FIG. 1A

Heavy Chain IgG1 Constant Region

```
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg     60
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg    120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca    180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc    240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc    300
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga    360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccc    420
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg    480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac    540
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag    600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc    660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag    720
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc    780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg    840
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg    900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg    960
cagaagagcc tctccctgtc tccgggtaaa                                     990
```

FIG. 1B

```
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS     60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG    120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN    180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE    240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW    300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                     330
```

FIG. 2A

Kappa Chain Constant Region

```
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct      60
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag     120
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac     180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag     240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag     300
agcttcaaca ggggagagtg t                                               321
```

FIG. 2B

```
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD      60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                   107
```

FIG. 3A

1119 Heavy Chain Variable Region

```
gaggtgcagc tggtacagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc      60
tcctgtaagg gttctggata caactttacc agctactgga tcggctgggt gcgccagatg     120
cccgggaaag gcctggagtt gatggggatc atctatcctg gtgactctga taccagatac     180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac     240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc     300
tacttttact tcgatctctg gggccgtggc accctggtca ccgtctctag t              351
```

FIG. 3B

```
EVQLVQSGAE VKKPGESLKI SCKGSGYNFT SYWIGWVRQM PGKGLELMGI IYPGDSDTRY      60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCGSGS YFYFDLWGRG TLVTVSS         117
```

FIG. 4A

1119 Kappa Chain Variable Region

```
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa     120
cctggccagg ctcccaggct cctcatatat ggtgcatcca gcagggccac tggcatccca     180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag     240
cctgaagatt ttgcagtgta ttactgtcag cggtctggtg gctcatcatt cactttcggc     300
cctgggacca aagtggatat caaa                                            324
```

FIG. 4B

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY GASSRATGIP      60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RSGGSSFTFG PGTKVDIK                  108
```

FIG. 5A

1118 Heavy Chain Variable Region

```
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc     60
tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg    120
cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac    180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac    240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc    300
tactggtact tcgatctctg gggccgtggc accctggtca ccgtctctag t             351
```

FIG. 5B

```
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY     60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCGSGS YWYFDLWGRG TLVTVSS       117
```

FIG. 5C

1118* Heavy Chain Variable Region

```
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY     60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCGSGS YWYFDLRGRG TLVTVSS       117
```

FIG. 5D

1118* Heavy Chain Variable Region

```
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc     60
tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg    120
cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac    180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac    240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc    300
tactggtact tcgatctccg gggccgtggc accctggtca ccgtctctag t             351
```

FIG. 6A

1118 Kappa Chain Variable Region

```
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgttagc agcagctcct tagcctggta ccagcagaaa     120
cctggccagg ctcccaggct cctcatatat ggtgcatcca gcagggccac tggcatccca     180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag     240
cctgaagatt ttgcagtgta ttactgtcag cggtctggtg gctcatcatt cactttcggc     300
cctgggacca aagtggatat caaa                                            324
```

FIG. 6B

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSSLAWYQQK PGQAPRLLIY GASSRATGIP      60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RSGGSSFTFG PGTKVDIK                  108
```

FIG. 7A

1121 Heavy Chain Variable Region

```
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc      60
tcctgtaagg gttctggata caactttacc agctactgga tcggctgggt gcgccagatg     120
cccgggaaag gcctggagtt gatggggatc atctatcctg gtgactctga taccagatac     180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac     240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc     300
tactggtact tcgatctctg gggccgtggc accctggtca ccgtctctag t              351
```

FIG. 7B

```
EVQLVQSGAE VKKPGESLKI SCKGSGYNFT SYWIGWVRQM PGKGLELMGI IYPGDSDTRY      60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCGSGS YWYFDLWGRG TLVTVSS         117
```

FIG. 8A

1121 Kappa Chain Variable Region

```
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa     120
cctggccagg ctcccaggct cctcatatat ggtgcatcca gcagggccac tggcatccca     180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag     240
cctgaagatt ttgcagtgta ttactgtcag cggtctggtg gctcatcatt cactttcggc     300
cctgggacca aagtggatat caaa                                            324
```

FIG. 8B

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY GASSRATGIP      60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RSGGSSFTFG PGTKVDIK                  108
```

FIG. 8C

1121* Kappa Chain Variable Region

```
EIVLTQSPGT LSLSPGERAT LSCRASQSII SSYLAWYQQK PGQTPRLLIY GVSSRATGIP      60
DRFSGSGSGT DFTLTITRLE PEDFAVYYCQ QYGNSFMYTF GQGTKLEIK                 109
```

FIG. 8D

1121* Kappa Chain Variable Region

```
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtattatc agcagctact tagcctggta ccagcagaaa     120
cctggccaga ctcccaggct cctcatctat ggtgtatcca gcagggccac tggcatccca     180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcac cagactggag     240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta actcatttat gtacactttt     300
ggccagggga ccaagctgga gatcaaa                                         327
```

Fig. 9

A549 Assay

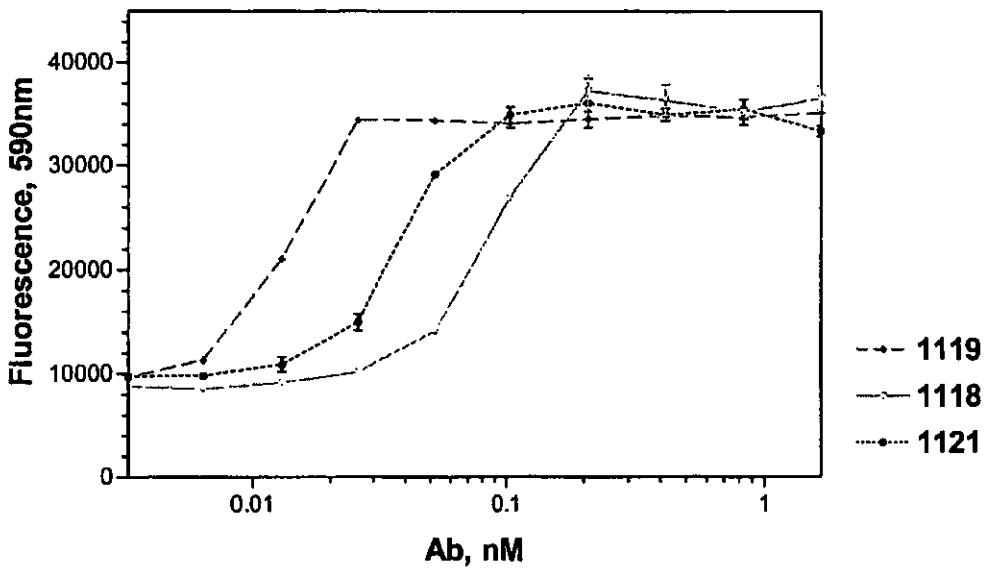


Fig. 10

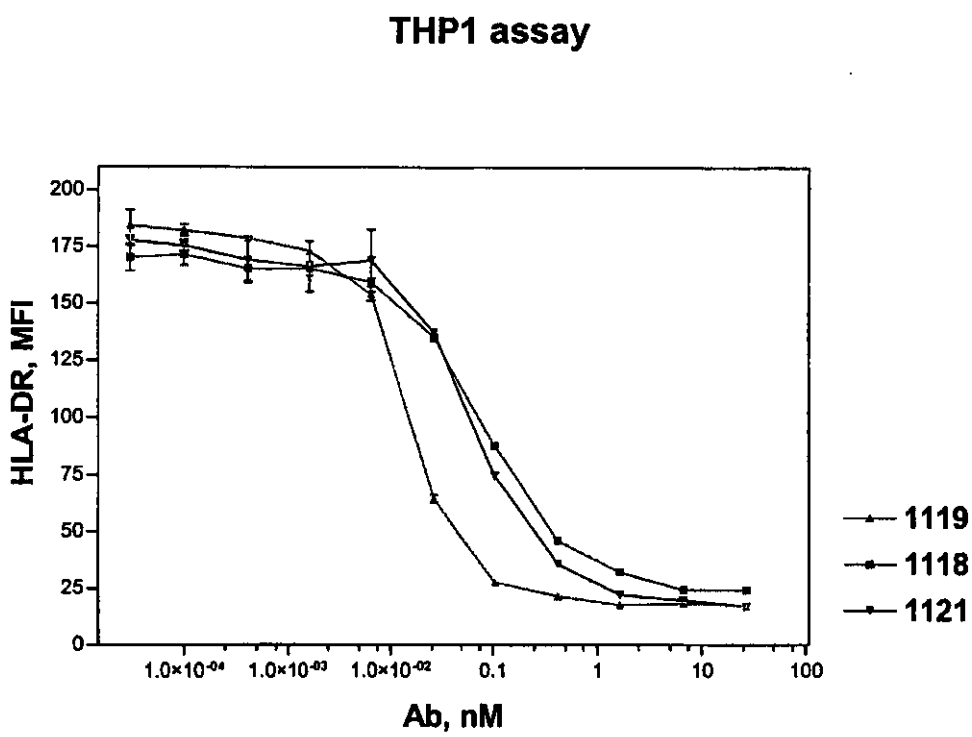
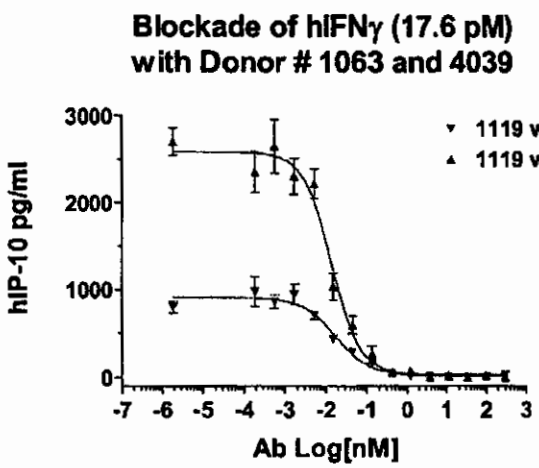

THP1 assay
HLA-DR, MFI
200
175
150
125
100
75
50
25
0
1.0×10-04
1.0×10-03
1.0×10-02
0.1
1
10
100
Ab, nM
1119
1118
1121

Fig. 11



	IC50 (pM)	95%CI
1119 with # 1063	132	53-328
1119 with # 4039	81	35-187

	hIFNγ EC50 (pM)	95%CI
Donor # 1063	82	55-122
Donor # 4039	56	40-78

FIG. 12

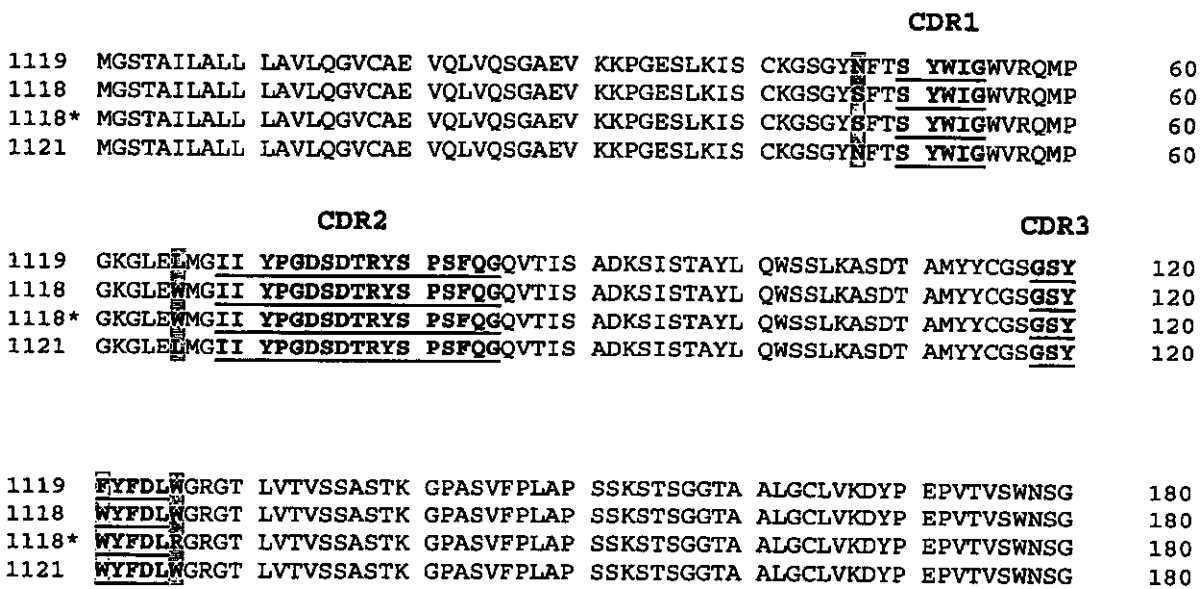

CDR1
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1118 MGSTAILALL LAVLQGVCAE VQLVQSGAEV KKPGESLKIS CKGSGYSFTS YWIGWVRQMP 60
1118* MGSTAILALL LAVLQGVCAE VQLVQSGAEV KKPGESLKIS CKGSGYSFTS YWIGWVRQMP 60
1121 MGSTAILALL LAVLQGVCAE VQLVQSGAEV KKPGESLKIS CKGSGYNFTS YWIGWVRQMP 60
CDR2
CDR3
1119 GKGLELMGII YPGDSDTRYS PSFQGQVTIS ADKSISTAYL QWSSLKASDT AMYYCGSGSY 120
1118 GKGLEWMGII YPGDSDTRYS PSFQGQVTIS ADKSISTAYL QWSSLKASDT AMYYCGSGSY 120
1118* GKGLEWMGII YPGDSDTRYS PSFQGQVTIS ADKSISTAYL QWSSLKASDT AMYYCGSGSY 120
1121 GKGLELMGII YPGDSDTRYS PSFQGQVTIS ADKSISTAYL QWSSLKASDT AMYYCGSGSY 120
1119 FYFDLWGRGT LVTVSSASTK GPASVFPLAP SSKSTSGGTA ALGCLVKDYP EPVTVSWNSG 180
1118 WYFDLWGRGT LVTVSSASTK GPASVFPLAP SSKSTSGGTA ALGCLVKDYP EPVTVSWNSG 180
1118* WYFDLRGRGT LVTVSSASTK GPASVFPLAP SSKSTSGGTA ALGCLVKDYP EPVTVSWNSG 180
1121 WYFDLWGRGT LVTVSSASTK GPASVFPLAP SSKSTSGGTA ALGCLVKDYP EPVTVSWNSG 180

FIG. 13

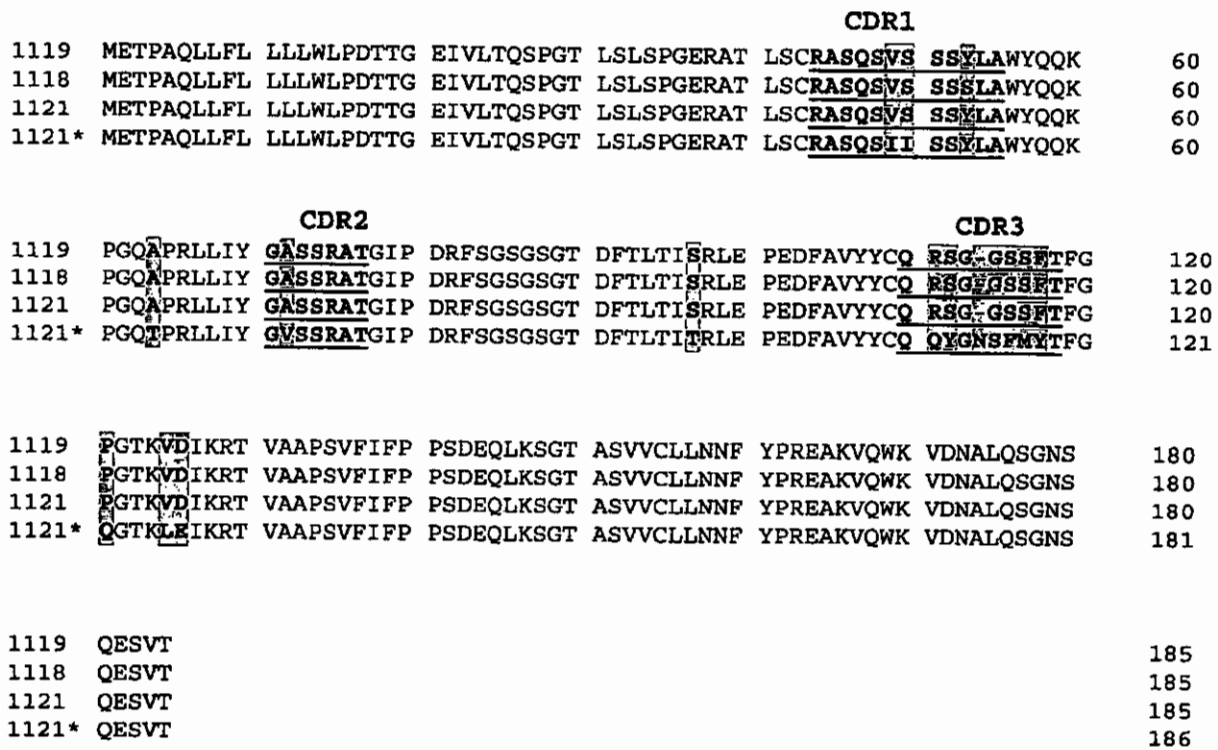

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CDR2
CDR3
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1118 METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSSLAWYQQK 60
1121 METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK 60
1121* METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRASQSII SSYLAWYQQK 60
1119 PGQAPRLLIY GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RSG-GSSFTFG 120
1118 PGQAPRLLIY GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RSGFGSSFTFG 120
1121 PGQAPRLLIY GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RSG-GSSFTFG 120
1121* PGQTPRLLIY GVSSRATGIP DRFSGSGSGT DFTLTITRLE PEDFAVYYCQ QYGNSFMYTFG 121
1119 PGTKVDIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS 180
1118 PGTKVDIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS 180
1121 PGTKVDIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS 180
1121* QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS 181
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1121 QESVT 185
1121* QESVT 186

Figure 14

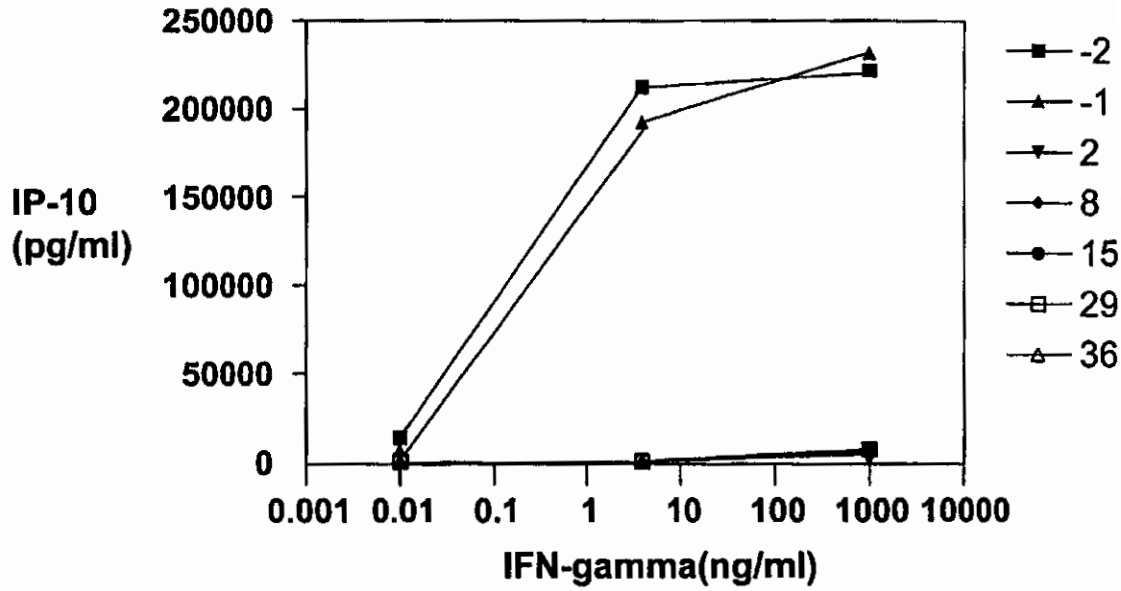
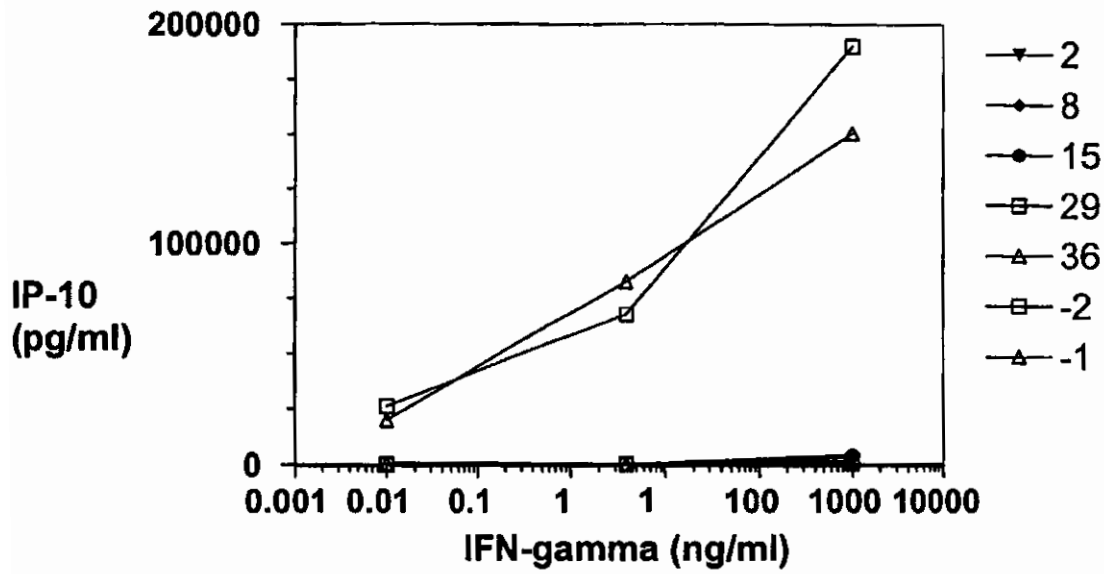

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200000
150000
100000
50000
0
IP-10
(pg/ml)
0.001
0.01
0.1
1
10
100
1000
10000
IFN-gamma(ng/ml)
-2
-1
2
8
15
29
36

Figure 15


200000
100000
0
IP-10
(pg/ml)
0.001
0.01
0.1
1
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100
1000
10000
IFN-gamma (ng/ml)
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8
15
29
36
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01-1635-B.ST25

SEQUENCE LISTING

<110> Amgen, Inc.
Welcher, Andrew
Chute, Hilary
Li, Luke
Huang, Haichun

<120> Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamma Pathway Inhibitors

<130> 01-1635-B

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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 Ser Leu Gly Thr Gln Thr
65 70 75 80

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
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Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240

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01-1635-B.ST25

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35 40 45

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

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
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cccgggaaag gcctggagtt gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc 300

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

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

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Gly Ser Gly Ser Tyr Phe Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
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<210> 7

<211> 324

<212> DNA

<213> Homo Sapiens

<400> 7

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc     60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa    120

cctggccagg ctcccaggct cctcatatat ggtgcatcca gcagggccac tggcatccca    180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag    240

cctgaagatt ttgcagtgta ttactgtcag cggtctggtg gctcatcatt cactttcggc    300

cctgggacca aagtggatat caaa                                           324
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<210> 8

<211> 108

<212> PRT

<213> Homo sapiens

<400> 8

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 Arg Ser Gly Gly Ser Ser
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 9

<211> 351

<212> DNA

<213> Homo Sapiens

<400> 9
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc 300

tactggtact tcgatctctg gggccgtggc accctggtca ccgtctctag t 351

<210> 10

<211> 117

<212> PRT

<213> Homo sapiens

<400> 10

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Gly Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 11

<211> 324

<212> DNA

<213> Homo Sapiens

<400> 11
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctcct tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatatat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cggtctggtg gctcatcatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 12

<211> 108

<212> PRT

<213> Homo sapiens

<400> 12

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

Ser 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 Arg Ser Gly Gly Ser Ser
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 13

<211> 351

<212> DNA

<213> Homo Sapiens

<400> 13
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata caactttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtt gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc 300

tactggtact tcgatctctg gggccgtggc accctggtca ccgtctctag t 351

<210> 14

<211> 117

<212> PRT

<213> Homo sapiens

<400> 14

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

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

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Gly Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 15

<211> 324

<212> DNA

<213> Homo Sapiens

<400> 15
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatatat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cggtctggtg gctcatcatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 16

<211> 108

<212> PRT

<213> Homo sapiens

<400> 16

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 Arg Ser Gly Gly Ser Ser
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 17

<211> 447

<212> PRT

<213> homo sapiens

<400> 17

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

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

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Gly Ser Gly Ser Tyr Phe Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 18

<211> 215

<212> PRT

<213> Homo sapiens

<400> 18

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 Arg Ser Gly Gly Ser Ser
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 19

<211> 447

<212> PRT

<213> Homo sapiens

<400> 19

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Gly Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110
```

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<210> 20

<211> 215

<212> PRT

<213> Homo sapiens

<400> 20

```
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

Ser 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 Arg Ser Gly Gly Ser Ser
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 21

<211> 447

<212> PRT

<213> Homo sapiens

01-1635-B.ST25

<400> 21

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

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

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Gly Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320
```

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 22

<211> 215

<212> PRT

<213> Homo sapiens

<400> 22

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 Arg Ser Gly Gly Ser Ser
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 23

<211> 24

<212> DNA

<213> artificial

<220>

<223> oligunucleotide primer for PCR

<220>

<221> misc_feature

<222> (18)..(23)

<223> n is a, c, t, or g

<400> 23
ggccggatag gcctccannn nnnt 24

<210> 24

<211> 21

<212> DNA

<213> artificial

<220>

<223> olignucleotide primer for PCR

<400> 24
ggggtcaggc tggaactgag g 21

<210> 25

<211> 19

<212> DNA

<213> artificial

<220>

<223> oligonucleotide primer for PCR

<400> 25
tgaggacgct gaccacacg 19

<210> 26

<211> 48

<212> DNA

<213> artificial

<220>

<223> oligonucleotide primer for PCR

<400> 26
acaacaaagc ttctagacca ccatggaaac cccagctcag cttctctt 48

<210> 27

<211> 33

<212> DNA

<213> artificial

<220>

<223> oligonucleotide primer for PCR

<400> 27
cttgtcgact caacactctc ccctgttgaa gct 33

<210> 28

<211> 44

<212> DNA

<213> artificial

<220>

<223> oligonucleotide primer for PCR

<400> 28
cagcagaagc ttctagacca ccatggggtc aaccgccatc ctcg 44

<210> 29

<211> 42

<212> DNA

<213> artificial

<220>

<223> oligonucleotide primer for PCR

<400> 29
cttggtggag gcactagaga cggtgaccag ggtgccacgg cc 42

<210> 30

<211> 117

<212> PRT

<213> homo sapiens

<400> 30

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Gly Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Arg Gly Arg Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 31

<211> 109

<212> PRT

<213> homo sapiens

<400> 31

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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 Ile Ile Ser Ser
            20                  25                  30

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

Ile Tyr Gly Val 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 Thr Arg Leu Glu
65                  70                  75                  80

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

Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 32

<211> 447

<212> PRT

<213> Homo sapiens

<400> 32

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Gly Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Arg Gly Arg Gly Thr Leu
```

```
                100                 105                 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ile Ser Ser
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Val 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 Thr Arg Leu Glu
65 70 75 80

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

Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
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Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
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Lys Ser Phe Asn Arg Gly Glu Cys
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<400> 34

Ser Tyr Trp Ile Gly
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Gly

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Gly Ser Tyr Phe Tyr Phe Asp Leu
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Gly Ser Tyr Trp Tyr Phe Asp Leu
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<211> 12

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<213> Homo sapiens

<400> 38

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<210> 39

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<213> Homo sapiens

<400> 39

Arg Ala Ser Gln Ser Val Ser Ser Ser Ser Leu Ala
1 5 10

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<212> PRT

<213> Homo sapiens

<400> 40

Arg Ala Ser Gln Ser Ile Ile Ser Ser Tyr Leu Ala
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Gly Ala Ser Ser Arg Ala Thr
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Gly Val Ser Ser Arg Ala Thr
1 5

<210> 43

<211> 9

<212> PRT

<213> Homo sapiens

<400> 43

Gln Arg Ser Gly Gly Ser Ser Phe Thr
1 5

<210> 44

<211> 10

<212> PRT

<213> Homo sapiens

<400> 44

Gln Gln Tyr Gly Asn Ser Phe Met Tyr Thr
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<212> DNA

<213> Homo sapiens

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<223> X is any amino acid

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<212> PRT

<213> Homo sapiens

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<210> 50

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Phe Gly Xaa Gly
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<211> 20

<212> PRT

<213> Homo sapiens

<400> 52

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Gly Ser Thr Gly
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<210> 53

<211> 26

<212> PRT

<213> Homo sapiens

<400> 53

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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
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<211> 19

<212> PRT

<213> Homo sapiens

<400> 54

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Val Cys Ala

<210> 55

<211> 20

<212> PRT

<213> Homo sapiens

<400> 55

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Asp Thr Thr Gly
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<211> 351

<212> DNA

<213> Homo sapiens

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cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgg ttcggggagc 300

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<211> 327

<212> DNA

<213> Homo sapiens

<400> 57

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cctggccaga ctcccaggct cctcatctat ggtgtatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcac cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta actcatttat gtacactttt 300

ggccagggga ccaagctgga gatcaaa 327