATAATCAATCAACAACGATATCTTTTTGATAGATA

2460 2470 2480 2490 2500
TTTATAAAAACTTTATCTTTTTTTATTTTTTCAAGTTGCGCAAAATAATAA

2510 2520 2530 2540 2550
AATTAAAATAAATATAAAAACTGTAAAAAGAAAAAAAAAAGTGTAAAGGT

2560 2570 2580 2590 2600
TTATTAATTATTTAATTATTATTCACTTTTTGTAATTATTTTTTTATTTT

2610 2620 2630 2640 2650
GAAGAATAATGATGGATATTTTATATAAAAAAAAAAAGAGATACTGAAAA

2660 2670 2680 2690 2700
AATAATAATTATAAAAAAAAAAAAAAAAAATAGAATTTTAAAGTTTTAGT

2710 2720 2730 2740 2750
ACAAATGGATGATTTTTTTTTTTTTTTTTTTTTTTTCCCAAATAATTCAA

2760 2770 2780 2790 2800
GTAATAACAACAAAGAACGGATATTCTGATGCCTAATTAAAAAAGAAATT

2810 2820 2830 2840 2850
TTTAAATAAAAAATGGGTTTTTTTTAAGTAAAGTTATTTGAAATTGATTG

FIGURE 1

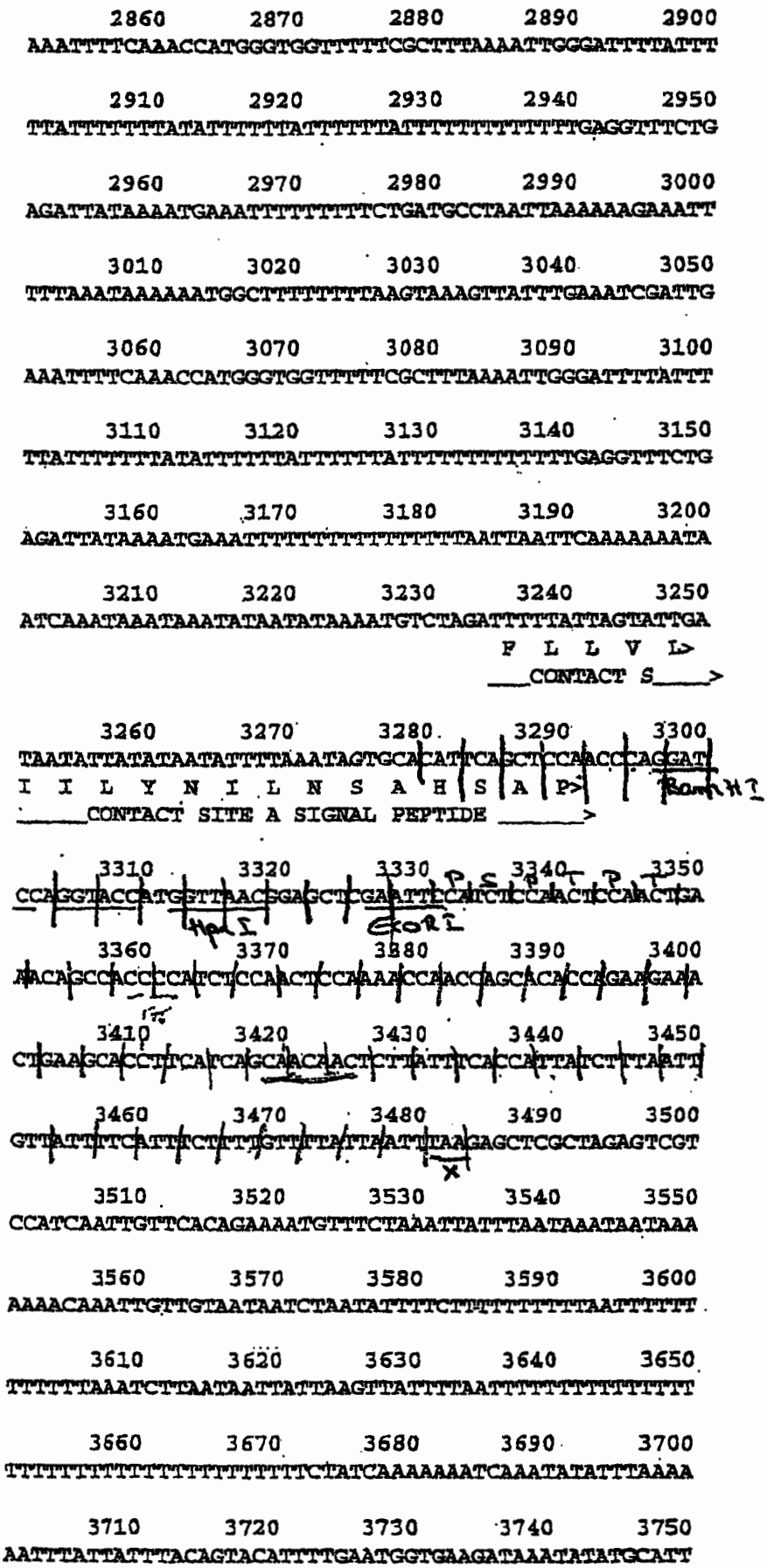

2860 2870 2880 2890 2900
AAATTTTCAAACCATGGGTGGTTTTTCGCTTTAAAATTGGGATTTTATTT
2910 2920 2930 2940 2950
TTATTTTTTTTATATTTTTTATTTTTTATTTTTTTTTTTTTGAGGTTTCTG
2960 2970 2980 2990 3000
AGATTATAAAATGAAATTTTTTTTTTCTGATGCCTAATTAAAAAAGAAATT
3010 3020 3030 3040 3050
TTTAAATAAAAAATGGCTTTTTTTTTAAGTAAAGTTATTTGAAATCGATTG
3060 3070 3080 3090 3100
AAATTTTCAAACCATGGGTGGTTTTTCGCTTTAAAATTGGGATTTTATTT
3110 3120 3130 3140 3150
TTATTTTTTTATATTTTTTATTTTTTATTTTTTTTTTTTTGAGGTTTCTG
3160 3170 3180 3190 3200
AGATTATAAAATGAAATTTTTTTTTTTTTTTTTTTAATTAATTCAAAAAAATA
3210 3220 3230 3240 3250
ATCAAATAAATAAATATAATATAAAATGTCTAGATTTTTATTAGTATTGA
F L L V L>
___CONTACT S____>
3260 3270 3280 3290 3300
TAATATTATATAATATTTTAAATAGTGCACATTCAGCTCCAACCCAGGAT
I I L Y N I L N S A H S A P>
_____CONTACT SITE A SIGNAL PEPTIDE _____>
3310 3320 3330 3340 3350
CCAGGTACCATGGTTAACGGAGCTCGAATTCATCTCCAACTCCAACTCA
HpaI
EcoRI
3360 3370 3380 3390 3400
AACAGCCACCCCATCTCCAACTCCAAAACCAACCAGCACACCAGAAGAAA
3410 3420 3430 3440 3450
CTGAAGCACCTTCATCAGCAACAACTCTTATTCACCATTATCTTTAATT
3460 3470 3480 3490 3500
GTTATTTCATTTCTTTGTTTTATTAATTAAGAGCTCGCTAGAGTCGT
X
3510 3520 3530 3540 3550
CCATCAATTGTTCACAGAAAATGTTTCTAAATTATTTAATAAATAATAAA
3560 3570 3580 3590 3600
AAAACAAATTGTTGTAATAATCTAATATTTTCTTTTTTTTTTAATTTTTT
3610 3620 3630 3640 3650
TTTTTTAAATCTTAATAATTATTAAGTTATTTTAATTTTTTTTTTTTTT
3660 3670 3680 3690 3700
TTTTTTTTTTTTTTTTTTTTTTTTCTATCAAAAAAATCAAATATATTTAAAA
3710 3720 3730 3740 3750
AATTTATTATTTACAGTACATTTTGAATGGTGAAGATAAATATATGCATT

FIGURE 1


```
      3760       3770       3780       3790       3800
AGATGTAAAAGGCGACTGGTCGTCCATCAATTGTTCACAGAAAATGTTTC

      3810       3820       3830       3840       3850
TAAATTATTTAATAAATAATAAAAAAACAAATTGTTGTAATAATCTAATA

      3860       3870       3880       3890       3900
TTTTCTTTTTTTTTTTAATTTTTTTTTTTTTTAAATCTTAATAATTATTAAGT

      3910       3920       3930       3940       3950
TATTTTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTATC

      3960       3970       3980       3990       4000
AAAAAAATCAAATATATTTAAAAAATTTATTATTTACAGTACATTTTGAA

      4010       4020       4030       4040       4050
TGGTGAAGATAAATATATGCATTAGATGTAAAAGGCGACTCGAAAGCTTG

      4060       4070       4080       4090       4100
GCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC

      4110       4120       4130       4140       4150
AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTG

      4160       4170       4180       4190       4200
CCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT

      4210       4220       4230       4240       4250
TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG

      4260       4270       4280       4290       4300
CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCA

      4310       4320       4330       4340       4350
CTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCAC

      4360       4370       4380       4390       4400
TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA

      4410       4420       4430       4440       4450
GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCG

      4460       4470       4480       4490       4500
CGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAA

      4510       4520       4530       4540       4550
AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA

      4560       4570       4580       4590       4600
CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCC

      4610       4620       4630       4640       4650
TGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCG

      4660       4670       4680       4690       4700
CTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG
```

```
      4710       4720       4730       4740       4750
CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCG

      4760       4770       4780       4790       4800
CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA

      4810       4820       4830       4840       4850
TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT

      4860       4870       4880       4890       4900
AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA

      4910       4920       4930       4940       4950
GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA

      4960       4970       4980       4990       5000
AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGG

      5010       5020       5030       5040       5050
TGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTC

      5060       5070       5080       5090       5100
AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAA

      5110       5120       5130       5140       5150
AACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCAC

      5160       5170       5180       5190       5200
CTAGATCCTTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATAT

      5210       5220       5230       5240       5250
ATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCTGTGAGGCACCT

      5260       5270       5280       5290       5300
ATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGT

      5310       5320       5330       5340       5350
CGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTG

      5360       5370       5380       5390       5400
CAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATA

      5410       5420       5430       5440       5450
AACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATC

      5460       5470       5480       5490       5500
CGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTT

      5510       5520       5530       5540       5550
CGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTG

      5560       5570       5580       5590       5600
GTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACG

      5610       5620       5630       5640       5650
ATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCT
```

FIGURE 1


```
      5660       5670       5680       5690       5700
CCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCA

      5710       5720       5730       5740       5750
CTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGT

      5760       5770       5780       5790       5800
AAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAAT

      5810       5820       5830       5840       5850
AGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAAT

      5860       5870       5880       5890       5900
ACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTC

      5910       5920       5930       5940       5950
TTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGA

      5960       5970       5980       5990       6000
TGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACC

      6010       6020       6030       6040       6050
AGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGG

      6060       6070       6080       6090       6100
AATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAAT

      6110       6120       6130       6140       6150
ATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTT

      6160       6170       6180       6190       6200
GAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCG

      6210       6220       6230       6240       6250
AAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCT

      6260       6270       6280
ATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
```

FIGURE 1

Sequence Range: 1 to 6283

Enzyme	#Cuts	Positions					
BamHI	1	3297					
BcoI	2	1750	2296				
BglI	1	5416					
BscCI	2	1667	1744				
BsiBI	1	448					
BsiLI	10	762	999	1378	1735	3295	3302
		4143	4431	4552	4565		
BsiXI	3	1933	2291	3044			
BsiZI	7	584	1078	5338	5417	5434	5656
		6272					
ClaI	3	1933	2291	3044			
EcoRI	1	3326					
EcoRV	1	2434					
HindIII	2	1504	4044				
HpaI	1	3315					
KpnI	1	3308					
NciI	8	65	100	833	1751	1752	4783
		5479	5830				
NcoI	3	2862	3062	3308			
NruI	1	1969					
PvuII	1	4227					
RsaI	8	186	777	1791	2700	3306	3717
		3990	5776				
SacI	2	3324	3488				
SmaI	1	1752					
StuI	1	1002					
XbaI	1	3229					
XhoI	1	2296					

FIGURE 1

BglII
BsiCI
BsiMI
BsiQI
NotI
PstI
SacII
SalI
SfiI
SpeI
SphI

FIGURE 2

cag gat cca TTT
TCTGGAAGTG AGGCCACAGC AGCTATCCTT AGCAGAGCAC CCTGGAGTCT
GCAAAGTGTT AATCCAGGCC TAAAGACAAA TTCTTCTAAG GAGCCTAAAT
TCACCAAGTG CCGTTCACCT GAGCGAGAGA CTTTTTCATG CCACTGGACA
GATGAGGTTC ATCATGGTAC AAAGAACCTA GGACCCATAC AGCTGTTCTA
TACCAGAAGG AACACTCAAG AATGGACTCA AGAATGGAAA GAATGCCCTG
ATTATGTTTC TGCTGGGGAA AACAGCTGTT ACTTTAATTC ATCGTTTACC
TCCATCTGGA TACCTTATTG TATCAAGCTA ACTAGCAATG GTGGTACAGT
GGATGAAAAG TGTTTCTCTG TTGATGAAAT AGTGCAACCA GATCCACCCA
TTGCCCTCAA CTGGACTTTA CTGAACGTCA GTTTAACTGG GATTCATGCA
GATATCCAAG TGAGATGGGA AGCACCACGC AATGCAGATA TTCAGAAAGG
ATGGATGGTT CTGGAGTATG AACTTCAATA CAAAGAAGTA AATGAAACTA
AATGGAAAAT GATGGACCCT ATATTGACAA CATCAGTTCC AGTGTACTCA
TTGAAAGTGG ATAAGGAATA TGAAGTACGC GTGAGATCCA AACAACGAAA
CTCTGGAAAT TATGGCGAGT TCAGTGAGGT GCTCTATGTA ACACTTCCTC
AGATGAGCCA ATTTACATGT GAAGAAGATT TCTAC cga att cca

FIGURE 3


```
  1  TTTTCTGGAA GTGAGGCCAC AGCAGCTATC CTTAGCAGAG CACCCTGGAG
 51  TCTGCAAAGT GTTAATCCAG GCCTAAAGAC AAATTCTTCT AAGGAGCCTA
101  AATTCACCAA GTGCCGTTCA CCTGAGCGAG AGACTTTTTC ATGCCACTGG
151  ACAGATGAGG TTCATCATGG TACAAAGAAC CTAGGACCCA TACAGCTGTT
201  CTATACCAGA AGGAACACTC AAGAATGGAC TCAAGAATGG AAAGAATGCC
251  CTGATTATGT TTCTGCTGGG GAAAACAGCT GTTACTTTAA TTCATCGTTT
301  ACCTCCATCT GGATACCTTA TTGTATCAAG CTAACTAGCA ATGGTGGTAC
351  AGTGGATGAA AAGTGTTTCT CTGTTGATGA AATAGTGCAA CCAGATCCAC
401  CCATTGCCCT CAACTGGACT TTACTGAACG TCAGTTTAAC TGGGATTCAT
451  GCAGATATCC AAGTGAGATG GGAAGCACCA CGCAATGCAG ATATTCAGAA
501  AGGATGGATG GTTCTGGAGT ATGAACTTCA ATACAAAGAA GTAAATGAAA
551  CTAAATGGAA AATGATGGAC CCTATATTGA CAACATCAGT TCCAGTGTAC
601  TCATTGAAAG TGGATAAGGA ATATGAAGTA CGCGTGAGAT CCAAACAACG
651  AAACTCTGGA AATTATGGCG AGTTCAGTGA GGTGCTCTAT GTAACACTTC
701  CTCAGATGAG CCAATTTACA TGTGAAGAAG ATTTCTACcg aattccaTct
751  ccaactccaa ctgaaacagc caccccatct ccaactccaA aaccaaccag
801  cacaccagaa gaaactgaag caccttcatc agcaAcaact cttatttcac
851  cattatcttt aattgttatt ttcattTctt ttgttttatt aatttaa

  1  FSGSEATAAI LSRAPWSLQS VNPGLKTNSS KEPKFTKCRS PERETFSCHW
 51  TDEVHHGTKN LGPIQLFYTR RNTQEWTQEW KECPDYVSAG ENSCYFNSSF
101  TSIWIPYCIK LTSNGGTVDE KCFSVDEIVQ PDPPIALNWT LLNVSLTGIH
151  ADIQVRWEAP RNADIQKGWM VLEYELQYKE VNETKWKMMD PILTTSVPVY
201  SLKVDKEYEV RVRSKQRNSG NYGEFSEVLY VTLPQMSQFT CEEDFYRIPS
251  PTPTETATPS PTPKPTSTPE ETEAPSSATT LISPLSLIVI FISFVLLI*
```



FIGURE 4

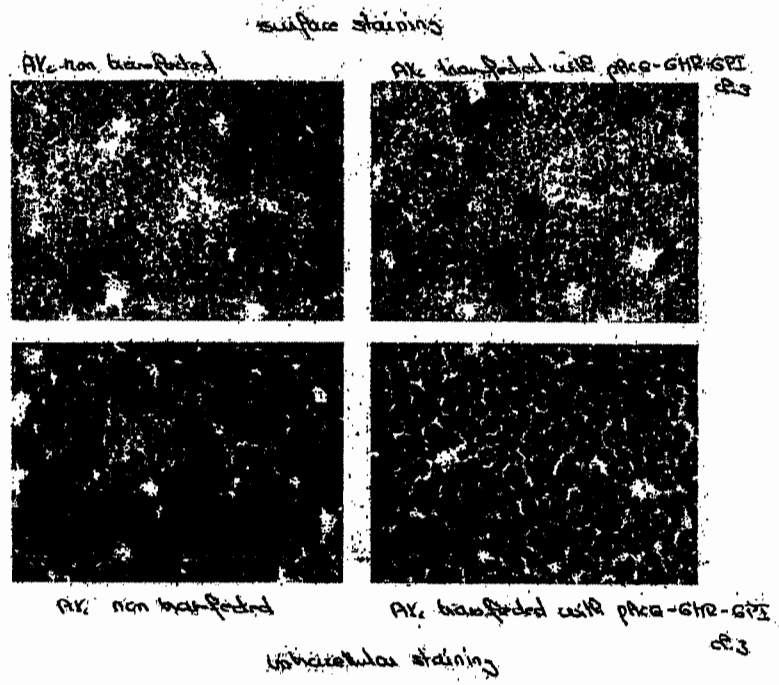


FIGURE 5

FIGURE 6

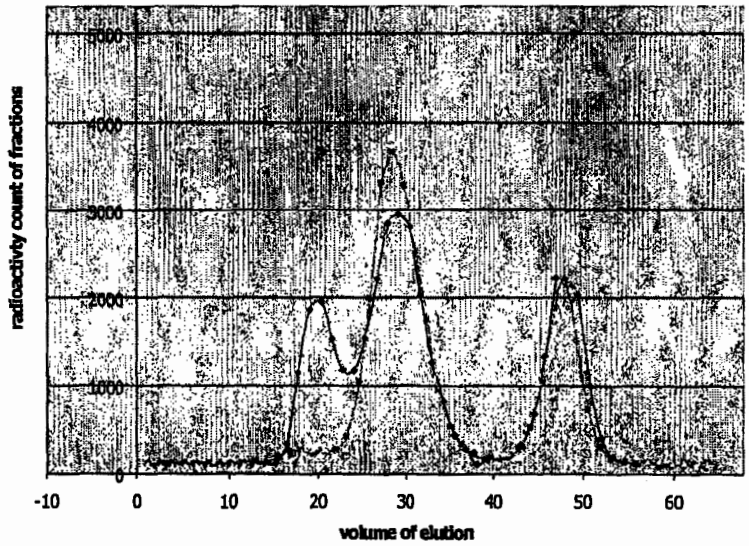

radioactivity count of fractions
0
1000
2000
3000
-10
0
10
20
30
40
50
60
volume of elution

FIGURE 7

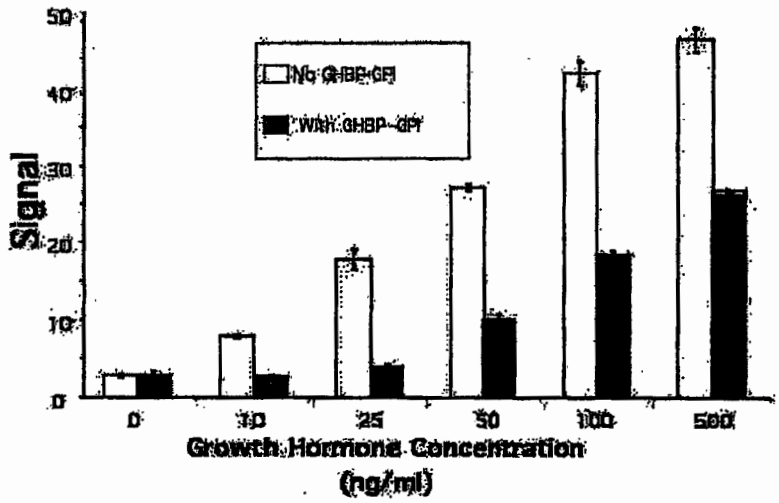

50
40
30
20
10
0
Signal
No GHBP-GFI
With GHBP-GFI
0
10
25
50
100
500
Growth Hormone Concentration
(ng/ml)

FIGURE 8


```
   1 GCGCGCGTTG ACATTGATTA TTGACTAGTT ATTAATAGTA ATCAATTACG GGGTCATTAG
  61 TTCATAGCCC ATATATGGAG TTCCGCGTTA CATAACTTAC GGTAAATGGC CCGCCTGGCT
 121 GACCGCCCAA CGACCCCCGC CCATTGACGT CAATAATGAC GTATGTTCCC ATAGTAACGC
 181 CAATAGGGAC TTTCCATTGA CGTCAATGGG TGGACTATTT ACGGTAAACT GCCCACTTGG
 241 CAGTACATCA AGTGTATCAT ATGCCAAGTA CGCCCCCTAT TGACGTCAAT GACGGTAAAT
 301 GGCCCGCCTG GCATTATGCC CAGTACATGA CCTTATGGGA CTTTCCTACT TGGCAGTACA
 361 TCTACGTATT AGTCATCGCT ATTACCATGG TGATGCGGTT TTGGCAGTAC ATCAATGGGC
 421 GTGGATAGCG GTTTGACTCA CGGGGATTTC CAAGTCTCCA CCCCATTGAC GTCAATGGGA
 481 GTTTGTTTTG GCACCAAAAT CAACGGGACT TTCCAAAATG TCGTAACAAC TCCGCCCCAT
 541 TGACGCAAAT GGGCGGTAGG CGTGTACGGT GGGAGGTCTA TATAAGCAGA GCTCTCTGGC
 601 TAACTAGAGA ACCCACTGCT TACTGGCTTA TCGAAATTAA TACGACTCAC TATAGGGAGA
 661 CCCAAGCTTG GTACCGAGCT CGGATCCACT AGTAACGGCC GCCAGTGTGC TGGAATTCTG
 721 CAGATATCGA CAAGCTGGTC AAGTGTGGCG GCATAAGCCT GCTGGTTCAG AACACATCCT
 781 GGATGCTGCT GCTGCTGCTT TCCCTCTCCC TCCTCCAAGC CCTAGACTTC ATTTCTCTGT
 841 GACTCGAGCA TGCATCTAGA GGGCCCTATT CTATAGTGTC ACCTAAATGC TAGAGCTCGC
 901 TGATCAGCCT CGACTGTGCC TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTCCCCCGTG
 961 CCTTCCTTGA CCCTGGAAGG TGCCACTCCC ACTGTCCTTT CCTAATAAAA TGAGGAAATT
1021 GCATCGCATT GTCTGAGTAG GTGTCATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC
1081 AAGGGGGAGG ATTGGGAAGA CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGCT
1141 TCTGAGGCGG AAAGAACCAG TGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC
1201 AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT
1261 GCTGGCGTTT TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG
1321 TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC
1381 CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTTCTCCC
1441 TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT CGGTGTAGGT
1501 CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT
1561 ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC
1621 AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
1681 GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA
1741 GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA CCACCGCTGG
1801 TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG GATCTCAAGA
1861 AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG
1921 GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG
1981 AAGTTTTAAA TCAATCTAAA GTATATATGA GTAACCTGAG GCTATGGCAG GGCCTGCCGC
2041 CCCGACGTTG GCTGCGAGCC CTGGGCCTTC ACCCGAACTT GGGGGGTGGG GTGGGGAAAA
2101 GGAAGAAACG CGGGCGTATT GGCCCCAATG GGGTCTCGGT GGGGTATCGA CAGAGTGCCA
2161 GCCCTGGGAC CGAACCCCGC GTTTATGAAC AAACGACCCA ACACCGTGCG TTTTATTCTG
2221 TCTTTTTTATT GCCGTCATAG CGCGGGTTCC TTCCGGTATT GTCTCCTTCC GTGTTTCAGT
2281 TAGCCTCCCC CTAGGGTGGG CGAAGAACTC CAGCATGAGA TCCCCGCGCT GGAGGATCAT
2341 CCAGCCGGCG TCCCGGAAAA CGATTCCGAA GCCCAACCTT TCATAGAAGG CGGCGGTGGA
2401 ATCGAAATCT CGTGATGGCA GGTTGGGCGT CGCTTGGTCG GTCATTTCGA ACCCCAGAGT
2461 CCCGCTCAGA AGAACTCGTC AAGAAGGCGA TAGAAGGCGA TGCGCTGCGA ATCGGGAGCG
2521 GCGATACCGT AAAGCACGAG GAAGCGGTCA GCCCATTCGC CGCCAAGCTC TTCAGCAATA
2581 TCACGGGTAG CCAACGCTAT GTCCTGATAG CGGTCCGCCA CACCCAGCCG GCCACAGTCG
2641 ATGAATCCAG AAAAGCGGCC ATTTTCCACC ATGATATTCG GCAAGCAGGC ATCGCCATGG
2701 GTCACGACGA GATCCTCGCC GTCGGGCATG CTCGCCTTGA GCCTGGCGAA CAGTTCGGCT
2761 GGCGCGAGCC CCTGATGCTC TTGATCATCC TGATCGACAA GACCGGCTTC CATCCGAGTA
2821 CGTGCTCGCT CGATGCGATG TTTCGCTTGG TGGTCGAATG GGCAGGTAGC CGGATCAAGC
2881 GTATGCAGCC GCCGCATTGC ATCAGCCATG ATGGATACTT TCTCGGCAGG AGCAAGGTGA
2941 GATGACAGGA GATCCTGCCC CGGCACTTCG CCCAATAGCA GCCAGTCCCT TCCCGCTTCA
3001 GTGACAACGT CGAGCACAGC TGCGCAAGGA ACGCCCGTCG TGGCCAGCCA CGATAGCCGC
3061 GCTGCCTCGT CTTGCAGTTC ATTCAGGGCA CCGGACAGGT CGGTCTTGAC AAAAAGAACC
3121 GGGCGCCCCT GCGCTGACAG CCGGAACACG GCGGCATCAG AGCAGCCGAT TGTCTGTTGT
3181 GCCCAGTCAT AGCCGAATAG CCTCTCCACC CAAGCGGCCG GAGAACCTGC GTGCAATCCA
3241 TCTTGTTCAA TCATGCGAAA CGATCCTCAT CCTGTCTCTT GATCGATCTT TGCAAAAGCC
3301 TAGGCCTCCA AAAAAGCCTC CTCACTACTT CTGGAATAGC TCAGAGGCCG AGGCGGCCTC
3361 GGCCTCTGCA TAAATAAAAA AAATTAGTCA GCCATGGGGC GGAGAATGGG CGGAACTGGG
3421 CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT ATGGTTGCTG ACTAATTGAG
```

FIGURE 8 (continued)


```
3481 ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG GACTTTCCAC ACCTGGTTGC
3541 TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT GGGGAGCCTG GGGACTTTCC
3601 ACACCCTAAC TGACACACAT TCCACAGCTG GTTCTTTCCG CCTCAGGACT CTTCCTTTTT
3661 CAATAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT
3721 CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCGTTCA TCCATAGTTG CCTGACTCCC
3781 CGTCGTGTAG ATAACTACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT
3841 ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG
3901 GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG
3961 CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC
4021 TACAGGCATC GTGGTGTCAC GCTCGTCGTT TGGTATGGCT TCATTCAGCT CCGGTTCCCA
4081 ACGATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG
4141 TCCTCCGATC GTTGTCAGAA GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCAGC
4201 ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA
4261 CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC
4321 AATACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG
4381 TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC
4441 CACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC
4501 AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGGAATAAGG GCGACACGGA AATGTTGAAT
4561 ACTCATACTC TTCCTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG
4621 CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC GCACATTTCC
4681 CCGAAAAGTG CCACCTGACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT
4741 TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
4801 CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC GGGGGCTCCC
4861 TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG ATTAGGGTGA
4921 TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC
4981 CACGTTCTTT AATAGTGGAC TCTTGTTCCA AACTGGAACA ACACTCAACC CTATCTCGGT
5041 CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA AAAATGAGCT
5101 GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGCTTACAA TTTAC
```

Figure 9

601 TAACTAGAGA ACCCACTGCT TACTGGCTTA TCGAAATTAA TACGACTCAC TATAGGGAGA
661 CCCAAGCTTG GTACCGAGCT CG **(BamHI in bold)**

gatcctctagactcgaggtcctacaggt (sequence from original GHR vector)
atggatctctggcagctgctgttgaccttggcactggcaggatcaagtgatgct (GHR signal)
ttttctggaagtgaggccacagcagctatccttagcagagcaccctggagtctgcaaagtgttaatccaggcctaaagac
aaattcttctaaggagcctaaattcaccaagtgccgttcacctgagcgagagacttttcatgccactggacagatgagg
ttcatcatggtacaaagaacctaggacccatacagctgttctataccagaaggaacactcaagaatggactcaagaatgg
aaagaatgccctgattatgtttctgctggggaaaacagctgttactttaattcatcgtttacctccatctggatacctta
ttgtatcaagctaactagcaatggtggtacagtggatgaaaagtgtttctctgttgatgaaatagtgcaaccagatccac
ccattgccctcaactggactttactgaacgtcagtttaactgggattcatgcagatatccaagtgagatgggaagcacca
cgcaatgcagatattcagaaaggatggatggttctggagtatgaacttcaatacaaagaagtaaatgaaactaaatggaa
aatgatggaccctatattgacaacatcagttccagtgtactcattgaaagtggataaggaatatgaagtgcgtgtgagat
ccaaacaacgaaactctggaaattatggcgagttcagtgaggtgctctatgtaacacttcctcagatgagccaatttaca
tgtgaagaagatttctac (GHR extracellular domain)
GGG (inserted codon to keep in frame and generate EcorI site in bold)
AAT TCT G.
721 CA GAT ATC GAC AAG CTG GTC AAG TGT GGC G GCATAAGCCT GCTGGTTCAG

1 RIL*TRGPTG ***MDLWQLLLLTL*** ***ALAGSSDAFS*** **GSEATAAILS RAPWSLQSVN**

51 **PGLKTNSSKE PKFTKCRSPE RETFSCHWTD EVHHGTKNLG PIQLFYTRRN**

101 **TQEWTQEWKE CPDYVSAGEN SCYFNSSFTS IWIPYCIKLT SNGGTVDEKC**

151 **FSVDEIVQPD PPIALNWTLL NVSLTGIHAD IQVRWEAPRN ADIQKGWMVL**

201 **EYELQYKEVN ETKWKMMDPI LTTSVPVYSL KVDKEYEVRV RSKQRNSGNY**

251 **GRFSEVLYVT LPQMSQFTCE EDFYGNSADI** DKLVKCGGIS LLVQNTSWML

301 LLLLSLSLLQ ALDFISL*LE HASRGPYSIV SPKC*SSLIS LDCAF*LPAI

351 CCLPLPRAFL DPGRCHSHCP FLIK*GNCIA LSE*VSFYSG GWGGAGQ

FIGURE 10

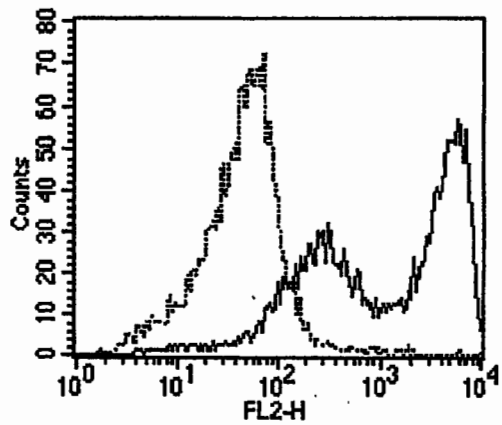


FIGURE 11

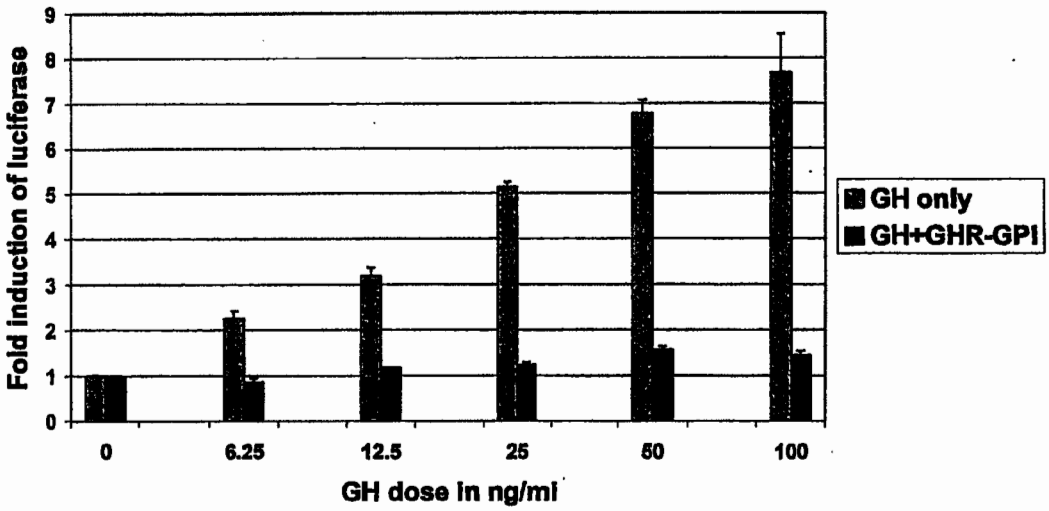

Fold induction of luciferase
9
8
7
6
5
4
3
2
1
0
0
6.25
12.5
25
50
100
GH dose in ng/ml
GH only
GH+GHR-GPI

FIGURE 12

sample number	date	cells	tranfection	GHBP (pM)
1	29/5/02.	CHO cells	pcdna3	<70
2	29/5/02.	CHO cells	GHRfl	93
5	6/6/02.	CHO cells	pcdna3	<70
6	6/6/02.	CHO cells	GHRfl	408
9	13/6/02.	CHO cells	pcdna3	<70
10	13/6/02.	CHO cells	GHRfl	<70
13	29/5/02.	HI cells	no	192
14	6/6/02.	HI cells	no	455
15	13/6/02.	HI cells	no	171
16	3/8/01.	293cells	no	<70
17	3/8/01.	293cells	GHRfl	193
20	18/7/02.	CHO cells	pcdna3	<70
21	18/7/02.	CHO cells	GHRfl	752
22	18/7/02.	CHO cells	GHR-GPI	>8000
23	18/7/02.	HI cells	no	72

pcDNA3 cells transfected with vector only
GHRfl cells transfected with wild-type GH reptor
HI cells – stable clone 293 cells expressing wild-type GH receptor
GHR-GPI cells transfected with GHR linked to GPI

FIGURE 13


```
   1 mglstvpdll lplvllellv giypsgvigl vphlgdrekr dsvcpqgkyi hpqnnsicct
  61 kchkgtylyn dcpgpgqdtd crecesgsft asenhlrhcl scskcrkemg qveissctvd
 121 rdtvcgcrkn qyrhywsenl fqcfncslcl ngtvhlscqe kqntvctcha gfflrenecv
 181 scsnckksle ctklclpqie nvkgtedsgt tvllplviff glcllsllfi glmyryqrwk
 241 sklysivcgk stpekegele gtttkplapn psfsptpgft ptlgfspvps stftssstyt
 301 pgdcpnfaap rrevappyqg adpilatala sdpipnplqk wedsahkpqs ldtddpatly
 361 avvenvpplr wkefvrrlgl sdheidrlel qngrclreaq ysmlatwrrr tprreatlel
 421 lgrvlrdmdl lgcledieea lcgpaalppa psllr

   1 cggcccagtg atcttgaacc ccaaaggcca gaactggagc ctcagtccag agaattctga
  61 gaaaattaaa gcagagagga ggggagagat cactgggacc aggccgtgat ctctatgccc
 121 gagtctcaac cctcaactgt caccccaagg cacttgggac gtcctggaca gaccgagtcc
 181 cgggaagccc cagcactgcc gctgccacac tgccctgagc ccaaatgggg gagtgagagg
                     MetGl yLeuSer…
 241 ccatagctgt ctggcatggg cctctccacc gtgcctgacc tgctgctgcc gctggtgctc
                       Il eTyrProSer…
 301 ctggagctgt tggtgggaat ataccctca ggggttattg gactggtccc tcacctaggg
 361 gacagggaga agagagatag tgtgtgtccc caaggaaaat atatccaccc tcaaaataat
 421 tcgatttgct gtaccaagtg ccacaaagga acctacttgt acaatgactg tccaggcccg
 481 gggcaggata cggactgcag ggagtgtgag agcggctcct tcaccgcttc agaaaaccac
 541 ctcagacact gcctcagctg ctccaaatgc cgaaaggaaa tgggtcaggt ggagatctct
 601 tcttgcacag tggaccggga caccgtgtgt ggctgcagga agaaccagta ccggcattat
 661 tggagtgaaa acctttcca gtgcttcaat tgcagcctct gcctcaatgg gaccgtgcac
 721 ctctcctgcc aggagaaaca gaacaccgtg tgcacctgcc atgcaggttt ctttctaaga
 781 gaaaacgagt gtgtctcctg tagtaactgt aagaaaagcc tggagtgcac gaagttgtgc
                                                        Va lLeuLeuPro..
 841 ctaccccaga ttgagaatgt taagggcact gaggactcag gcaccacagt gctgttgccc
 901 ctggtcattt tctttggtct ttgccttta tccctcctct tcattggttt aatgtatcgc
 961 taccaacggt ggaagtccaa gctctactcc attgtttgtg ggaaatcgac acctgaaaaa
1021 gaggggagc ttgaaggaac tactactaag cccctggccc caaacccaag cttcagtccc
1081 actccaggct tcacccccac cctgggcttc agtcccgtgc ccagttccac cttcacctcc
1141 agctccacct ataccccccgg tgactgtccc aactttgcgg ctccccgcag agaggtggca
1201 ccaccctatc agggggctga ccccatcctt gcgacagccc tcgcctccga ccccatcccc
1261 aacccccttc agaagtggga ggacagcgcc cacaagccac agagcctaga cactgatgac
1321 cccgcgacgc tgtacgccgt ggtggagaac gtgcccccgt tgcgctggaa ggaattcgtg
1381 cggcgcctag ggctgagcga ccacgagatc gatcggctgg agctgcagaa cgggcgctgc
1441 ctgcgcgagg cgcaatacag catgctggcg acctggaggc ggcgcacgcc gcggcgcgag
1501 gccacgctgg agctgctggg acgcgtgctc cgcgacatgg acctgctggg ctgcctggag
1561 gacatcgagg aggcgctttg cggccccgcc gccctcccgc ccgcgcccag tcttctcaga
1621 tgaggctgcg cccctgcggg cagctctaag gaccgtcctg cgagatcgcc ttccaacccc
1681 actttttttct ggaaaggagg ggtcctgcag gggcaagcag gagctagcag ccgcctactt
1741 ggtgctaacc cctcgatgta catagctttt ctcagctgcc tgcgcgccgc cgacagtcag
1801 cgctgtgcgc gcggagagag gtgcgccgtg ggctcaagag cctgagtggg tggtttgcga
1861 ggatgaggga cgctatgcct catgcccgtt ttgggtgtcc tcaccagcaa ggctgctcgg
1921 gggcccctgg ttcgtccctg agccttttte acagtgcata agcagttttt tttgtttttg
1981 ttttgttttg ttttgttttt aaatcaatca tgttacacta atagaaactt ggcactcctg
2041 tgccctctgc ctggacaagc acatagcaag ctgaactgtc ctaaggcagg ggcgagcacg
2101 gaacaatggg gccttcagct ggagctgtgg acttttgtac atacactaaa attctgaagt
2161 t
```

FIGURE 14

RIL*TRGPTG ***mglstvpdll lplvllellv*** giypsgvigl vphlgdrekr dsvcpqgkyi
hpqnnsicct kchkgtylyn dcpgpgqdtd crecesgsft asenhlrhcl scskcrkemg
qveissctvd rdtvcgcrkn qyrhywsenl fqcfncslcl ngtvhlscqe kqntvctcha
gfflrenecv scsnckksle ctklclpqie nvkgtedsgt tGNSADI DKLVKCGGIS
LLVQNTSWML LLLLSLSLLQ ALDFISL*LE HASRGPYSIV SPKC*SSLIS LDCAF*LPAI
CCLPLPRAFL DPGRCHSHCP FLIK*GNCIA LSE*VSFYSG GWGGAGQ

FIGURE 15


```
  1  MICQKFCVVL LHWEFIYVIT AF NLSYPITP WRFKLSCMPP NSTYDYFLLP
 51  AGLSKNTSNS NGHYETAVEP KFNSSGTHFS NLSKTTFHCC FRSEQDRNCS
101  LCADNIEGKT FVSTVNSLVF QQIDANWNIQ CWLKGDLKLF ICYVESLFKN
151  LFRNYNYKVH LLYVLPEVLE DSPLVPQKGS FQMVHCNCSV HECCECLVPV
201  PTAKLNDTLL MCLKITSGGV IFQSPLMSVQ PINMVKPDPP LGLHMEITDD
251  GNLKISWSSP PLVPFPLQYQ VKYSENSTTV IREADKIVSA TSLLVDSILP
301  GSSYEVQVRG KRLDGPGIWS DWSTPRVFTT QDVIYFPPKI LTSVGSNVSF
351  HCIYKKENKI VPSKEIVWWM NLAEKIPQSQ YDVVSDHVSK VTFFNLNETK
401  PRGKFTYDAV YCCNEHECHH RYAELYVIDV NINISCETDG YLTKMTCRWS
451  TSTIQSLAES TLQLRYHRSS LYCSDIPSIH PISEPKDCYL QSDGFYECIF
501  QPIFLLSGYT MWIRINHSLG SLDSPPTCVL PDSVVKPLPP SSVKAEITIN
551  IGLLKISWEK PVFPENNLQF QIRYGLSGKE VQWKMYEVYD AKSKSVSLPV
601  PDLCAVYAVQ VRCKRLDGLG YWSNWSNPAY TVVMDIKVPM RGPEFWRIIN
651  GDTMKKEKNV TLLWKPLMKN DSLCSVQRYV INHHTSCNGT WSEDVGNHTK
701  FTFLWTEQAH TVTVLAINSI GASVANFNLT FSWPMSKVNI VQSLSAYPLN
751  SSCVIVSWIL SPSDYKLMYF IIEWKNLNED GEIKWLRISS SVKKYYIHDH
801  FIPIEKYQFS LYPIFMEGVG KPKIINSFTQ DDIEKHQS GN SADIDKLVKC
851  GGISLLVQNT SWMLLLLLSL SLLQALDFIS L*LEHASRGP YSIVSPKC*S
901  SLISLDCAF* LPAICCLPLP RAFLDPGR
```

FIGURE 16

Cytokines and accession numbers.

Cytokine	Accession Number
Homo sapiens growth hormone (GH)	**XM_044413; XM_044403**
Homo sapiens leptin	**U43168**
Homo sapiens erythropoietin (EPO)	**XM_011627**
Gallus gallus prolactin	**AF288765**
Homo sapiens tumor necrosis factor (TNF)	**XM_041847; XM_011402**
Homo sapiens interleukin 2 (IL2)	**XM_035510; XM_035509; XM_035511**
Homo sapiens interleukin 3 (IL3)	**XM_029116; XM_029114; XM_003752**
Homo sapiens interleukin 4 (IL4)	**XM_034870**
Homo sapiens interleukin 5 (IL5)	**XM_003778**
Homo sapiens interleukin 6 (IL6)	**XM_033638**
Homo sapiens interleukin 7 (IL7)	**XM_005266**
Homo sapiens interleukin 8 (IL8)	*XM_031289*
Homo sapiens interleukin 9 (IL9)	**XM_003760**
Homo sapiens interleukin 10 (IL10)	**AY029171**
Homo sapiens interleukin 11 (IL11)	**XM_035922; XM_008906**
Cavia porcellus interleukin-12 p35 subunit (IL12 p35)	**AB025723**
Homo sapiens interleukin 13 (IL13)	**XM_054533; XM_054534**
Homo sapiens interleukin 14 (IL14)	*XM_034511*
Homo sapiens interleukin 15 (IL15)	**XM_043810; XM_043811; XM_003529**
Homo sapiens granulocyte colony stimulating factor (G-CSF)	**NM_000759**
Homo sapiens granulocyte macrophage CSF (GM-CSF)	**XM_003751; XM_029118**
Homo sapiens ciliary neurotrophic factor (CNTF)	**XM_006012**
Homo sapiens cardiotrophin-1 (CT-1)	**XM_008119; NM_001330**
Homo sapiens leukemia inhibitory factor (LIF)	**XM_038018; XM_009915**
Homo sapiens oncostatin M (OSM)	**XM_054688; XM_009916**
Homo sapiens interferon α (IFNA)	**M54886, M38682**
Homo sapiens interferon γ (IFNG)	**NM_000619**

- **This data was obtained from the National Centre for Biotechnology Information site (URL: http://www.ncbi.nlm.nih.gov/)**