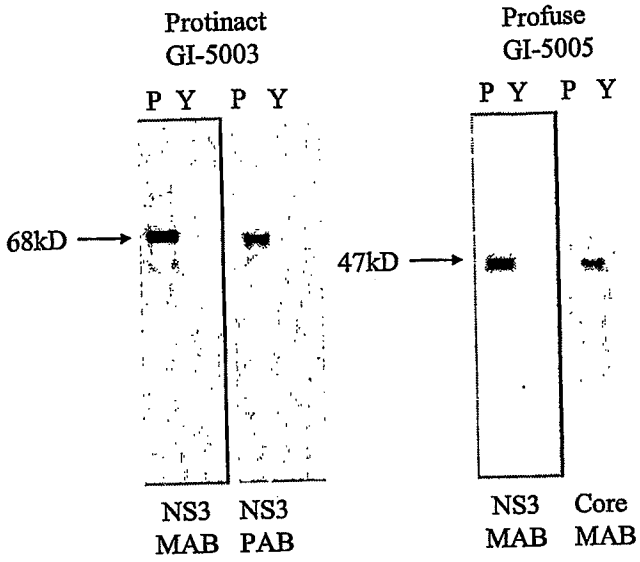
FIG. 1A



P = Profuse or Protinact
Y = YEX (vector only)

FIG. 1B

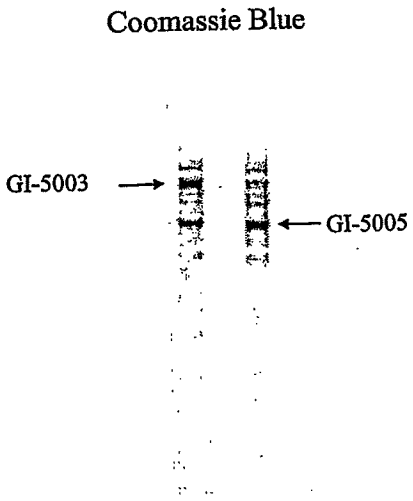


FIG. 1C

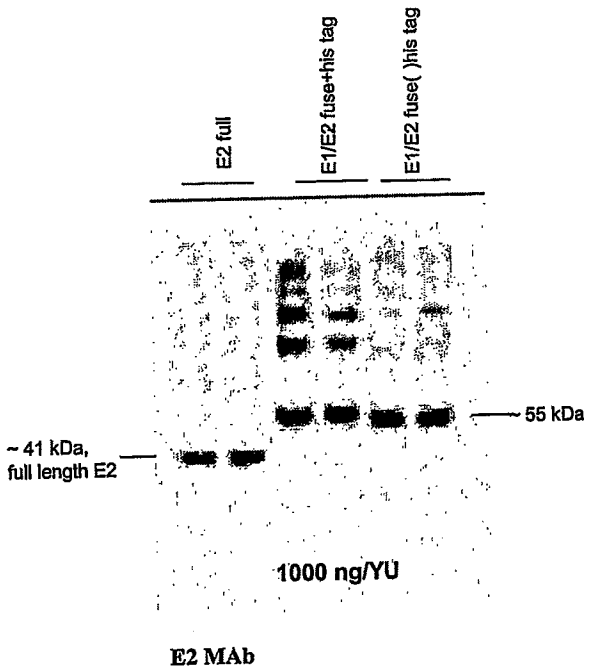


FIG. 1D

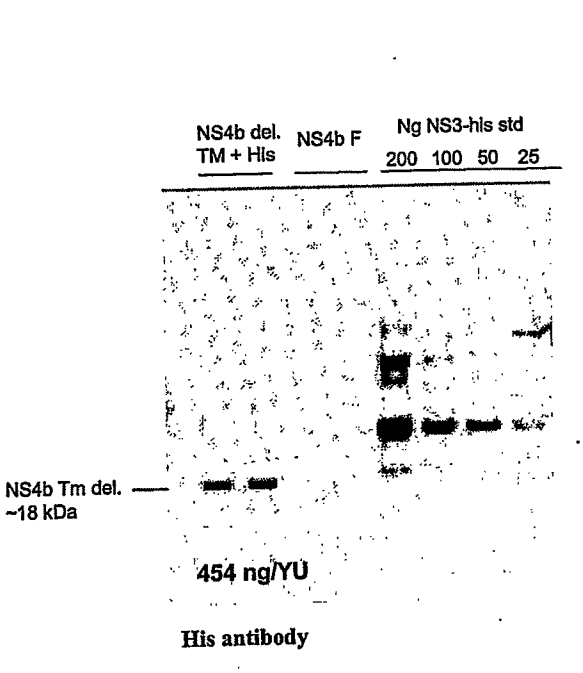


FIG. 2

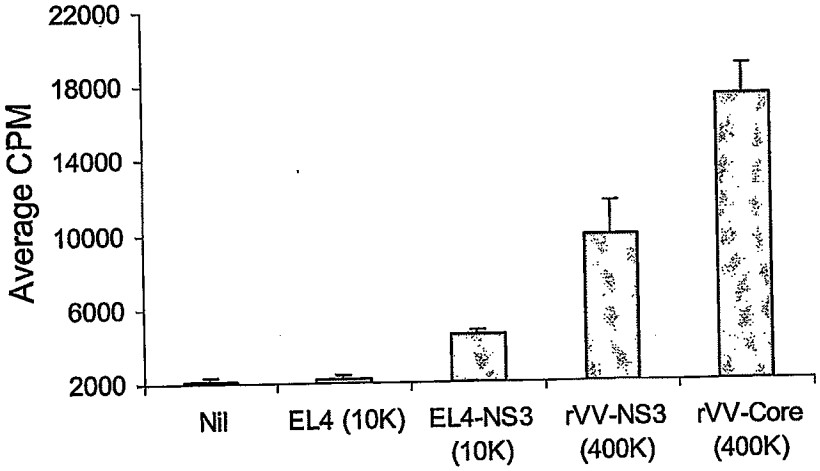


FIG. 3A

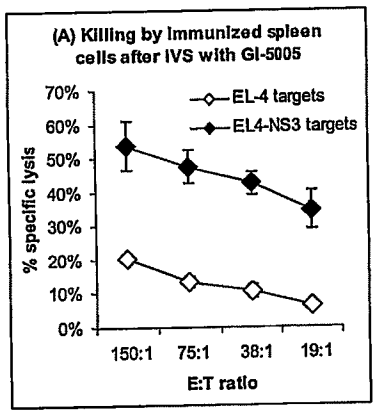


FIG. 3B

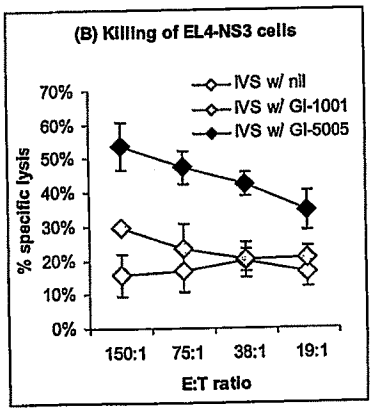


FIG. 3C

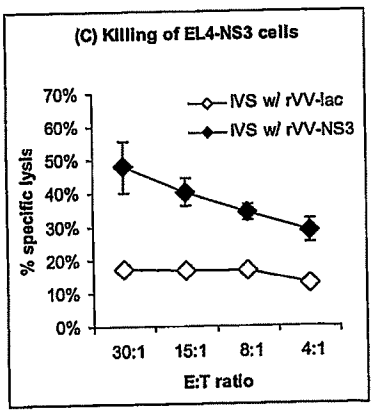


FIG. 4A

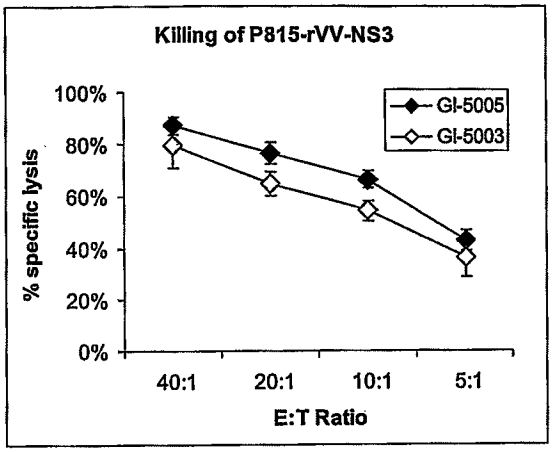


FIG. 4B

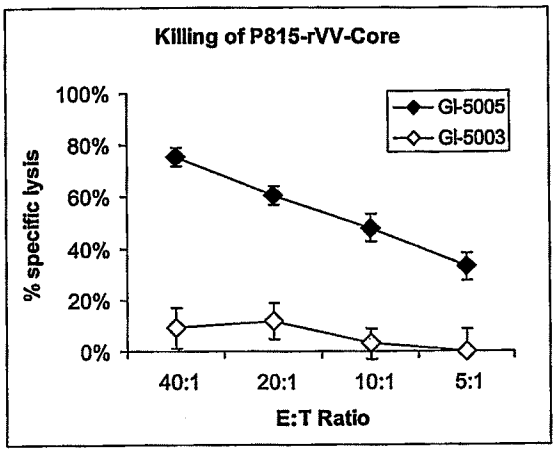


FIG. 5

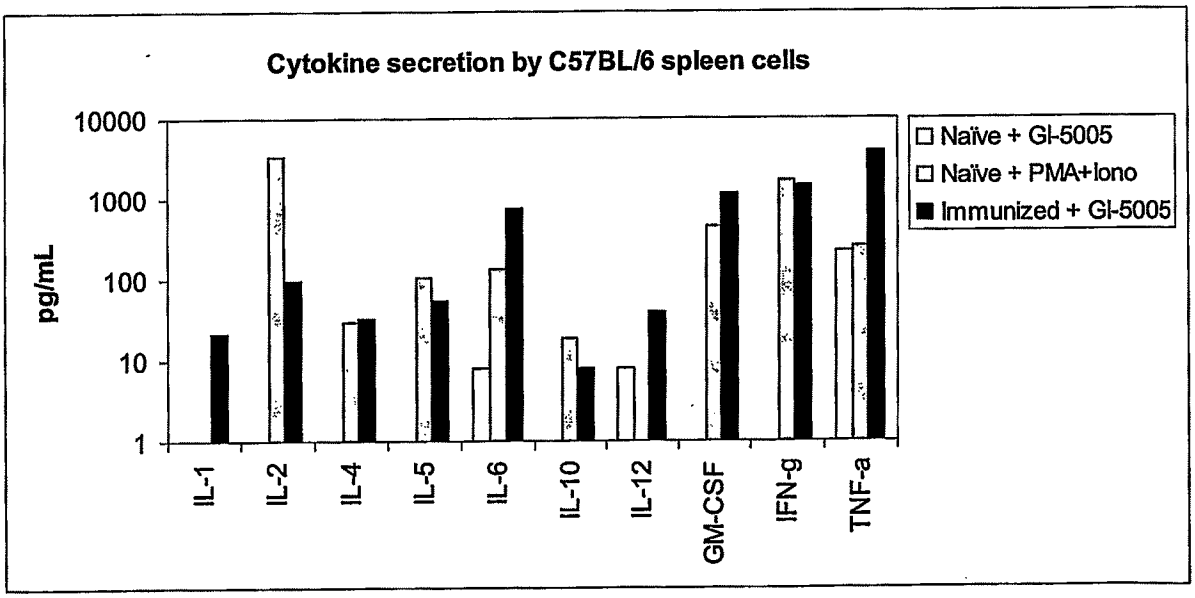


FIG. 6

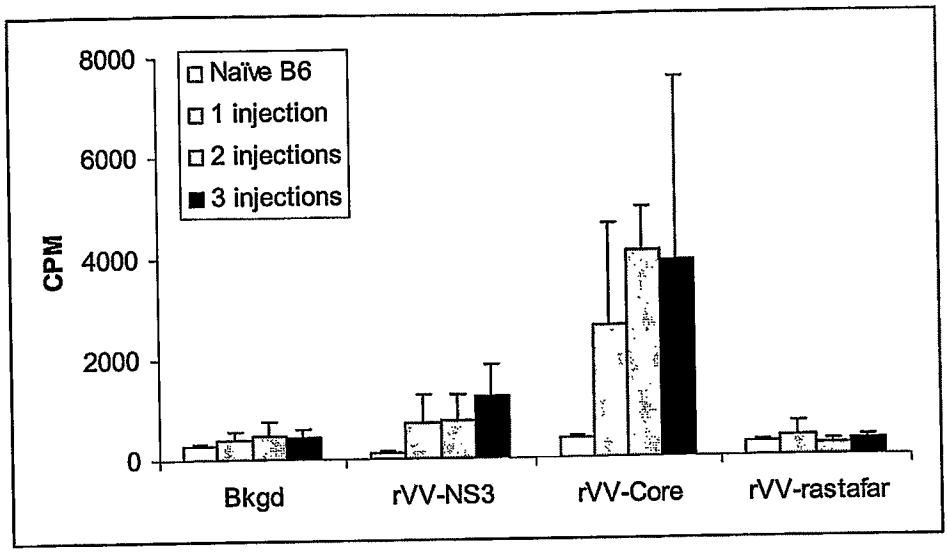


FIG. 7A

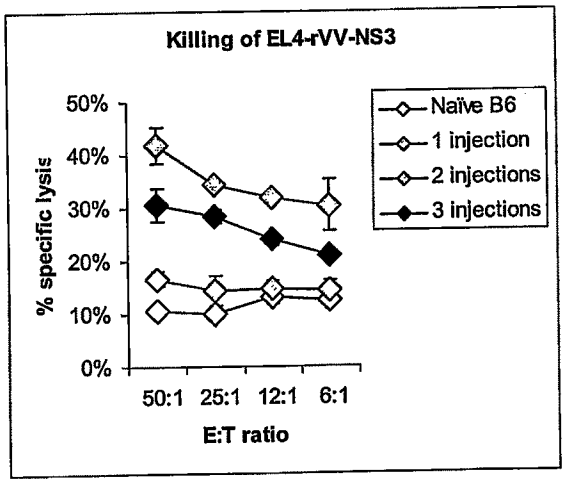
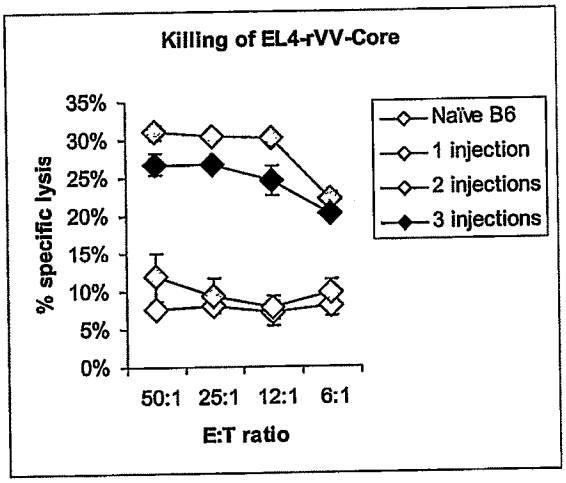


FIG. 7B



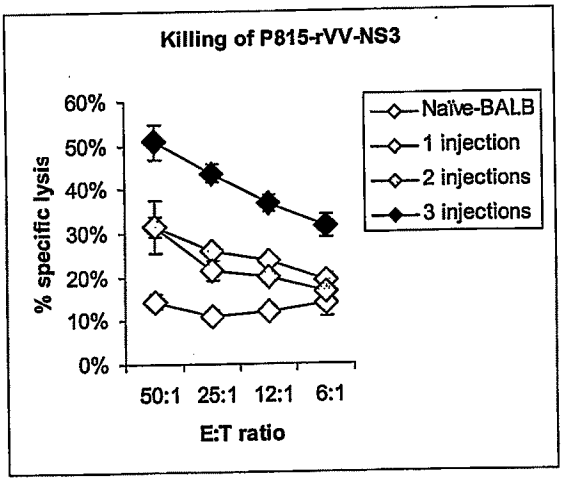


FIG. 7C

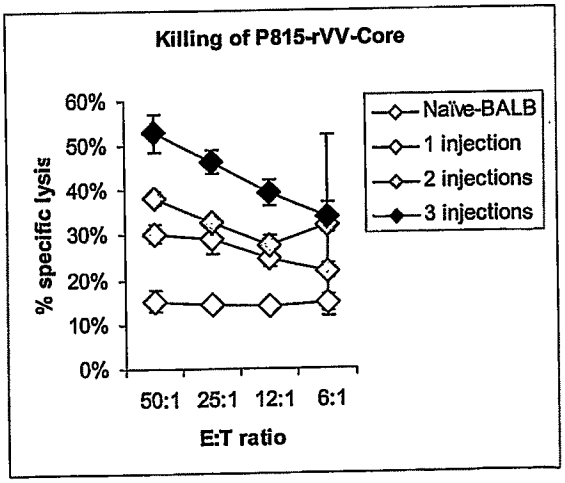


FIG. 7D

FIG. 8A

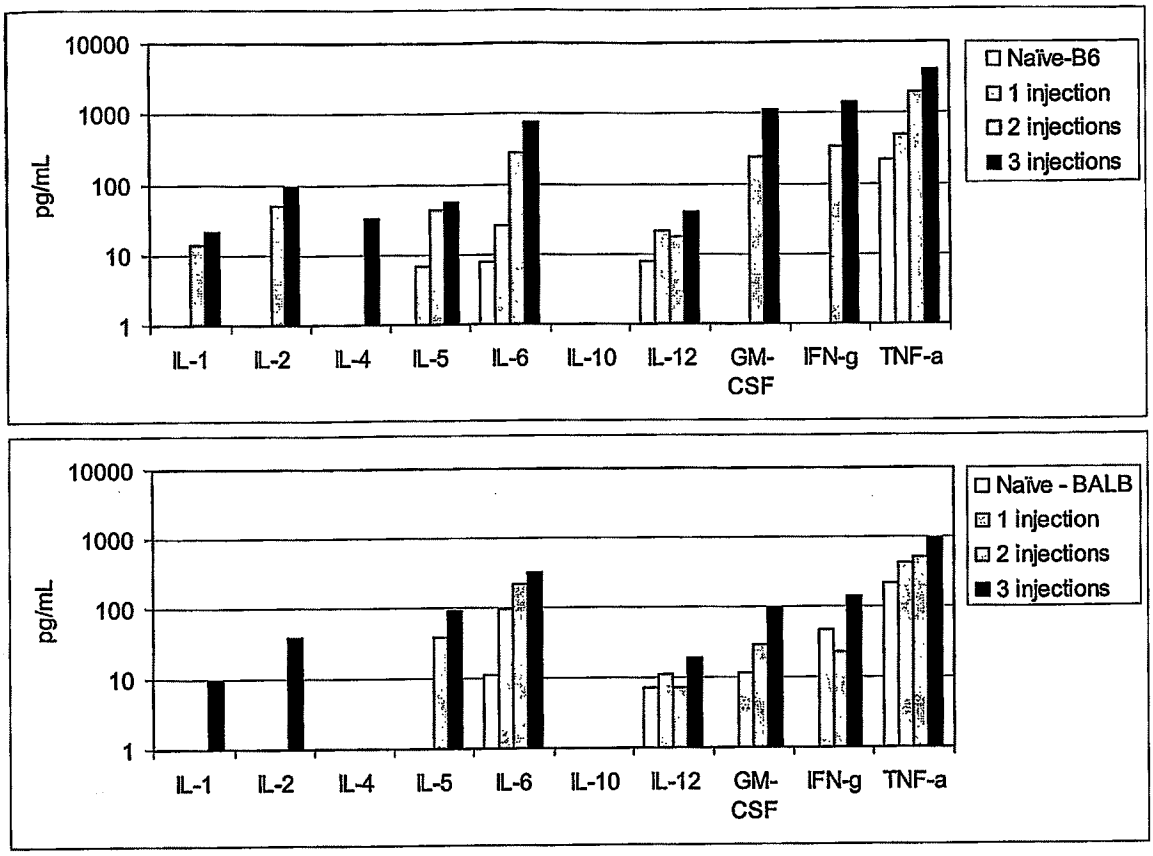


FIG. 8B

FIG. 9

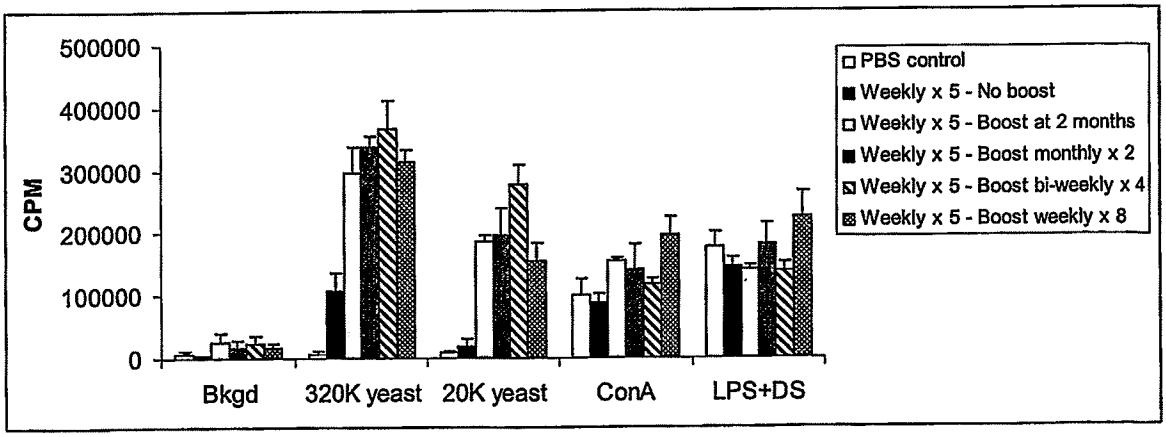


FIG. 10

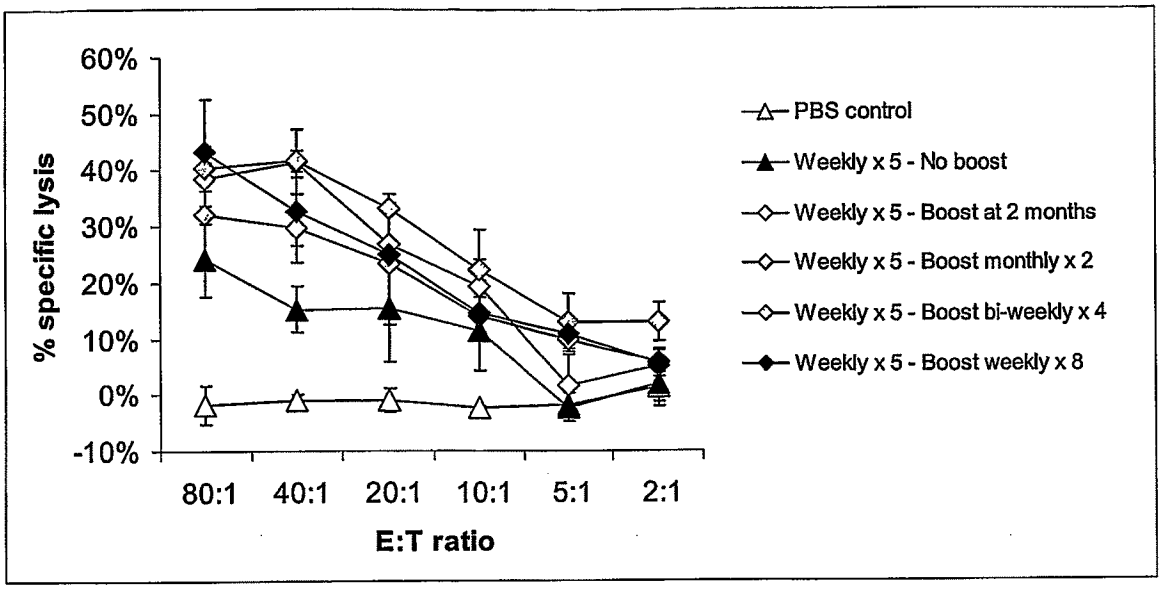


FIG. 11A

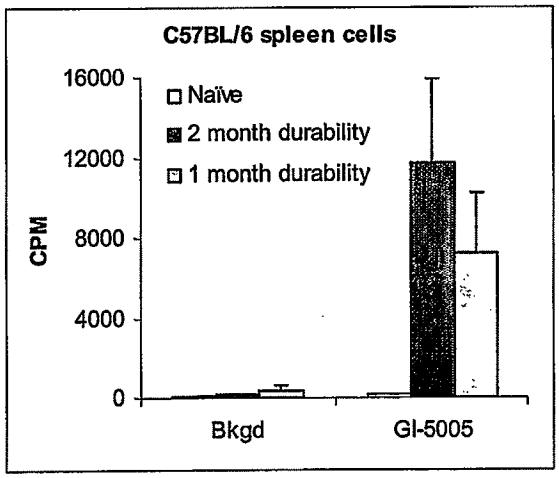


FIG. 11B

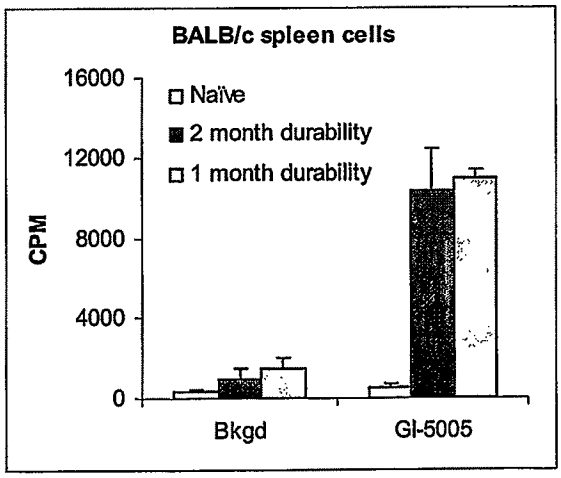


FIG. 12A

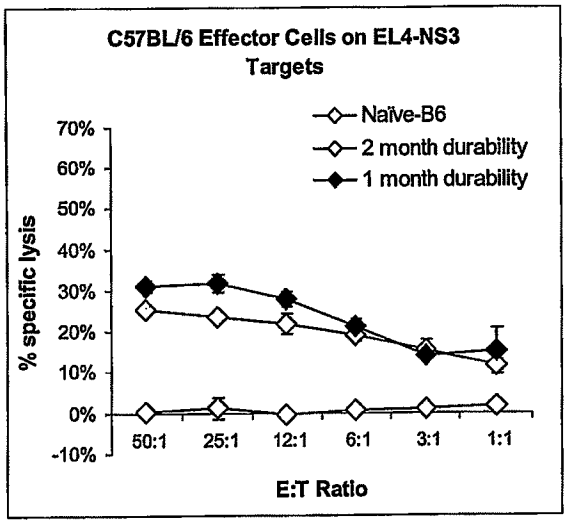


FIG. 12B

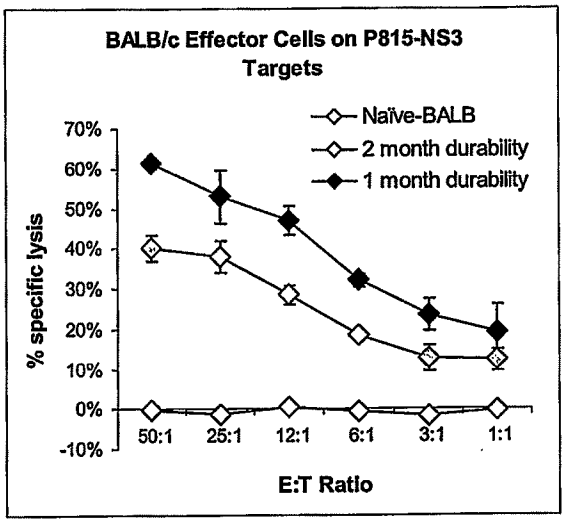


FIG. 13A

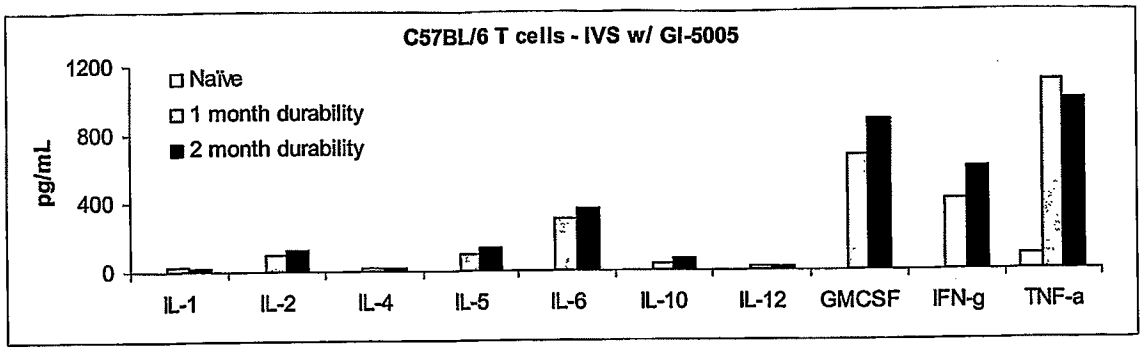


FIG. 13B

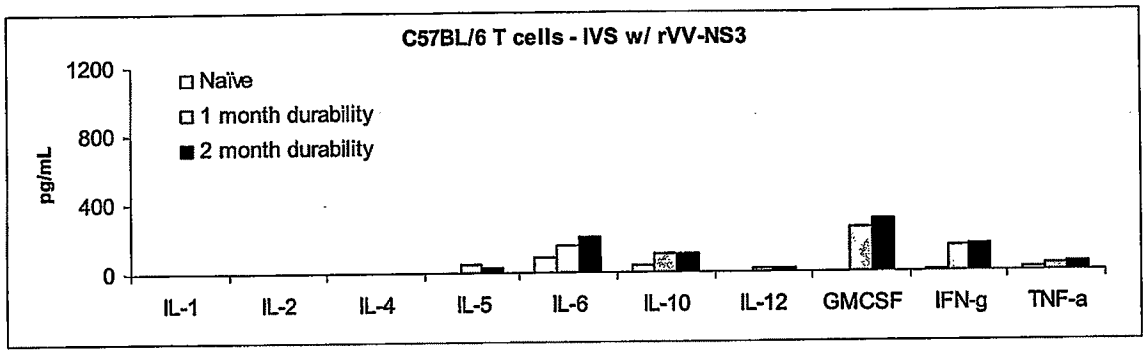


FIG. 13C

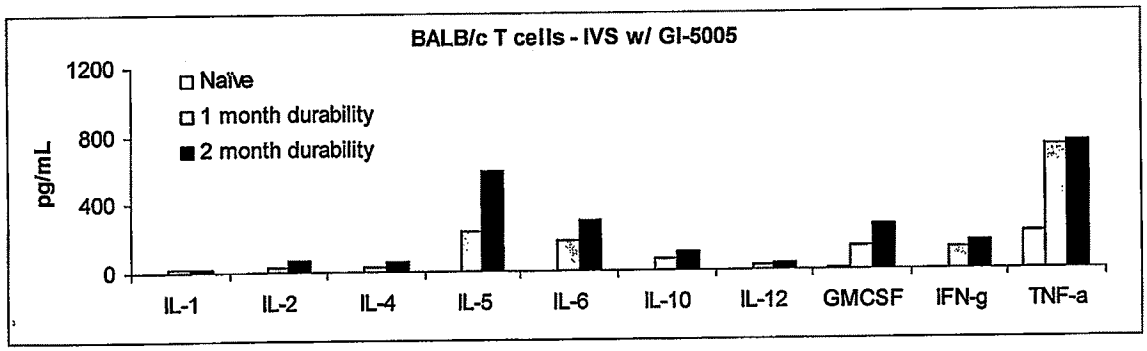


FIG. 13D

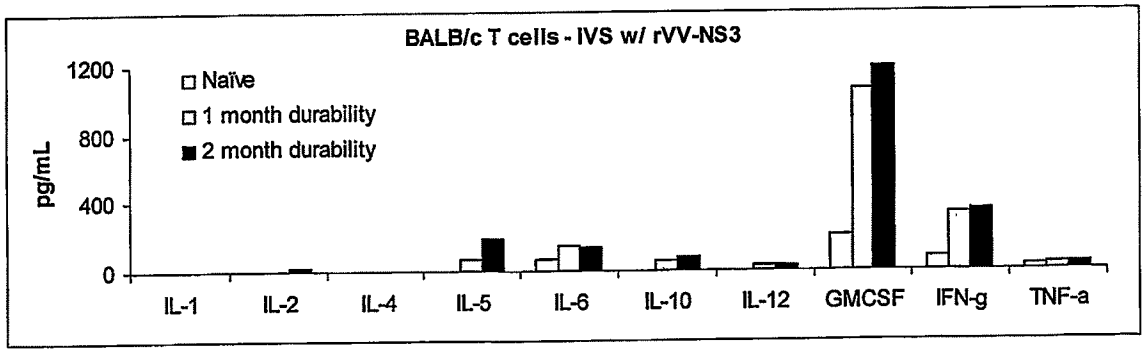


FIG. 14A

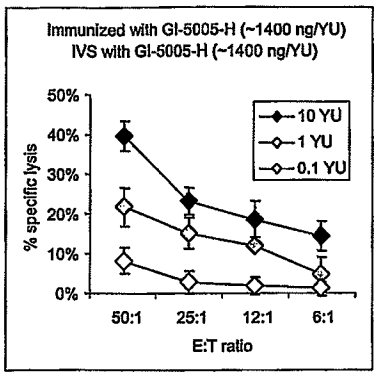


FIG. 14B

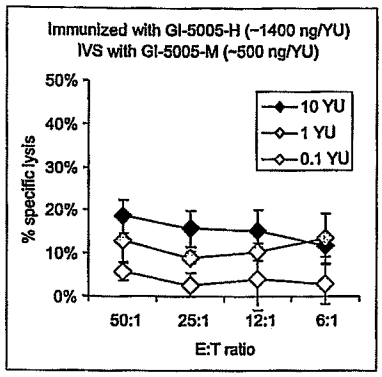


FIG. 14C

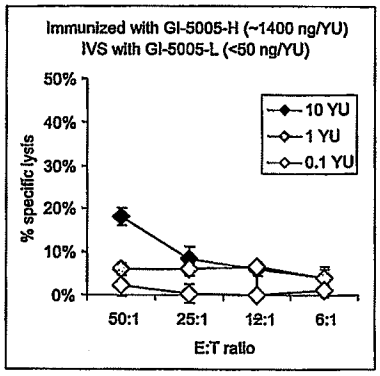


FIG. 14D

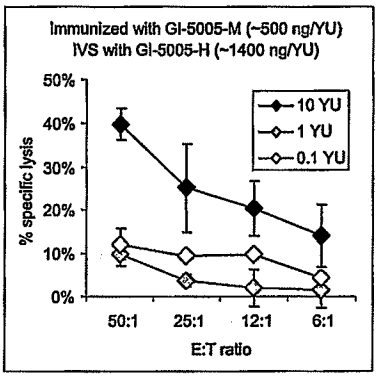


FIG. 14E

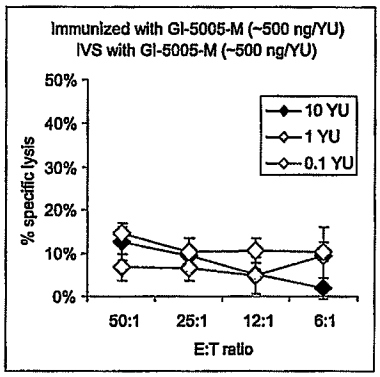


FIG. 14F

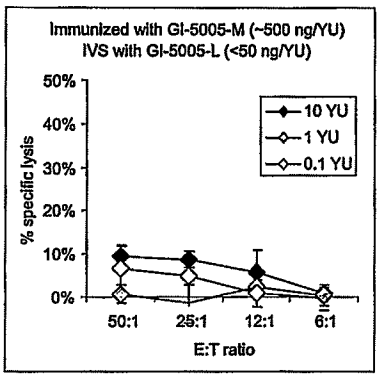


FIG. 14G

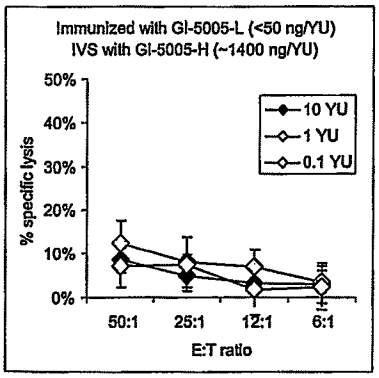


FIG. 14H

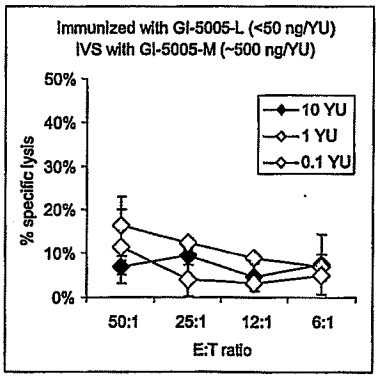


FIG. 14I

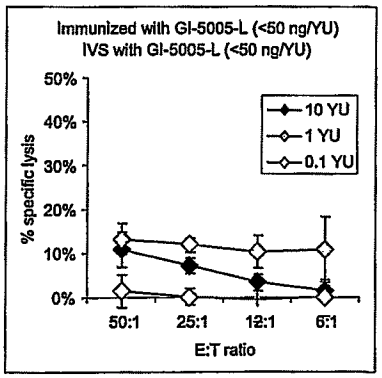


FIG. 15A

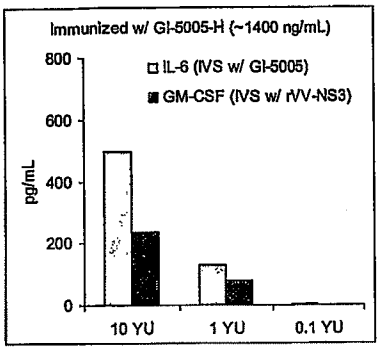


FIG. 15B

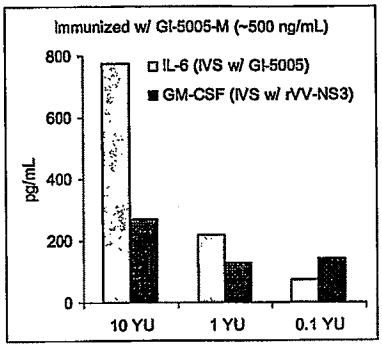


FIG. 15C

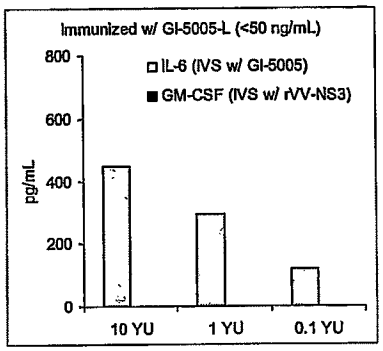


FIG. 16

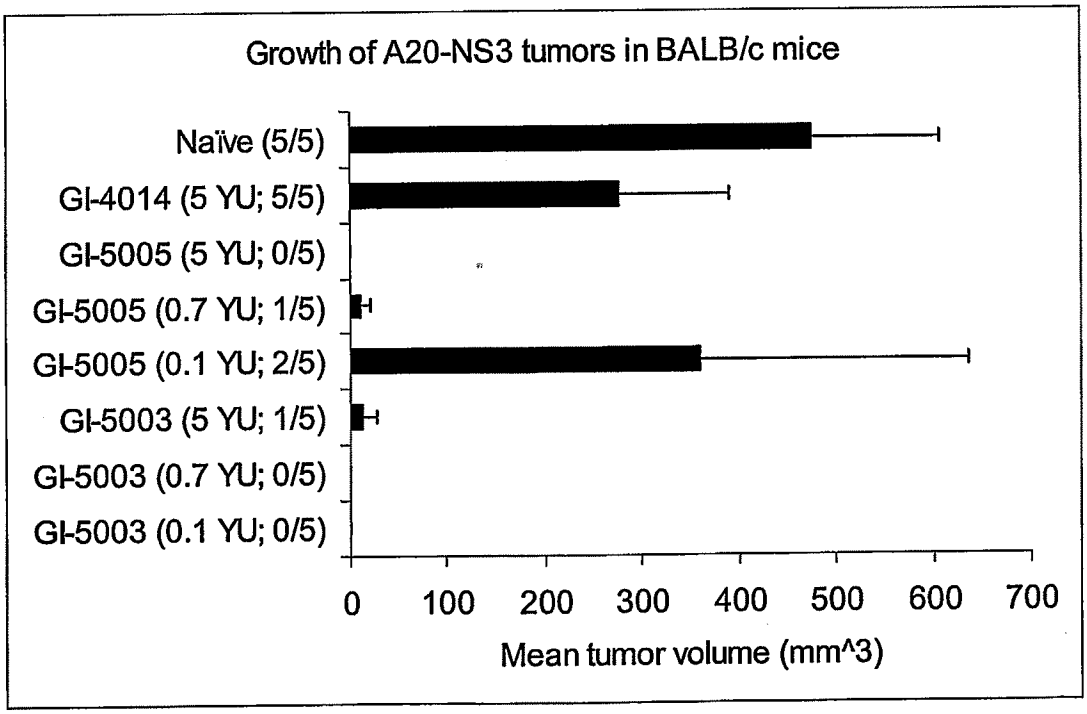


FIG. 17

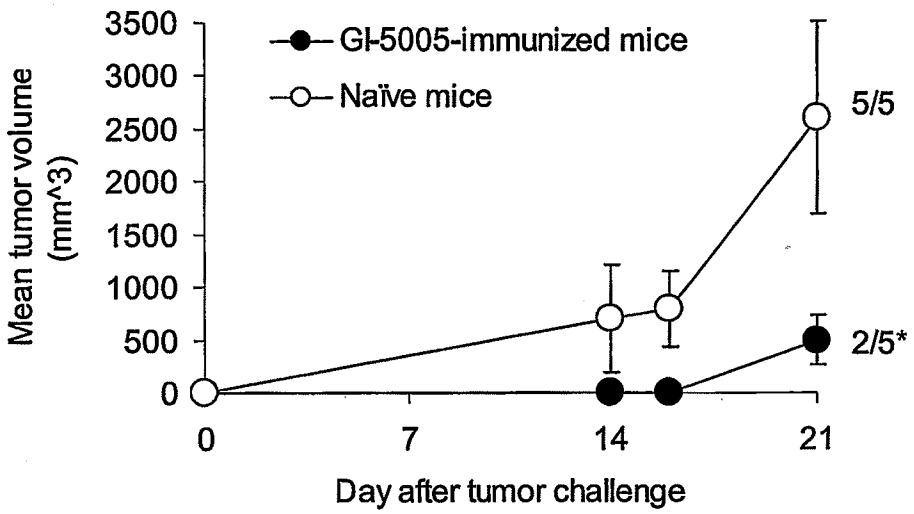

Mean tumor volume (mm^3)
3500
3000
2500
2000
1500
1000
500
0
GI-5005-immunized mice
Naïve mice
5/5
2/5*
0
7
14
21
Day after tumor challenge

FIG. 18

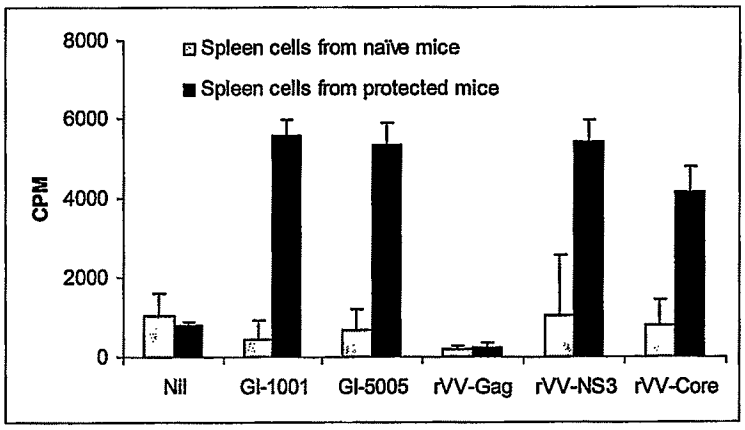

Spleen cells from naïve mice
Spleen cells from protected mice
CPM
8000
6000
4000
2000
0
Nil
GI-1001
GI-5005
rVV-Gag
rVV-NS3
rVV-Core

FIG. 19

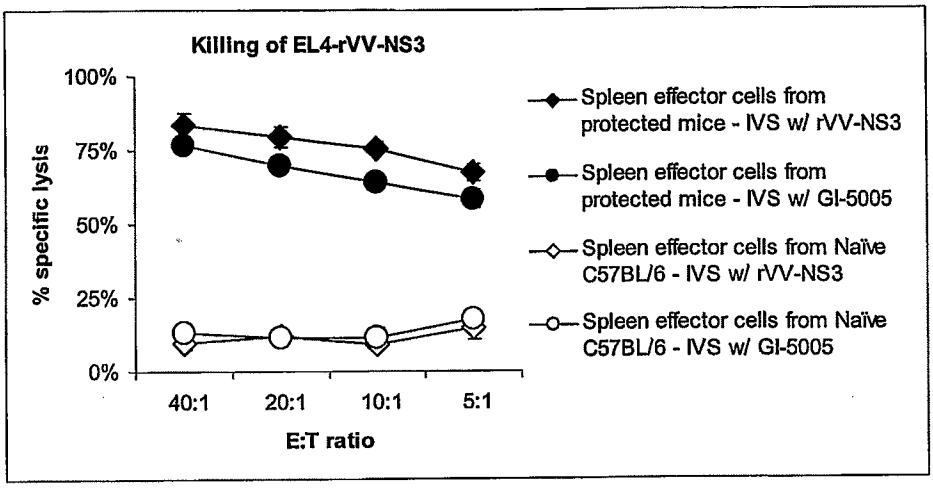

Killing of EL4-rVV-NS3
100%
75%
50%
25%
0%
% specific lysis
40:1
20:1
10:1
5:1
E:T ratio
Spleen effector cells from protected mice - IVS w/ rVV-NS3
Spleen effector cells from protected mice - IVS w/ GI-5005
Spleen effector cells from Naïve C57BL/6 - IVS w/ rVV-NS3
Spleen effector cells from Naïve C57BL/6 - IVS w/ GI-5005

FIG. 20

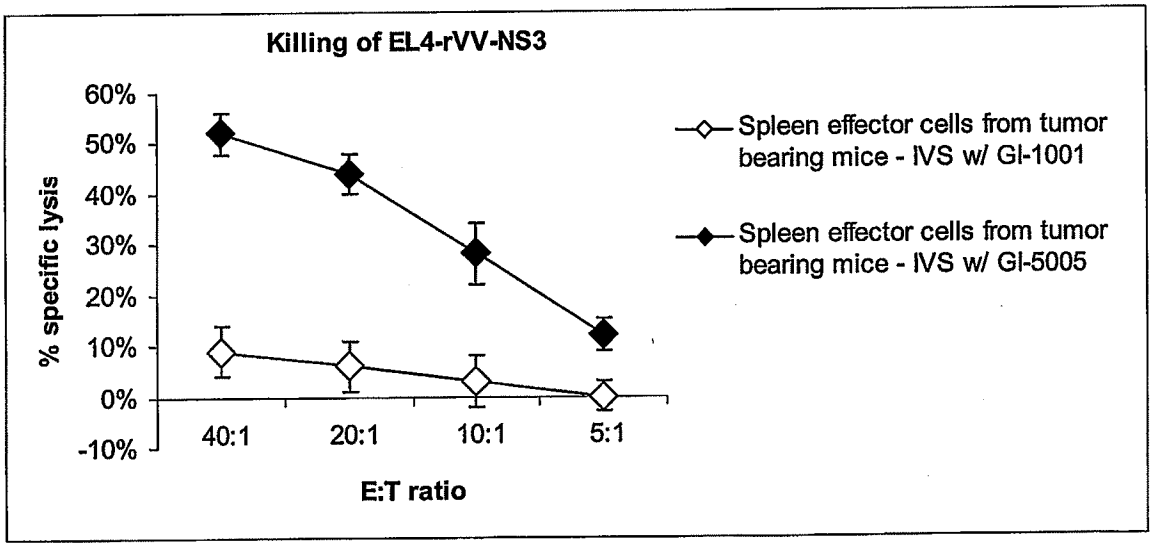

Killing of EL4-rVV-NS3
60%
50%
40%
30%
20%
10%
0%
-10%
% specific lysis
40:1
20:1
10:1
5:1
E:T ratio
Spleen effector cells from tumor bearing mice - IVS w/ GI-1001
Spleen effector cells from tumor bearing mice - IVS w/ GI-5005

FIG. 21

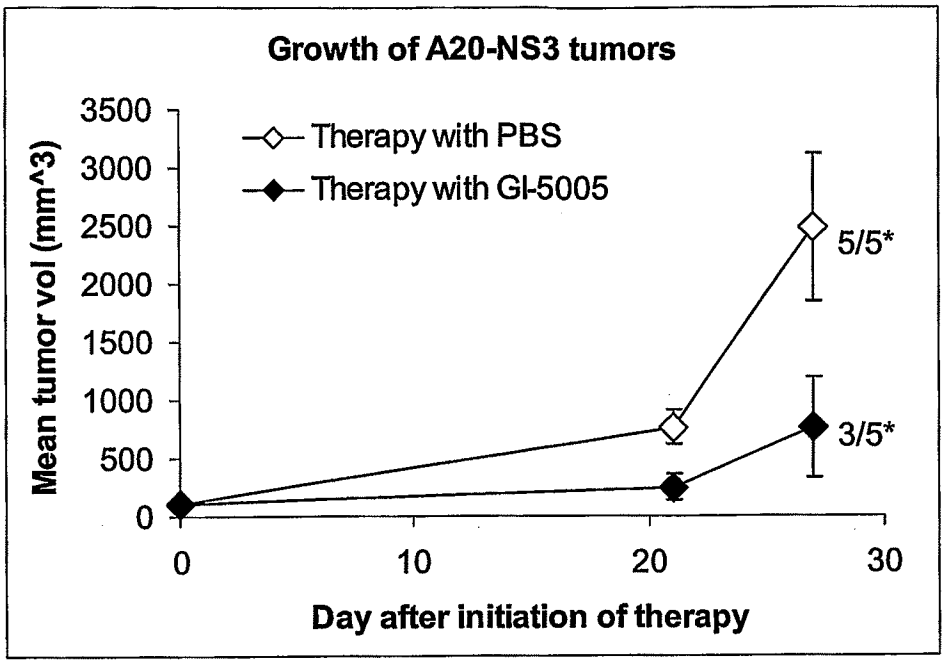


FIG. 22A

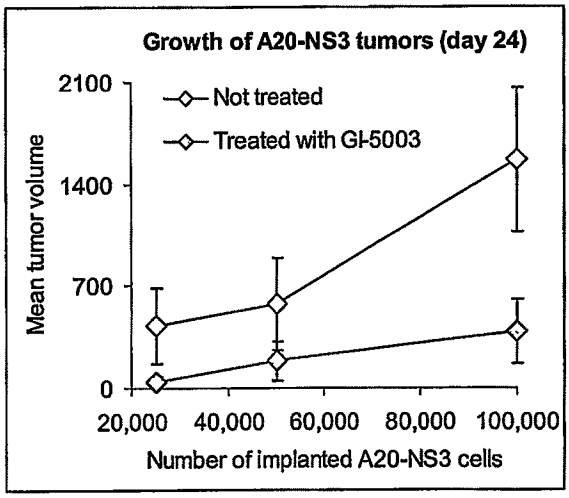


FIG. 22B

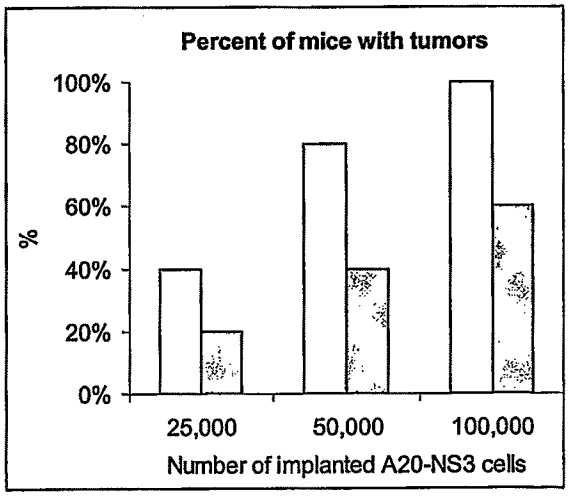


FIG. 23A

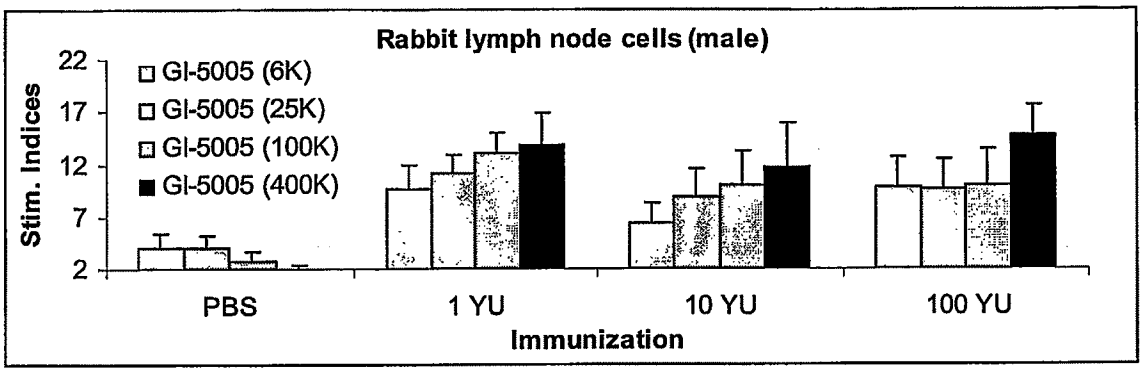
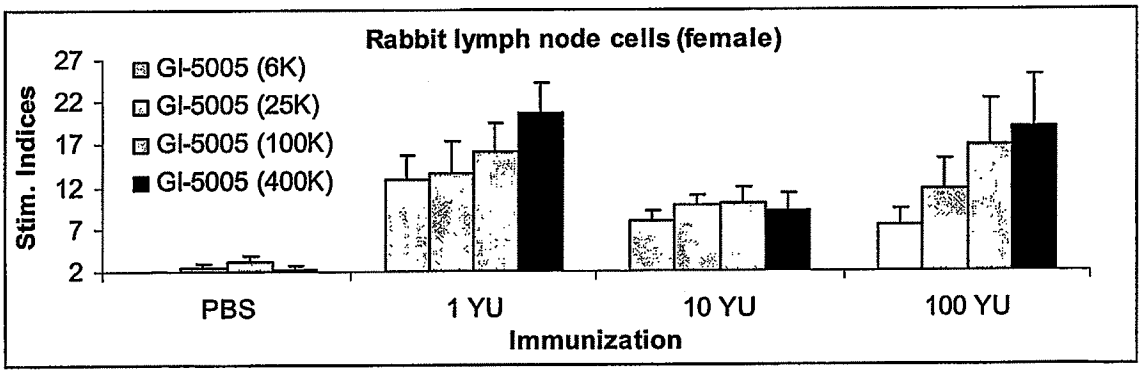


FIG. 23B



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20 25 30

Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg
35 40 45

Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro
50 55 60

Ala Gly His Ala Val Gly Leu Phe Arg Ala Ala Val Cys Thr Arg Gly
65 70 75 80

Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu Gly Thr Thr
85 90 95

Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro
100 105 110

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

Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu
130 135 140

Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met
145 150 155 160

Ser Lys Ala His Gly Val Asp Pro Asn Ile Arg Thr Gly Val Arg Thr
165 170 175

Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu
180 185 190

```
Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp
        195                 200                 205

Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val
    210                 215                 220

Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr
225                 230                 235                 240

Ala Thr Pro Pro Gly Ser Val Thr Val Ser His Pro Asn Ile Glu Glu
                245                 250                 255

Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Thr Ser Thr Asn
            260                 265                 270

Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
        275                 280                 285

Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
    290                 295                 300

Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
305                 310                 315                 320

Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
                325                 330                 335

Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
            340                 345                 350

Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
        355                 360                 365

Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser
    370                 375                 380

Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp
385                 390                 395                 400

Leu Met Gly Tyr Ile Pro Leu Val Glu Asp
                405                 410
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<210> 3
<211> 1914
<212> DNA
<213> Artificial

<220>
<223> recombinant fusion protein construct

<400> 3

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atcgtgtcaa ctgctaccca aaccttcctg gcaacgtgca tcaatggggt atgctggact 180

gtctaccacg gggccggaac gaggaccatc gcatcaccca agggtcctgt catccagatg 240

tataccaatg tggaccaaga ccttgtgggc tggcccgctc ctcaaggttc ccgctcattg 300

acaccctgta cctgcggctc ctcggacctt tacctggtca cgaggcacgc cgatgtcatt 360

cccgtgcgcc ggcgaggtga tagcaggggt agcctgcttt cgccccggcc catttcctac 420

ttgaaaggct ccgctggggg tccgctgttg tgccccgcgg gacacgccgt gggcctattc 480

agggccgcgg tgtgcacccg tggagtggct aaagcggtgg actttatccc tgtggagaac 540

ctagggacaa ccatgagatc cccggtgttc acggacaact cctctccacc agcagtgccc 600

cagagcttcc aggtggccca cctgcatgct cccaccggca gcggtaagag caccaaggtc 660

ccggctgcgt acgcagccca gggctacaag gtgttggtgc tcaacccctc tgttgctgca 720

acgctgggct ttggtgctta catgtccaag gcccatgggg ttgatcctaa tatcaggacc 780

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gcgagactgg ttgtgctcgc cactgctacc cctccgggct ccgtcactgt gtcccatcct 1020

aacatcgagg aggttgctct gtccaccacc ggagagatcc ccttttacgg caaggctatc 1080

cccctcgagg tgatcaaggg gggaagacat ctcatcttct gccactcaaa gaagaagtgc 1140

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gcgtacatga acaccccggg gcttcccgtg tgccaggacc atcttgaatt ttgggagggc 1620

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gagaactttc cttacctggt agcgtaccaa gccaccgtgt gcgctagggc tcaagcccct 1740

cccccatcgt gggaccagat gtggaagtgt ttgatccgcc ttaaacccac cctccatggg 1800

ccaacacccc tgctatacag actgggcgct gttcagaatg aagtcaccct gacgcaccca 1860

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<210> 4
<211> 637
<212> PRT
<213> Artificial

<220>
<223> recombinant fusion protein

<400> 4

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Met Ala Asp Glu Ala Pro Ala Pro Ile Thr Ala Tyr Ala Gln Gln Thr
1               5                  10                  15

Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys
            20                  25                  30

Asn Gln Val Glu Gly Glu Val Gln Ile Val Ser Thr Ala Thr Gln Thr
        35                  40                  45

Phe Leu Ala Thr Cys Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly
    50                  55                  60

Ala Gly Thr Arg Thr Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met
65                  70                  75                  80

Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly
                85                  90                  95

Ser Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu
            100                 105                 110

Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser
        115                 120                 125

Arg Gly Ser Leu Leu Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser
    130                 135                 140

Ala Gly Gly Pro Leu Leu Cys Pro Ala Gly His Ala Val Gly Leu Phe
145                 150                 155                 160

Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile
                165                 170                 175

Pro Val Glu Asn Leu Gly Thr Thr Met Arg Ser Pro Val Phe Thr Asp
            180                 185                 190

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

His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr
210 215 220

Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala
225 230 235 240

Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly Val Asp Pro
245 250 255

Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr
260 265 270

Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly
275 280 285

Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr
290 295 300

Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly
305 310 315 320

Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr
325 330 335

Val Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu
340 345 350

Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly
355 360 365

Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala
370 375 380

Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly
385 390 395 400

Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ser
405 410 415

Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile
420 425 430

Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro
435 440 445

Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala Val Ser Arg
450 455 460

Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg
465 470 475 480

Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val
485 490 495

Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro
500 505 510

Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu
515 520 525

Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly
530 535 540

Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly
545 550 555 560

Glu Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg
565 570 575

Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile
580 585 590

Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu
595 600 605

Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr
610 615 620

Ile Met Thr Cys Met Ser Ala Asp Leu Glu Val Val Thr
625 630 635

<210> 5
<211> 1491
<212> DNA
<213> Artificial

<220>
<223> recombinant fusion protein construct

<400> 5
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gattgcccta actcgagtat tgtgtacgag gcggccgatg ccatcctgca cactccgggg 120

tgtgtccctt gcgttcgcga gggtaacgcc tcgaggtgtt gggtggcggt gacccccacg 180

gtggccacca gggacggcaa actccccaca acgcagcttc gacgtcatat cgatctgctt 240

gtcgggagcg ccaccctctg ctcggccctc tacgtggggg acctgtgcgg gtctgtcttt 300

cttgttggtc aactgtttac cttctctccc aggcgccact ggacgacgca agactgcaat 360

tgttctatct atcccggcca tataacgggt catcgcatgg catgggatat gatgatgaac 420

tggtccccta cggcagcgtt ggtggtagct cagctgctcc ggatcccaca agccatcatg 480

gacatggaaa cccacgtcac cgggggaagt gccggccgca ccacggctgg gcttgttggt 540

ctccttacac caggcgccaa gcagaacatc caactgatca acaccaacgg cagttggcac 600

atcaatagca cggccttgaa ctgcaatgaa agccttaaca ccggctggtt agcagggctc 660

ttctatcagc acaaattcaa ctcttcaggc tgtcctgaga ggttggccag ctgccgacgc 720

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gaacgccccc actgctggca ctaccctcca agaccttgtg gcattgtgcc cgcaaagagc 840

gtgtgtggcc cggtatattg cttcactccc agccccgtgg tggtgggaac gaccgacagg 900

tcgggcgcgc ctacctacag ctggggtgca aatgatacgg atgtcttcgt ccttaacaac 960

accaggccac cgctgggcaa ttggttcggt tgtacctgga tgaactcaac tggattcacc 1020

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cccactgatt gtttccgcaa gcatccggaa gccacatact ctcggtgcgg ctccggtccc 1140

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atcaattaca ccatattcaa agtcaggatg tacgtgggag gggtcgagca caggctggaa 1260

gcggcctgca actggacgcg gggcgaacgc tgtgatctgg aagacaggga caggtccgag 1320

ctcagcccat tgctgctgtc caccacacag tggcaggtcc ttccgtgttc tttcacgacc 1380

ctgccagcct tgtccaccgg cctcatccac ctccaccaga acattgtgga cgtgcagtac 1440

ttgtacgggg tagggtcaag catcgcgtcc tgggccatta agtgggagta g 1491

<210> 6
<211> 496
<212> PRT
<213> Artificial

<220>
<223> recombinant fusion protein

<400> 6

Met Ala Asp Glu Ala Pro Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr
1 5 10 15

His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala
20 25 30

Asp Ala Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly
35 40 45

Asn Ala Ser Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg
50 55 60

```
Asp Gly Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu
65                  70                  75                  80

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

Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg
            100                 105                 110

His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile
        115                 120                 125

Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr
    130                 135                 140

Ala Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Met
145                 150                 155                 160

Asp Met Glu Thr His Val Thr Gly Gly Ser Ala Gly Arg Thr Thr Ala
                165                 170                 175

Gly Leu Val Gly Leu Leu Thr Pro Gly Ala Lys Gln Asn Ile Gln Leu
            180                 185                 190

Ile Asn Thr Asn Gly Ser Trp His Ile Asn Ser Thr Ala Leu Asn Cys
        195                 200                 205

Asn Glu Ser Leu Asn Thr Gly Trp Leu Ala Gly Leu Phe Tyr Gln His
    210                 215                 220

Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Arg
225                 230                 235                 240

Leu Thr Asp Phe Ala Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly
                245                 250                 255

Ser Gly Leu Asp Glu Arg Pro Tyr Cys Trp His Tyr Pro Pro Arg Pro
            260                 265                 270

Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe
        275                 280                 285

Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro
    290                 295                 300

Thr Tyr Ser Trp Gly Ala Asn Asp Thr Asp Val Phe Val Leu Asn Asn
305                 310                 315                 320
```

Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser
325 330 335

Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly Gly
340 345 350

Val Gly Asn Asn Thr Leu Leu Cys Pro Thr Asp Cys Phe Arg Lys His
355 360 365

Pro Glu Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro
370 375 380

Arg Cys Met Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr
385 390 395 400

Ile Asn Tyr Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu
405 410 415

His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp
420 425 430

Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr
435 440 445

Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu
450 455 460

Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr
465 470 475 480

Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp Glu
485 490 495

<210> 7
<211> 483
<212> DNA
<213> Artificial

<220>
<223> recombinant fusion protein construct

<400> 7
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atcacccctg ctgtccagac caactggcag aaactcgagg tcttctgggc gaagcacatg 180

tggaatttca tcagtgggat acaatacttg gcgggcctgt caactagtcc tggagccctt 240

gtagtcggtg tggtctgcgc agcaatactg cgccggcacg ttggcccggg cgagggggca 300

gtgcaatgga tgaaccggct aatagccttc gcctcccggg ggaaccatgt ttcccccacg 360

cactacgtgc cggagagcga tgcagccgcc cgcgtcactg ccatactcag cagcctcact 420

gtaacccagc tcctgaggcg actgcatcag tggataagct cggagtgtac cactccatgc 480

tag 483

<210> 8
<211> 160
<212> PRT
<213> Artificial

<220>
<223> recombinant fusion protein

<400> 8

Met Ala Asp Glu Ala Pro Ser Gln His Leu Pro Tyr Ile Glu Gln Gly
1 5 10 15

Met Met Leu Ala Glu Gln Phe Lys Gln Lys Ala Leu Gly Leu Leu Gln
20 25 30

Thr Ala Ser Arg His Ala Glu Val Ile Thr Pro Ala Val Gln Thr Asn
35 40 45

Trp Gln Lys Leu Glu Val Phe Trp Ala Lys His Met Trp Asn Phe Ile
50 55 60

Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Ser Pro Gly Ala Leu
65 70 75 80

Val Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro
85 90 95

Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser
100 105 110

Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala
115 120 125

Ala Ala Arg Val Thr Ala Ile Leu Ser Ser Leu Thr Val Thr Gln Leu
130 135 140

Leu Arg Arg Leu His Gln Trp Ile Ser Ser Glu Cys Thr Thr Pro Cys
145 150 155 160

<210> 9
<211> 6
<212> PRT
<213> Artificial

<220>
<223> synthetic peptide

<400> 9

Met Ala Asp Glu Ala Pro
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial

<220>
<223> synthetic peptide

<400> 10

Gly Gly Gly His His His His His His
1 5

<210> 11
<211> 2256
<212> DNA
<213> Artificial

<220>
<223> recombinant fusion protein construct

<400> 11
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aaccgtcgcc cacaggacgt caagttcccg ggtggcggtc agatcgttgg tggagtttac 120

ttgttgccgc gcaggggccc tagattgggt gtgcgcgcga cgaggaagac ttccgagcgg 180

tcgcaacctc gaggtagacg tcagcctatc cccaaggcac gtcggcccga gggcaggacc 240

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tacataccgc tcgtcggcgc ccctcttgga ggcgctgcca gggccctggc gcatggcgtc 480

cgggttctgg aagacggcgt gaactatgca acagggaacc ttcctggttg ctctttctct 540

atcttccttc tggccctgct ctcttgcctg actgtgcccg cttcagccta ccaagtgcgc 600

aattcctcgg ggctttacca tgtcaccaat gattgcccta actcgagtat tgtgtacgag 660

gcggccgatg ccatcctgca cactccgggg tgtgtccctt gcgttcgcga gggtaacgcc 720

tcgaggtgtt gggtggcggt gacccccacg gtggccacca gggacggcaa actccccaca 780

acgcagcttc gacgtcatat cgatctgctt gtcgggagcg ccaccctctg ctcggccctc 840

tacgtggggg acctgtgcgg gtctgtcttt cttgttggtc aactgtttac cttctctccc 900

aggcgccact ggacgacgca agactgcaat tgttctatct atcccggcca tataacgggt 960

catcgcatgg catgggatat gatgatgaac tggtccccta cggcagcgtt ggtggtagct 1020

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ctggcgggca tagcgtattt ctccatggtg gggaactggg cgaaggtcct ggtagtgctg 1140

ctgctatttg ccggcgtcga cgcggaaacc cacgtcaccg ggggaagtgc cggccgcacc 1200

acggctgggc ttgttggtct ccttacacca ggcgccaagc agaacatcca actgatcaac 1260

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gacagggaca ggtccgagct cagcccattg ctgctgtcca ccacacagtg gcaggtcctt 2040

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attgtggacg tgcagtactt gtacggggta gggtcaagca tcgcgtcctg ggccattaag 2160

tgggagtacg tcgttctcct gttcctcctg cttgcagacg cgcgcgtctg ctcctgcttg 2220

tggatgatgt tactcatatc ccaagcggag gcgtag 2256

<210> 12
<211> 751
<212> PRT
<213> Artificial

<220>
<223> recombinant fusion protein

<400> 12

Met Ala Asp Glu Ala Pro Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr
1 5 10 15

Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
20 25 30

Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg
35 40 45

Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg
50 55 60

Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr
65 70 75 80

Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys
85 90 95

Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp
100 105 110

Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile
115 120 125

Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu
130 135 140

Val Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val
145 150 155 160

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

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val
180 185 190

Pro Ala Ser Ala Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val
195 200 205

Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala
210 215 220

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala
225 230 235 240

Ser Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly
245 250 255

Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly
260 265 270

Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser
275 280 285

```
Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp
    290                 295                 300

Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly
305                 310                 315                 320

His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Ala Ala
                325                 330                 335

Leu Val Val Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Met Asp Met
            340                 345                 350

Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser
        355                 360                 365

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala
    370                 375                 380

Gly Val Asp Ala Glu Thr His Val Thr Gly Gly Ser Ala Gly Arg Thr
385                 390                 395                 400

Thr Ala Gly Leu Val Gly Leu Leu Thr Pro Gly Ala Lys Gln Asn Ile
                405                 410                 415

Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn Ser Thr Ala Leu
            420                 425                 430

Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Leu Ala Gly Leu Phe Tyr
        435                 440                 445

Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys
    450                 455                 460

Arg Arg Leu Thr Asp Phe Ala Gln Gly Trp Gly Pro Ile Ser Tyr Ala
465                 470                 475                 480

Asn Gly Ser Gly Leu Asp Glu Arg Pro Tyr Cys Trp His Tyr Pro Pro
                485                 490                 495

Arg Pro Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val Tyr
            500                 505                 510

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly
        515                 520                 525

Ala Pro Thr Tyr Ser Trp Gly Ala Asn Asp Thr Asp Val Phe Val Leu
    530                 535                 540
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Asn Asn Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met
545 550 555 560

Asn Ser Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile
565 570 575

Gly Gly Val Gly Asn Asn Thr Leu Leu Cys Pro Thr Asp Cys Phe Arg
580 585 590

Lys His Pro Glu Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile
595 600 605

Thr Pro Arg Cys Met Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro
610 615 620

Cys Thr Ile Asn Tyr Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
625 630 635 640

Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
645 650 655

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
660 665 670

Ser Thr Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro
675 680 685

Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val
690 695 700

Gln Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys
705 710 715 720

Trp Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val
725 730 735

Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala
740 745 750

<210> 13
<211> 1908
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<213> Artificial

<220>
<223> recombinant fusion protein construct

<400> 13
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ttgttgccgc gcaggggccc tagattgggt gtgcgcgcga cgaggaagac ttccgagcgg 180

tcgcaacctc gaggtagacg tcagcctatc cccaaggcac gtcggcccga gggcaggacc 240

tgggctcagc ccgggtaccc ttggcccctc tatggcaatg agggttgcgg gtgggcggga 300

tggctcctgt ctccccgtgg ctctcggcct agctggggcc ccacagaccc ccggcgtagg 360

tcgcgcaatt tgggtaaggt catcgatacc cttacgtgcg gcttcgccga cctcatgggg 420

tacataccgc tcgtctacca agtgcgcaat tcctcggggc tttaccatgt caccaatgat 480

tgccctaact cgagtattgt gtacgaggcg gccgatgcca tcctgcacac tccggggtgt 540

gtcccttgcg ttcgcgaggg taacgcctcg aggtgttggg tggcggtgac ccccacggtg 600

gccaccaggg acggcaaact ccccacaacg cagcttcgac gtcatatcga tctgcttgtc 660

gggagcgcca ccctctgctc ggccctctac gtgggggacc tgtgcgggtc tgtctttctt 720

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atggaaaccc acgtcaccgg gggaagtgcc ggccgcacca cggctgggct tgttggtctc 960

cttacaccag gcgccaagca gaacatccaa ctgatcaaca ccaacggcag ttggcacatc 1020

aatagcacgg ccttgaactg caatgaaagc cttaacaccg gctggttagc agggctcttc 1080

tatcagcaca aattcaactc ttcaggctgt cctgagaggt tggccagctg ccgacgcctt 1140

accgattttg cccagggctg gggtcctatc agttatgcca acggaagcgg cctcgacgaa 1200

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<210> 14
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<212> PRT
<213> Artificial

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<400> 14

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Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
20 25 30

Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg
35 40 45

Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg
50 55 60

Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr
65 70 75 80

Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys
85 90 95

Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp
100 105 110

Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile
115 120 125

Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu
130 135 140

Val Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
145 150 155 160

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu His
165 170 175

Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser Arg Cys
180 185 190

Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro
195 200 205

Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala Thr
210 215 220

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Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu
225                 230                 235                 240

Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln
                245                 250                 255

Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
            260                 265                 270

Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Ala Ala Leu Val Val
        275                 280                 285

Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Met Asp Met Glu Thr His
    290                 295                 300

Val Thr Gly Gly Ser Ala Gly Arg Thr Thr Ala Gly Leu Val Gly Leu
305                 310                 315                 320

Leu Thr Pro Gly Ala Lys Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly
                325                 330                 335

Ser Trp His Ile Asn Ser Thr Ala Leu Asn Cys Asn Glu Ser Leu Asn
            340                 345                 350

Thr Gly Trp Leu Ala Gly Leu Phe Tyr Gln His Lys Phe Asn Ser Ser
        355                 360                 365

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Arg Leu Thr Asp Phe Ala
    370                 375                 380

Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly Leu Asp Glu
385                 390                 395                 400

Arg Pro Tyr Cys Trp His Tyr Pro Pro Arg Pro Cys Gly Ile Val Pro
                405                 410                 415

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val
            420                 425                 430

Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr Tyr Ser Trp Gly
        435                 440                 445

Ala Asn Asp Thr Asp Val Phe Val Leu Asn Asn Thr Arg Pro Pro Leu
    450                 455                 460

Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys
465                 470                 475                 480
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Val Cys Gly Ala Pro Pro Cys Val Ile Gly Gly Val Gly Asn Asn Thr
485 490 495

Leu Leu Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr
500 505 510

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Met Val Asp
515 520 525

Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile Asn Tyr Thr Ile
530 535 540

Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala
545 550 555 560

Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp
565 570 575

Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gln Trp Gln Val
580 585 590

Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile
595 600 605

His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly
610 615 620

Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp Glu
625 630 635

<210> 15
<211> 2538
<212> DNA
<213> Artificial

<220>
<223> recombinant fusion protein construct

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atcgtgtcaa ctgctaccca aaccttcctg gcaacgtgca tcaatggggt atgctggact 180

gtctaccacg gggccggaac gaggaccatc gcatcaccca agggtcctgt catccagatg 240

tataccaatg tggaccaaga ccttgtgggc tggcccgctc ctcaaggttc ccgctcattg 300

acaccctgta cctgcggctc ctcggacctt tacctggtca cgaggcacgc cgatgtcatt 360

cccgtgcgcc ggcgaggtga tagcaggggt agcctgcttt cgccccggcc catttcctac 420

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ctagggacaa ccatgagatc cccggtgttc acggacaact cctctccacc agcagtgccc 600

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gtcatagtgg gcaggattgt cttgtccggg aagccggcaa ttatacctga cagggaggtt 2040

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catgtttccc ccacgcacta cgtgccggag agcgatgcag ccgcccgcgt cactgccata 2460

ctcagcagcc tcactgtaac ccagctcctg aggcgactgc atcagtggat aagctcggag 2520

tgtaccactc catgctag 2538

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<212> PRT
<213> Artificial

<220>
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<400> 16

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Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys
20 25 30

Asn Gln Val Glu Gly Glu Val Gln Ile Val Ser Thr Ala Thr Gln Thr
35 40 45

Phe Leu Ala Thr Cys Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly
50 55 60

Ala Gly Thr Arg Thr Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met
65 70 75 80

Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly
85 90 95

Ser Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu
100 105 110

Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser
115 120 125

Arg Gly Ser Leu Leu Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser
130 135 140

Ala Gly Gly Pro Leu Leu Cys Pro Ala Gly His Ala Val Gly Leu Phe
145 150 155 160

Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile
165 170 175

Pro Val Glu Asn Leu Gly Thr Thr Met Arg Ser Pro Val Phe Thr Asp
180 185 190

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Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu
        195                 200                 205

His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr
    210                 215                 220

Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala
225                 230                 235                 240

Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly Val Asp Pro
                245                 250                 255

Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr
            260                 265                 270

Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly
        275                 280                 285

Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr
    290                 295                 300

Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly
305                 310                 315                 320

Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr
                325                 330                 335

Val Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu
            340                 345                 350

Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly
        355                 360                 365

Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala
    370                 375                 380

Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly
385                 390                 395                 400

Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ser
                405                 410                 415

Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile
            420                 425                 430

Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro
        435                 440                 445
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Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala Val Ser Arg
450 455 460

Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg
465 470 475 480

Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val
485 490 495

Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro
500 505 510

Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu
515 520 525

Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly
530 535 540

Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly
545 550 555 560

Glu Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg
565 570 575

Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile
580 585 590

Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu
595 600 605

Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr
610 615 620

Ile Met Thr Cys Met Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp
625 630 635 640

Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser
645 650 655

Thr Gly Cys Val Val Ile Val Gly Arg Ile Val Leu Ser Gly Lys Pro
660 665 670

Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln Glu Phe Asp Glu Met
675 680 685

Glu Glu Cys Ser Gln His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu
690 695 700

Ala Glu Gln Phe Lys Gln Lys Ala Leu Gly Leu Leu Gln Thr Ala Ser
705 710 715 720

Arg His Ala Glu Val Ile Thr Pro Ala Val Gln Thr Asn Trp Gln Lys
725 730 735

Leu Glu Val Phe Trp Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile
740 745 750

Gln Tyr Leu Ala Gly Leu Ser Thr Ser Pro Gly Ala Leu Val Val Gly
755 760 765

Val Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro Gly Glu Gly
770 775 780

Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn
785 790 795 800

His Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg
805 810 815

Val Thr Ala Ile Leu Ser Ser Leu Thr Val Thr Gln Leu Leu Arg Arg
820 825 830

Leu His Gln Trp Ile Ser Ser Glu Cys Thr Thr Pro Cys
835 840 845

<210> 17
<211> 2982
<212> DNA
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<220>
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ccctttgtgt cctgccagcg cgggtatagg ggggtctggc gaggagacgg cattatgcac 180

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gtcggtccta ggacctgcag gaacatgtgg agtgggacgt tccccattaa cgcctacacc 300

acgggccccc gtactccccc tcctgcgccg aactataagt tcgcgctgtg gagggtgtct 360

gcagaggaat acgtggagat aaggcgggtg ggggacttcc actacgtatc gggtatgact 420

actgacaatc ttaaatgccc gtgccagatc ccatcgcccg aatttttcac agaattggac 480

ggggtgcgcc tacataggtt tgcgcccccc tgcaagccct tgctgcggga ggaggtatca 540

ttcagagtag gactccacga gtacccggtg gggtcgcaat taccttgcga gcccgaaccg 600

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gggagaaggt tggcgagagg gtcacccccc tctatggcca gctcctcggc cagccagctg 720

tccgctccat ctctcaaggc aacttgcacc gccaaccatg actcccctga cgccgagctc 780

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gagaacaaag tggtgattct ggactccttc gatccgcttg tggcagagga ggatgagcgg 900

gaggtctccg tacccgcaga aattctgcgg aagtctcgga gattcgcccg ggccctgccc 960

gtttgggcgc ggccggacta caacccccccg ctagtagaga cgtggaaaaa gcctgactac 1020

gaaccacctg tggtccatgg ctgcccgcta ccacctccac ggtcccctcc tgtgcctccg 1080

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aactgggcag taagaacaaa gctcaaactc actccaatat ag 2982

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<211> 993
<212> PRT
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<400> 18

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20 25 30

Leu Met Pro Gln Leu Pro Gly Ile Pro Phe Val Ser Cys Gln Arg Gly
35 40 45

Tyr Arg Gly Val Trp Arg Gly Asp Gly Ile Met His Thr Arg Cys His
50 55 60

Cys Gly Ala Glu Ile Thr Gly His Val Lys Asn Gly Thr Met Arg Ile
65 70 75 80

Val Gly Pro Arg Thr Cys Arg Asn Met Trp Ser Gly Thr Phe Pro Ile
85 90 95

Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro Leu Pro Ala Pro Asn Tyr
100 105 110

Lys Phe Ala Leu Trp Arg Val Ser Ala Glu Glu Tyr Val Glu Ile Arg
115 120 125

Arg Val Gly Asp Phe His Tyr Val Ser Gly Met Thr Thr Asp Asn Leu
130 135 140

Lys Cys Pro Cys Gln Ile Pro Ser Pro Glu Phe Phe Thr Glu Leu Asp
145 150 155 160

Gly Val Arg Leu His Arg Phe Ala Pro Pro Cys Lys Pro Leu Leu Arg
165 170 175

Glu Glu Val Ser Phe Arg Val Gly Leu His Glu Tyr Pro Val Gly Ser
180 185 190

Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met
195 200 205

Leu Thr Asp Pro Ser His Ile Thr Ala Glu Ala Ala Gly Arg Arg Leu
210 215 220

Ala Arg Gly Ser Pro Pro Ser Met Ala Ser Ser Ser Ala Ser Gln Leu
225 230 235 240

Ser Ala Pro Ser Leu Lys Ala Thr Cys Thr Ala Asn His Asp Ser Pro
245 250 255

Asp Ala Glu Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly
260 265 270

Gly Asn Ile Thr Arg Val Glu Ser Glu Asn Lys Val Val Ile Leu Asp
275 280 285

Ser Phe Asp Pro Leu Val Ala Glu Glu Asp Glu Arg Glu Val Ser Val
290 295 300

Pro Ala Glu Ile Leu Arg Lys Ser Arg Arg Phe Ala Arg Ala Leu Pro
305 310 315 320

Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys
325 330 335

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Leu Pro Pro Ile Ile Gln Arg Leu His Gly Leu Ser Ala Phe Ser Leu
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His Ser Tyr Ser Pro Gly Glu Ile Asn Arg Val Ala Ala Cys Leu Arg
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Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu
625                 630                 635                 640

Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp
                645                 650                 655

Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gln Trp
            660                 665                 670

Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
        675                 680                 685

Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly
    690                 695                 700

Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp Glu Tyr Val Val
705                 710                 715                 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp
                725                 730                 735

Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
            740                 745                 750

Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly Leu Val Ser Phe
        755                 760                 765

Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly Arg Trp Val Pro
    770                 775                 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Met Trp Pro Leu Leu Leu Leu Leu
785                 790                 795                 800

Leu Ala Leu Pro Gln Arg Ala Tyr Ala Leu Asp Thr Glu Val Ala Ala
                805                 810                 815

Ser Cys Gly Gly Val Val Leu Val Gly Leu Met Ala Leu Thr Leu Ser
            820                 825                 830

Pro Tyr Tyr Lys Arg Tyr Ile Ser Trp Cys Met Trp Trp Leu Gln Tyr
        835                 840                 845

Phe Leu Thr Arg Val Glu Ala Gln Leu His Val Trp Val Pro Pro Leu
    850                 855                 860
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Asn Val Arg Gly Gly Arg Asp Ala Val Ile Leu Leu Met Cys Val Val
865                 870                 875                 880

His Pro Thr Leu Val Phe Asp Ile Thr Lys Leu Leu Leu Ala Ile Phe
                885                 890                 895

Gly Pro Leu Trp Ile Leu Gln Ala Ser Leu Leu Lys Val Pro Tyr Phe
            900                 905                 910

Val Arg Val Gln Gly Leu Leu Arg Ile Cys Ala Leu Ala Arg Lys Ile
        915                 920                 925

Ala Gly Gly His Tyr Val Gln Met Ala Ile Ile Lys Leu Gly Ala Leu
    930                 935                 940

Thr Gly Thr Tyr Val Tyr Asn His Leu Thr Pro Leu Arg Asp Trp Ala
945                 950                 955                 960

His Asn Gly Leu Arg Asp Leu Ala Val Ala Val Glu Pro Val Val Phe
                965                 970                 975

Ser Arg Met Glu Thr Lys Leu Ile Thr Trp Gly Ala Asp Thr Ala Ala
            980                 985                 990

Cys Gly Asp Ile Ile Asn Gly Leu  Pro Val Ser Ala Arg  Arg Gly Gln
        995                 1000                1005

Glu Ile  Leu Leu Gly Pro Ala  Asp Gly Met Val Ser  Lys Gly Trp
    1010                1015                1020

Arg Leu  Gln Ala Pro Ile Thr  Ala Tyr Thr Gln Gln  Thr Arg Gly
    1025                1030                1035

Leu Leu  Gly Cys Ile Ile Thr  Ser Leu Thr Gly Arg  Asp Lys Asn
    1040                1045                1050

Gln Val  Glu Gly Glu Val Gln  Ile Val Ser Thr Ala  Thr Gln Thr
    1055                1060                1065

Phe Leu  Ala Thr Cys Ile Asn  Gly Val Cys Trp Thr  Val Tyr His
    1070                1075                1080

Gly Ala  Gly Thr Arg Thr Ile  Ala Ser Pro Lys Gly  Pro Val Ile
    1085                1090                1095

Gln Met  Tyr Thr Asn Val Asp  Gln Asp Leu Val Gly  Trp Pro Ala
    1100                1105                1110
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Pro Gln  Gly Ser Arg Ser Leu  Ala Pro Cys Thr Cys  Gly Ser Ser
    1115                 1120                 1125

Asp Leu  Tyr Leu Val Thr Arg  His Ala Asp Val Ile  Pro Val Arg
    1130                 1135                 1140

Arg Arg  Gly Asp Ser Arg Gly  Ser Leu Leu Ser Pro  Arg Pro Ile
    1145                 1150                 1155

Ser Tyr  Leu Lys Gly Ser Ser  Gly Gly Pro Leu Leu  Cys Pro Ala
    1160                 1165                 1170

Gly His  Ala Val Gly Leu Phe  Arg Ala Ala Val Cys  Thr Arg Gly
    1175                 1180                 1185

Val Ala  Lys Ala Val Asp Phe  Ile Pro Val Glu Asn  Leu Gly Thr
    1190                 1195                 1200

Thr Met  Arg Ser Pro Val Phe  Thr Asp Asn Ser Ser  Pro Pro Ala
    1205                 1210                 1215

Val Pro  Gln Ser Phe Gln Val  Ala His Leu His Ala  Pro Thr Gly
    1220                 1225                 1230

Ser Gly  Lys Ser Thr Lys Val  Pro Ala Ala Tyr Ala  Ala Gln Gly
    1235                 1240                 1245

Tyr Lys  Val Leu Val Leu Asn  Pro Ser Val Ala Ala  Thr Leu Gly
    1250                 1255                 1260

Phe Gly  Ala Tyr Met Ser Lys  Ala His Gly Val Asp  Pro Asn Ile
    1265                 1270                 1275

Arg Thr  Gly Val Arg Thr Ile  Thr Thr Gly Ser Pro  Ile Thr Tyr
    1280                 1285                 1290

Ser Thr  Tyr Gly Lys Phe Leu  Ala Asp Gly Gly Cys  Ser Gly Gly
    1295                 1300                 1305

Ala Tyr  Asp Ile Ile Ile Cys  Asp Glu Cys His Ser  Thr Asp Ala
    1310                 1315                 1320

Thr Ser  Ile Leu Gly Ile Gly  Thr Val Leu Asp Gln  Ala Glu Thr
    1325                 1330                 1335

Ala Gly  Ala Arg Leu Val Val  Leu Ala Thr Ala Thr  Pro Pro Gly
    1340                 1345                 1350
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Ser Val Thr Val Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser
1355 1360 1365

Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu
1370 1375 1380

Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys
1385 1390 1395

Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn
1400 1405 1410

Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr
1415 1420 1425

Ser Gly Asp Val Val Val Val Ser Thr Asp Ala Leu Met Thr Gly
1430 1435 1440

Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val
1445 1450 1455

Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
1460 1465 1470

Thr Thr Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg
1475 1480 1485

Gly Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala
1490 1495 1500

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys
1505 1510 1515

Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala
1520 1525 1530

Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu
1535 1540 1545

Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr
1550 1555 1560

Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln
1565 1570 1575

Ser Gly Glu Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val
1580 1585 1590

Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp
1595 1600 1605

Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro
1610 1615 1620

Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr
1625 1630 1635

His Pro Ile Thr Lys Tyr Ile Met Thr Cys Met Ser Ala Asp Leu
1640 1645 1650

Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala
1655 1660 1665

Ala Leu Ala Ala Tyr Cys Leu Ser Thr Gly Cys Val Val Ile Val
1670 1675 1680

Gly Arg Ile Val Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg
1685 1690 1695

Glu Val Leu Tyr Gln Glu Phe Asp Glu Met Glu Glu Cys Ser Gln
1700 1705 1710

His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu Ala Glu Gln Phe
1715 1720 1725

Lys Gln Lys Ala Leu Gly Leu Leu Gln Thr Ala Ser Arg His Ala
1730 1735 1740

Glu Val Ile Thr Pro Ala Val Gln Thr Asn Trp Gln Lys Leu Glu
1745 1750 1755

Val Phe Trp Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln
1760 1765 1770

Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala
1775 1780 1785

Ser Leu Met Ala Phe Thr Ala Ala Val Thr Ser Pro Leu Thr Thr
1790 1795 1800

Gly Gln Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala Ala
1805 1810 1815

Gln Leu Ala Ala Pro Gly Ala Ala Thr Ala Phe Val Gly Ala Gly
1820 1825 1830

Leu Ala Gly Ala Ala Ile Gly Ser Val Gly Leu Gly Lys Val Leu
1835 1840 1845

Val Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu
1850 1855 1860

Val Ala Phe Lys Ile Met Ser Gly Glu Val Pro Ser Thr Glu Asp
1865 1870 1875

Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val
1880 1885 1890

Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro
1895 1900 1905

Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala
1910 1915 1920

Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu Ser
1925 1930 1935

Asp Ala Ala Ala Arg Val Thr Ala Ile Leu Ser Ser Leu Thr Val
1940 1945 1950

Thr Gln Leu Leu Arg Arg Leu His Gln Trp Ile Ser Ser Glu Cys
1955 1960 1965

Thr Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Ile Trp Asp Trp
1970 1975 1980

Ile Cys Glu Val Leu Ser Asp Phe Lys Thr Trp Leu Lys Ala Lys
1985 1990 1995

Leu Met Pro Gln Leu Pro Gly Ile Pro Phe Val Ser Cys Gln Arg
2000 2005 2010

Gly Tyr Arg Gly Val Trp Arg Gly Asp Gly Ile Met His Thr Arg
2015 2020 2025

Cys His Cys Gly Ala Glu Ile Thr Gly His Val Lys Asn Gly Thr
2030 2035 2040

Met Arg Ile Val Gly Pro Arg Thr Cys Arg Asn Met Trp Ser Gly
2045 2050 2055

Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro Leu
2060 2065 2070

Pro Ala Pro Asn Tyr Lys Phe Ala Leu Trp Arg Val Ser Ala Glu
2075 2080 2085

Glu Tyr Val Glu Ile Arg Arg Val Gly Asp Phe His Tyr Val Ser
2090 2095 2100

Gly Met Thr Thr Asp Asn Leu Lys Cys Pro Cys Gln Ile Pro Ser
2105 2110 2115

Pro Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg Phe
2120 2125 2130

Ala Pro Pro Cys Lys Pro Leu Leu Arg Glu Glu Val Ser Phe Arg
2135 2140 2145

Val Gly Leu His Glu Tyr Pro Val Gly Ser Gln Leu Pro Cys Glu
2150 2155 2160

Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro
2165 2170 2175

Ser His Ile Thr Ala Glu Ala Ala Gly Arg Arg Leu Ala Arg Gly
2180 2185 2190

Ser Pro Pro Ser Met Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala
2195 2200 2205

Pro Ser Leu Lys Ala Thr Cys Thr Ala Asn His Asp Ser Pro Asp
2210 2215 2220

Ala Glu Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly
2225 2230 2235

Gly Asn Ile Thr Arg Val Glu Ser Glu Asn Lys Val Val Ile Leu
2240 2245 2250

Asp Ser Phe Asp Pro Leu Val Ala Glu Glu Asp Glu Arg Glu Val
2255 2260 2265

Ser Val Pro Ala Glu Ile Leu Arg Lys Ser Arg Arg Phe Ala Arg
2270 2275 2280

Ala Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val
2285 2290 2295

Glu Thr Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly
2300 2305 2310

Cys Pro Leu Pro Pro Pro Arg Ser Pro Pro Val Pro Pro Pro Arg
2315 2320 2325

Lys Lys Arg Thr Val Val Leu Thr Glu Ser Thr Leu Ser Thr Ala
2330 2335 2340

Leu Ala Glu Leu Ala Thr Lys Ser Phe Gly Ser Ser Ser Thr Ser
2345 2350 2355

Gly Ile Thr Gly Asp Asn Thr Thr Thr Ser Ser Glu Pro Ala Pro
2360 2365 2370

Ser Gly Cys Pro Pro Asp Ser Asp Val Glu Ser Tyr Ser Ser Met
2375 2380 2385

Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly
2390 2395 2400

Ser Trp Ser Thr Val Ser Ser Gly Ala Asp Thr Glu Asp Val Val
2405 2410 2415

Cys Cys Ser Met Ser Tyr Ser Trp Thr Gly Ala Leu Val Thr Pro
2420 2425 2430

Cys Ala Ala Glu Glu Gln Lys Leu Pro Ile Asn Ala Leu Ser Asn
2435 2440 2445

Ser Leu Leu Arg His His Asn Leu Val Tyr Ser Thr Thr Ser Arg
2450 2455 2460

Ser Ala Cys Gln Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln
2465 2470 2475

Val Leu Asp Ser His Tyr Gln Asp Val Leu Lys Glu Val Lys Ala
2480 2485 2490

Ala Ala Ser Lys Val Lys Ala Asn Leu Leu Ser Val Glu Glu Ala
2495 2500 2505

Cys Ser Leu Thr Pro Pro His Ser Ala Lys Ser Lys Phe Gly Tyr
2510 2515 2520

Gly Ala Lys Asp Val Arg Cys His Ala Arg Lys Ala Val Ala His
2525 2530 2535

Ile Asn Ser Val Trp Lys Asp Leu Leu Glu Asp Ser Val Thr Pro
2540 2545 2550

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Ile Asp  Thr Thr Ile Met Ala  Lys Asn Glu Val Phe  Cys Val Gln
    2555                 2560                 2565

Pro Glu  Lys Gly Gly Arg Lys  Pro Ala Arg Leu Ile  Val Phe Pro
    2570                 2575                 2580

Asp Leu  Gly Val Arg Val Cys  Glu Lys Met Ala Leu  Tyr Asp Val
    2585                 2590                 2595

Val Ser  Lys Leu Pro Leu Ala  Val Met Gly Ser Ser  Tyr Gly Phe
    2600                 2605                 2610

Gln Tyr  Ser Pro Gly Gln Arg  Val Glu Phe Leu Val  Gln Ala Trp
    2615                 2620                 2625

Lys Ser  Lys Lys Thr Pro Met  Gly Phe Ser Tyr Asp  Thr Arg Cys
    2630                 2635                 2640

Phe Asp  Ser Thr Val Thr Glu  Ser Asp Ile Arg Thr  Glu Glu Ala
    2645                 2650                 2655

Ile Tyr  Gln Cys Cys Asp Leu  Asp Pro Gln Ala Arg  Val Ala Ile
    2660                 2665                 2670

Lys Ser  Leu Thr Glu Arg Leu  Tyr Val Gly Gly Pro  Leu Thr Asn
    2675                 2680                 2685

Ser Arg  Gly Glu Asn Cys Gly  Tyr Arg Arg Cys Arg  Ala Ser Gly
    2690                 2695                 2700

Val Leu  Thr Thr Ser Cys Gly  Asn Thr Leu Thr Cys  Tyr Ile Lys
    2705                 2710                 2715

Ala Arg  Ala Ala Cys Arg Ala  Ala Gly Leu Gln Asp  Cys Thr Met
    2720                 2725                 2730

Leu Val  Cys Gly Asp Asp Leu  Val Val Ile Cys Glu  Ser Ala Gly
    2735                 2740                 2745

Val Gln  Glu Asp Ala Ala Asn  Leu Arg Ala Phe Thr  Glu Ala Met
    2750                 2755                 2760

Thr Arg  Tyr Ser Ala Pro Pro  Gly Asp Pro Pro Gln  Pro Glu Tyr
    2765                 2770                 2775

Asp Leu  Glu Leu Ile Thr Ser  Cys Ser Ser Asn Val  Ser Val Ala
    2780                 2785                 2790
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His Asp Gly Ala Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro
2795 2800 2805

Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr
2810 2815 2820

Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe Ala Pro Thr
2825 2830 2835

Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Val Leu
2840 2845 2850

Ile Ala Arg Asp Gln Leu Glu Gln Ala Leu Asn Cys Glu Ile Tyr
2855 2860 2865

Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Pro Ile Ile
2870 2875 2880

Gln Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser
2885 2890 2895

Pro Gly Glu Ile Asn Arg Val Ala Ala Cys Leu Arg Lys Leu Gly
2900 2905 2910

Val Pro Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ser Val Arg
2915 2920 2925

Ala Arg Leu Leu Ser Arg Gly Gly Arg Ala Ala Ile Cys Gly Lys
2930 2935 2940

Tyr Leu Phe Asn Trp Ala Val Arg Thr Lys Leu Lys Leu Thr Pro
2945 2950 2955

Ile Thr Ala Ala Gly Arg Leu Asp Leu Ser Gly Trp Phe Thr Ala
2960 2965 2970

Gly Tyr Ser Gly Gly Asp Ile Tyr His Ser Val Ser His Ala Arg
2975 2980 2985

Pro Arg Trp Phe Trp Phe Cys Leu Leu Leu Leu Ala Ala Gly Val
2990 2995 3000

Gly Ile Tyr Leu Leu Pro Asn Arg
3005 3010

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