```
Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
1               5                  10                  15
Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
            20                  25                  30
Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
        35                  40                  45
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
    50                  55                  60
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65                  70                  75                  80
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
                85                  90                  95
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
            100                 105                 110
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
        115                 120                 125
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
    130                 135                 140
Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145                 150                 155
```

FIG. 1

1 atgggcagca gccatcatca tcatcatcac agcagcggcc tggtgccgcg cggcagccat

61 ATGgcagccg ggagcatcac cacgctgccc gccttgcccg aggatggcgg cagcggcgcc

121 ttcccgcccg gccacttcaa ggaccccaag cggctgtact gcaaaaacgg gggcttcttc

181 ctgcgcatcc accccgacgg ccgagttgac ggggtccggg agaagagcga ccctcacatc

241 aagctacaac ttcaagcaga agagagagga gttgtgtcta tcaaaggagt gtgtgctaac

301 cgttacctgg ctatgaagga agatggaaga ttactggctt ctaaatgtgt tacggatgag

361 tgtttctttt ttgaacgatt ggaatctaat aactacaata cttaccggtc aaggaaatac

421 accagttggt atgtggcact gaaacgaact gggcagtata aacttggatc caaaacagga

481 cctgggcaga aagctatact ttttcttcca atgtctgcta agagcTAGct cgag

FIG. 2