```
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc      60
acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg     120
actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact     180
ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt     240
agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa     300
gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga     360
ggtggaggtg gaggtggagg tcctaaatct tgtgacaaaa ctcacacatg cccaccgtgc     420
ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac     480
accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa     540
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca     600
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg     660
caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca     720
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac     780
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc     840
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac     900
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag     960
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat    1020
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatag       1077
```

FIGURE 1

```
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1               5                  10                  15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
            20                  25                  30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
        35                  40                  45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
    50                  55                  60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65                  70                  75                  80

Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu
                85                  90                  95

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
            100                 105                 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro
        115                 120                 125

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
    130                 135                 140

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
145                 150                 155                 160

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                165                 170                 175

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            180                 185                 190

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        195                 200                 205

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    210                 215                 220
```

FIGURE 2A

```
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
225                 230                 235                 240

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                245                 250                 255

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
            260                 265                 270

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        275                 280                 285

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
    290                 295                 300

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
305                 310                 315                 320

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                325                 330                 335

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
            340                 345                 350

Ser Leu Ser Pro Gly Lys
        355
```

FIGURE 2B

CTGACGGACAGACAGACAGACACCGCCCCCAGCCCCAGCTACCACCTCCTCCCCGGCCGGCGGCG
GACAGTGGACGCGGCGGCGAGCCGCGGGCAGGGGCCGGAGCCCGCGCCCGGAGGCGGGGTGGAGG
GGGTCGGGGCTCGCGGCGTCGCACTGAAACTTTTCGTCCAACTTCTGGGCTGTTCTCGCTTCGGA
GGAGCCGTGGTCCGCGCGGGGGAAGCCGAGCCGAGCGGAGCCGCGAGAAGTGCTAGCTCGGGCCG
GGAGGAGCCGCAGCCGGAGGAGGGGGAGGAGGAAGAAGAGAAGGAAGAGGAGAGGGGGCCGCAGT
GGCGACTCGGCGCTCGGAAGCCGGGCTCATGGACGGGTGAGGCGGCGGTGTGCGCAGACAGTGCT
CCAGCCGCGCGCGCTCCCCAGGCCCTGGCCCGGGCCTCGGGCCGGGGAGGAAGAGTAGCTCGCCG
AGGCGCCGAGGAGAGCGGGCCGCCCCACAGCCCGAGCCGGAGAGGGAGCGCGAGCCGCGCCGGCC
CCGGTCGGGCCTCCGAAACCATGAACTTTCTGCTGTCTTGGGTGCATTGGAGCCTTGCCTTGCTG
CTCTACCTCCACCATGCCAAGTGGTCCCAGGCTGCACCCATGGCAGAAGGAGGAGGGCAGAATCA
TCACGAAGTGGTGAAGTTCATGGATGTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCTGG
TGGACATCTTCCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCTG
ATGCGATGCGGGGGCTGCTGCAATGACGAGGGCCTGGAGTGTGTGCCCACTGAGGAGTCCAACAT
CACCATGCAGATTATGCGGATCAAACCTCACCAAGGCCAGCACATAGGAGAGATGAGCTTCCTAC
AGCACAACAAATGTGAATGCAGACCAAAGAAAGATAGAGCAAGACAAGAAAAAAAATCAGTTCGA
GGAAAGGGAAAGGGGCAAAAACGAAAGCGCAAGAAATCCCGGTATAAGTCCTGGAGCGTTCCCTG
TGGGCCTTGCTCAGAGCGGAGAAAGCATTTGTTTGTACAAGATCCGCAGACGTGTAAATGTTCCT
GCAAAAACACAGACTCGCGTTGCAAGGCGAGGCAGCTTGAGTTAAACGAACGTACTTGCAGATGT
GACAAGCCGAGGCGGTGA

FIGURE 3

MTDRQTDTAPSPSYHLLPGRRRTVDAAASRGQGPEPAPGGGVEGVGARGVALKLFVQLLGCSRFG
GAVVRAGEAEPSGAARSASSGREEPQPEEGEEEEEKEEERGPQWRLGARKPGSWTGEAAVCADSA
PAARAPQALARASGRGGRVARRGAEESGPPHSPSRRGSASRAGPGRASETMNFLLSWVHWSLALL
LYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPL
MRCGGCCNDEGLECVPTEESNITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVR
GKGKGQKRKRKKSRYKSWSVPCGPCSERRKHLFVQDPQTCKCSCKNTDSRCKARQLELNERTCRC
DKPRR

FIGURE 4

```
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc      60

acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg     120

actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact     180

ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt     240

agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa     300

gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga     360

ggtggaggtg gaggtggagg tccttcctgt gtgcccctga tgcgatgcgg gggctgctgc     420

aattag                                                               426
```

FIGURE 5

```
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1               5                  10                  15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
            20                  25                  30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
        35                  40                  45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
    50                  55                  60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65                  70                  75                  80

Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu
                85                  90                  95

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
            100                 105                 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro
        115                 120                 125

Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn
    130                 135                 140
```

FIGURE 6

```
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc      60
acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg     120
actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact     180
ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt     240
agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa     300
gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga     360
ggtggaggtg gaggtggagg tccttcctgt gtgcccctga tgcgatgcgg gggctgctgc     420
aatcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag     480
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag     540
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc     600
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg     660
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc     720
ctctccctgt ctccgggtaa atag                                           744
```

FIGURE 7

```
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1               5                  10                  15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
            20                  25                  30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
        35                  40                  45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
    50                  55                  60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65                  70                  75                  80

Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu
                85                  90                  95

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
            100                 105                 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro
        115                 120                 125

Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Gln Pro Arg
    130                 135                 140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
145                 150                 155                 160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                165                 170                 175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            180                 185                 190

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        195                 200                 205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    210                 215                 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
225                 230                 235                 240

Leu Ser Leu Ser Pro Gly Lys
                245
```

FIGURE 8

ATCGAGGTCCGCGGGAGGCTCGGAGCGCGCCAGGCGGACACTCCTCTCGGCTCCTCCCCGGCAGC
GGCGGCGGCTCGGAGCGGGCTCCGGGGCTCGGGTGCAGCGGCCAGCGGGCGCCTGGCGGCGAGGA
TTACCCGGGGAAGTGGTTGTCTCCTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGGCCGG
CGGCGGCGAACGAGAGGACGGACTCTGGCGGCCGGGTCGTTGGCCGCGGGGAGCGCGGGCACCGG
GCGAGCAGGCCGCGTCGCGCTCACCATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGC
TGCTCAGCTGTCTGCTTCTCACAGGATCTAGTTCAGGTTCAAAATTAAAAGATCCTGAACTGAGT
TTAAAAGGCACCCAGCACATCATGCAAGCAGGCCAGACACTGCATCTCCAATGCAGGGGGGAAGC
AGCCCATAAATGGTCTTTGCCTGAAATGGTGAGTAAGGAAAGCGAAAGGCTGAGCATAACTAAAT
CTGCCTGTGGAAGAAATGGCAAACAATTCTGCAGTACTTTAACCTTGAACACAGCTCAAGCAAAC
CACACTGGCTTCTACAGCTGCAAATATCTAGCTGTACCTACTTCAAAGAAGAAGGAAACAGAATC
TGCAATCTATATATTTATTAGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCG
AAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATC
ACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGA
CAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAAG
CAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACAATCATA
GATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTTGTCCTCAATTG
TACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTACCCTGATGAAAAAAATA
AGAGAGCTTCCGTAAGGCGACGAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTT
CTTACTATTGACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAAGGAGTGGACC
ATCATTCAAATCTGTTAACACCTCAGTGCATATATATGATAAAGCATTCATCACTGTGAAACATC
GAAAACAGCAGGTGCTTGAAACCGTAGCTGGCAAGCGGTCTTACCGGCTCTCTATGAAAGTGAAG
GCATTTCCCTCGCCGGAAGTTGTATGGTTAAAAGATGGGTTACCTGCGACTGAGAAATCTGCTCG
CTATTTGACTCGTGGCTACTCGTTAATTATCAAGGACGTAACTGAAGAGGATGCAGGGAATTATA
CAATCTTGCTGAGCATAAAACAGTCAAATGTGTTTAAAAACCTCACTGCCACTCTAATTGTCAAT
GTGAAACCCCAGATTTACGAAAAGGCCGTGTCATCGTTTCCAGACCCGGCTCTCTACCCACTGGG
CAGCAGACAAATCCTGACTTGTACCGCATATGGTATCCCTCAACCTACAATCAAGTGGTTCTGGC
ACCCCTGTAACCATAATCATTCCGAAGCAAGGTGTGACTTTTGTTCCAATAATGAAGAGTCCTTT
ATCCTGGATGCTGACAGCAACATGGGAAACAGAATTGAGAGCATCACTCAGCGCATGGCAATAAT
AGAAGGAAAGAATAAGATGGCTAGCACCTTGGTTGTGGCTGACTCTAGAATTTCTGGAATCTACA
TTTGCATAGCTTCCAATAAAGTTGGGACTGTGGGAAGAAACATAAGCTTTTATATCACAGATGTG
CCAAATGGGTTTCATGTTAACTTGGAAAAAATGCCGACGGAAGGAGAGGACCTGAAACTGTCTTG
CACAGTTAACAAGTTCTTATACAGAGACGTTACTTGGATTTTACTGCGGACAGTTAATAACAGAA
CAATGCACTACAGTATTAGCAAGCAAAAAATGGCCATCACTAAGGAGCACTCCATCACTCTTAAT
CTTACCATCATGAATGTTTCCCTGCAAGATTCAGGCACCTATGCCTGCAGAGCCAGGAATGTATA
CACAGGGGAAGAAATCCTCCAGAAGAAAGAAATTACAATCAGAGATCAGGAAGCACCATACCTCC
TGCGAAACCTCAGTGATCACACAGTGGCCATCAGCAGTTCCACCACTTTAGACTGTCATGCTAAT
GGTGTCCCCGAGCCTCAGATCACTTGGTTTAAAAACAACCACAAAATACAACAAGAGCCTGGAAT
TATTTTAGGACCAGGAAGCAGCACGCTGTTTATTGAAAGAGTCACAGAAGAGGATGAAGGTGTCT
ATCACTGCAAAGCCACCAACCAGAAGGGCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGA
ACCTCGGACAAGTCTAATCTGGAGCTGATCACTCTAACATGCACCTGTGTGGCTGCGACTCTCTT
CTGGCTCCTATTAACCCTCTTTATCCGAAAAATGAAAAGGTCTTCTTCTGAAATAAAGACTGACT
ACCTATCAATTATAATGGACCCAGATGAAGTTCCTTTGGATGAGCAGTGTGAGCGGCTCCCTTAT
GATGCCAGCAAGTGGGAGTTTGCCCGGGAGAGACTTAAACTGGGCAAATCACTTGGAAGAGGGGC
TTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTACGTGCCGGACTGTGG
CTGTGAAAATGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGATGACTGAGCTAAAA
ATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGGGAGCCTGCACCAAGCAAGG
AGGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCCAACTACCTCAAGAGCA
AACGTGACTTATTTTTTCTCAACAAGGATGCAGCACTACACATGGAGCCTAAGAAAGAAAAAATG
GAGCCAGGCCTGGAACAAGGCAAGAAACCAAGACTAGATAGCGTCACCAGCAGCGAAAGCTTTGC
GAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTTGAGGAAGAGGAGGATTCTGACGGTT
TCTACAAGGAGCCCATCACTATGGAAGATCTGATTTCTTACAGTTTTCAAGTGGCCAGAGGCATG
GAGTTCCTGTCTTCCAGAAAGTGCATTCATCGGGACCTGGCAGCGAGAAACATTCTTTTATCTGA
GAACAACGTGGTGAAGATTTGTGATTTTGGCCTTGCCCGGGATATTTATAAGAACCCCGATTATG
TGAGAAAAGGAGATACTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATC
TACAGCACCAAGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGTGG

FIGURE 9A

GTCTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGA
TGAGAGCTCCTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTGCTGGCACAGAGAC
CCAAAAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAAGCAAATGT
ACAACAGGATGGTAAAGACTACATCCCAATCAATGCCATACTGACAGGAAATAGTGGGTTTACAT
ACTCAACTCCTGCCTTCTCTGAGGACTTCTTCAAGGAAAGTATTTCAGCTCCGAAGTTTAATTCA
GGAAGCTCTGATGATGTCAGATACGTAAATGCTTTCAAGTTCATGAGCCTGGAAAGAATCAAAAC
CTTTGAAGAACTTTTACCGAATGCCACCTCCATGTTTGATGACTACCAGGGCGACAGCAGCACTC
TGTTGGCCTCTCCCATGCTGAAGCGCTTCACCTGGACTGACAGCAAACCCAAGGCCTCGCTCAAG
ATTGACTTGAGAGTAACCAGTAAAAGTAAGGAGTCGGGGCTGTCTGATGTCAGCAGGCCCAGTTT
CTGCCATTCCAGCTGTGGGCACGTCAGCGAAGGCAAGCGCAGGTTCACCTACGACCACGCTGAGC
TGGAAAGGAAAATCGCGTGCTGCTCCCCGCCCCCAGACTACAACTCGGTGGTCCTGTACTCCACC
CCACCCATCTAGAGTTTGACACGAAGCCTTATTTCTAGAAGCACATGTGTATTTATACCCCCAGG
AAACTAGCTTTTGCCAGTATTATGCATATATAAGTTTACACCTTTATCTTTCCATGGGAGCCAGC
TGCTTTTTGTGATTTTTTTAATAGTGCTTTTTTTTTTTTGACTAACAAGAATGTAACTCCAGATA
GAGAAATAGTGACAAGTGAAGAACACTACTGCTAAATCCTCATGTTACTCAGTGTTAGAGAAATC
CTTCCTAAACCCAATGACTTCCCTGCTCCAACCCCCGCCACCTCAGGGCACGCAGGACCAGTTTG
ATTGAGGAGCTGCACTGATCACCCAATGCATCACGTACCCCACTGGGCCAGCCCTGCAGCCCAAA
ACCCAGGGCAACAAGCCCGTTAGCCCCAGGGATCACTGGCTGGCCTGAGCAACATCTCGGGAGTC
CTCTAGCAGGCCTAAGACATGTGAGGAGGAAAAGGAAAAAAAGCAAAAAGCAAGGGAGAAAAGAG
AAACCGGGAGAAGGCATGAGAAAGAATTTGAGACGCACCATGTGGGCACGGAGGGGGACGGGGCT
CAGCAATGCCATTTCAGTGGCTTCCCAGCTCTGACCCTTCTACATTTGAGGGCCCAGCCAGGAGC
AGATGGACAGCGATGAGGGGACATTTTCTGGATTCTGGGAGGCAAGAAAAGGACAAATATCTTTT
TTGGAACTAAAGCAAATTTTAGAACTTTACCTATGGAAGTGGTTCTATGTCCATTCTCATTCGTG
GCATGTTTTGATTTGTAGCACTGAGGGTGGCACTCAACTCTGAGCCCATACTTTTGGCTCCTCTA
GTAAGATGCACTGAAAACTTAGCCAGAGTTAGGTTGTCTCCAGGCCATGATGGCCTTACACTGAA
AATGTCACATTCTATTTTGGGTATTAATATATAGTCCAGACACTTAACTCAATTTCTTGGTATTA
TTCTGTTTTGCACAGTTAGTTGTGAAAGAAAGCTGAGAAGAATGAAAATGCAGTCCTGAGGAGAG
GAGTTTTCTCCATATCAAAACGAGGGCTGATGGAGGAAAAAGGTCAATAAGGTCAAGGGAAAACC
CCGTCTCTATACCAACCAAACCAATTCACCAACACAGTTGGGACCCAAAACACAGGAAGTCAGTC
ACGTTTCCTTTTCATTTAATGGGGATTCCACTATCTCACACTAATCTGAAAGGATGTGGAAGAGC
ATTAGCTGGCGCATATTAAGCACTTTAAGCTCCTTGAGTAAAAAGGTGGTATGTAATTTATGCAA
GGTATTTCTCCAGTTGGGACTCAGGATATTAGTTAATGAGCCATCACTAGAAGAAAAGCCCATTT
TCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGATGGGAATAGGGAGACAGGGTAGGAAAGG
GCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCTTGGATCGCTAAGCTGGCTCTGTTTGATG
CTATTTATGCAAGTTAGGGTCTATGTATTTATGATGTCTGCACCTTCTGCAGCCAGTCAGAAGCT
GGAGAGGCAACAGTGGATTGCTGCTTCTTGGGGAGAAGAGTATGCTTCCTTTTATCCATGTAATT
TAACTGTAGAACCTGAGCTCTAAGTAACCGAAGAATGTATGCCTCTGTTCTTATGTGCCACATCC
TTGTTTAAAGGCTCTCTGTATGAAGAGATGGGACCGTCATCAGCACATTCCCTAGTGAGCCTACT
GGCTCCTGGCAGCGGCTTTTGTGGAAGACTCACTAGCCAGAAGAGAGGAGTGGGACAGTCCTCTA
CCAAGATCTAAATCCAAACAAAAGCAGGCTAGAGCCAGAAGAGAGGACAAATCTTTGTTCTTCCT
CTTCTTTACATACGCAAACCACCTGTGACAGCTGGCAATTTTATAAATCAGGTAACTGGAAGGAG
GTTAAACACAGAAAAAAGAAGACCTCAGTCAATTCTCTACTTTTTTTTTTTTTTCCAAATCAGAT
AATAGCCCAGCAAATAGTGATAACAAATAAAACCTTAGCTATTCATGTCTTGATTTCAATAATTA
ATTCTTAATCATTAAGAGACCATAATAAATACTCCTTTTCAAGAGAAAAGCAAAACCATTAGAAT
TGTTACTCAGCTCCTTCAAACTCAGGTTTGTAGCATACATGAGTCCATCCATCAGTCAAAGAATG
GTTCCATCTGGAGTCTTAATGTAGAAAGAAAAATGGAGACTTGTAATAATGAGCTAGTTACAAAG
TGCTTGTTCATTAAAATAGCACTGAAAATTGAAACATGAATTAACTGATAATATTCCAATCATTT
GCCATTTATGACAAAAATGGTTGGCACTAACAAAGAACGAGCACTTCCTTTCAGAGTTTCTGAGA
TAATGTACGTGGAACAGTCTGGGTGGAATGGGGCTGAAACCATGTGCAAGTCTGTGTCTTGTCAG
TCCAAGAAGTGACACCGAGATGTTAATTTTAGGGACCCGTGCCTTGTTTCCTAGCCCACAAGAAT
GCAAACATCAAACAGATACTCGCTAGCCTCATTTAAATTGATTAAAGGAGGAGTGCATCTTTGGC
CGACAGTGGTGTAACTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGGTGTATGTG
TGTTTTGTGCATAACTATTTAAGGAAACTGGAATTTTAAAGTTACTTTTATACAAACCAAGAATA
TATGCTACAGATATAAGACAGACATGGTTTGGTCCTATATTTCTAGTCATGATGAATGTATTTTG
TATACCATCTTCATATAATAAACTTCCAAAACACA

FIGURE 9B

```
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1               5                  10                  15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
            20                  25                  30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
        35                  40                  45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
    50                  55                  60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65                  70                  75                  80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
                85                  90                  95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
            100                 105                 110

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
        115                 120                 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
    130                 135                 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145                 150                 155                 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
                165                 170                 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
            180                 185                 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
        195                 200                 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
    210                 215                 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225                 230                 235                 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
                245                 250                 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
            260                 265                 270

Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
        275                 280                 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
    290                 295                 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
305                 310                 315                 320
```

FIGURE 10A

```
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile Thr Val
                325                 330                 335

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

Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu Val Val
        355                 360                 365

Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu
    370                 375                 380

Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu Asp Ala
385                 390                 395                 400

Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val Phe Lys
                405                 410                 415

Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile Tyr Glu
            420                 425                 430

Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Leu Tyr Pro Leu Gly Ser
        435                 440                 445

Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro Thr Ile
    450                 455                 460

Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala Arg Cys
465                 470                 475                 480

Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala Asp Ser
                485                 490                 495

Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala Ile Ile
            500                 505                 510

Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp Ser Arg
        515                 520                 525

Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly Thr Val
    530                 535                 540

Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly Phe His
545                 550                 555                 560

Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys Leu Ser
                565                 570                 575

Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile Leu Leu
            580                 585                 590

Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys Gln Lys
        595                 600                 605

Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr Ile Met
    610                 615                 620

Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala Arg Asn
625                 630                 635                 640
```

FIGURE 10B

```
Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr Ile Arg
                645                 650                 655

Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His Thr Val
            660                 665                 670

Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly Val Pro
        675                 680                 685

Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln Gln Glu
    690                 695                 700

Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile Glu Arg
705                 710                 715                 720

Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr Asn Gln
                725                 730                 735

Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly Thr Ser
            740                 745                 750

Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr Cys Thr Cys Val Ala
        755                 760                 765

Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu Ile Arg Lys Met Lys
    770                 775                 780

Arg Ser Ser Ser Glu Ile Lys Thr Asp Tyr Leu Ser Ile Ile Met Asp
785                 790                 795                 800

Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Glu Arg Leu Pro Tyr Asp
                805                 810                 815

Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Leu Lys Leu Gly Lys Ser
            820                 825                 830

Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gln Ala Ser Ala Phe Gly
        835                 840                 845

Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys
    850                 855                 860

Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala Leu Met Thr Glu Leu Lys
865                 870                 875                 880

Ile Leu Thr His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly
                885                 890                 895

Ala Cys Thr Lys Gln Gly Gly Pro Leu Met Val Ile Val Glu Tyr Cys
            900                 905                 910

Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys Ser Lys Arg Asp Leu Phe
        915                 920                 925

Phe Leu Asn Lys Asp Ala Ala Leu His Met Glu Pro Lys Lys Glu Lys
    930                 935                 940
```

FIGURE 10C

```
Met Glu Pro Gly Leu Glu Gln Gly Lys Lys Pro Arg Leu Asp Ser Val
945                 950                 955                 960

Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly Phe Gln Glu Asp Lys Ser
                965                 970                 975

Leu Ser Asp Val Glu Glu Glu Glu Asp Ser Asp Gly Phe Tyr Lys Glu
            980                 985                 990

Pro Ile Thr Met Glu Asp Leu Ile  Ser Tyr Ser Phe Gln Val Ala Arg
        995                 1000                1005

Gly Met Glu Phe Leu Ser Ser Arg Lys Cys Ile His Arg Asp Leu
    1010                1015                1020

Ala Ala Arg Asn Ile Leu Leu Ser Glu Asn Asn Val Val Lys Ile
    1025                1030                1035

Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asn Pro Asp Tyr
    1040                1045                1050

Val Arg  Lys Gly Asp Thr Arg  Leu Pro Leu Lys Trp  Met Ala Pro
    1055                 1060                1065

Glu Ser Ile Phe Asp Lys Ile Tyr Ser Thr Lys Ser Asp Val Trp
    1070                1075                1080

Ser Tyr Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Ser
    1085                1090                1095

Pro Tyr Pro Gly Val Gln Met Asp Glu Asp Phe Cys Ser Arg Leu
    1100                1105                1110

Arg Glu Gly Met Arg Met Arg Ala Pro Glu Tyr Ser Thr Pro Glu
    1115                1120                1125

Ile Tyr Gln Ile Met Leu Asp Cys Trp His Arg Asp Pro Lys Glu
    1130                1135                1140

Arg Pro Arg Phe Ala Glu Leu Val Glu Lys Leu Gly Asp Leu Leu
    1145                1150                1155

Gln Ala Asn Val Gln Gln Asp Gly Lys Asp Tyr Ile Pro Ile Asn
    1160                1165                1170

Ala Ile Leu Thr Gly Asn Ser Gly Phe Thr Tyr Ser Thr Pro Ala
    1175                1180                1185

Phe Ser Glu Asp Phe Phe Lys Glu Ser Ile Ser Ala Pro Lys Phe
    1190                1195                1200

Asn Ser Gly Ser Ser Asp Asp Val Arg Tyr Val Asn Ala Phe Lys
    1205                1210                1215

Phe Met Ser Leu Glu Arg Ile Lys Thr Phe Glu Glu Leu Leu Pro
    1220                1225                1230

Asn Ala Thr Ser Met Phe Asp Asp Tyr Gln Gly Asp Ser Ser Thr
    1235                1240                1245
```

FIGURE 10D

```
Leu Leu  Ala Ser Pro Met Leu  Lys Arg Phe Thr Trp  Thr Asp Ser
    1250                1255                1260

Lys Pro  Lys Ala Ser Leu Lys  Ile Asp Leu Arg Val  Thr Ser Lys
    1265                1270                1275

Ser Lys  Glu Ser Gly Leu Ser  Asp Val Ser Arg Pro  Ser Phe Cys
    1280                1285                1290

His Ser  Ser Cys Gly His Val  Ser Glu Gly Lys Arg  Arg Phe Thr
    1295                1300                1305

Tyr Asp  His Ala Glu Leu Glu  Arg Lys Ile Ala Cys  Cys Ser Pro
    1310                1315                1320

Pro Pro  Asp Tyr Asn Ser Val  Val Leu Tyr Ser Thr  Pro Pro Ile
    1325                1330                1335
```

FIGURE 10E

```
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc      60
acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg     120
actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact     180
ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt     240
agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa     300
gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga     360
ggtggaggtg gaggtggagg tcagccccga gaaccacagg tgtacaccct gcccccatcc     420
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc     480
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg     540
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag     600
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac     660
cactacacgc agaagagcct ctccctgtct ccgggtaaat ag                       702
```

FIGURE 11

```
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1               5                  10                  15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
            20                  25                  30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
        35                  40                  45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
    50                  55                  60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65                  70                  75                  80

Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu
                85                  90                  95

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
            100                 105                 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Gln
        115                 120                 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    130                 135                 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145                 150                 155                 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                165                 170                 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            180                 185                 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        195                 200                 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    210                 215                 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

FIGURE 12

```
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag      60
gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc     120
tgtgcagcgt ctggattcac cttcagtaat tatggcatgc actgggtccg ccaggctcca     180
ggcaaggggc tggagtgggt ggcagctata tggtatgatg gaagtaataa atactatgca     240
gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gttgtatatg     300
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt attgtgcgag agagggtcgg     360
tgggtacgat atactacggt gactactatc ggatactact ttgactactg gggccaggga     420
accctggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc     480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc     540
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc     600
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc     660
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag     720
gtggacaaga gagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca     780
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc     840
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac     900
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag     960
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    1020
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc    1080
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc    1140
ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa    1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac    1260
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc    1320
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag    1380
gctctgcaca accactacac gcagaagagc ctctccctgt ccccgggtaa atga          1434
```

FIGURE 13

```
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1               5                  10                  15

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

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

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

Glu Trp Val Ala Ala Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65                  70                  75                  80

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

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

Tyr Tyr Cys Ala Arg Glu Gly Arg Trp Val Arg Tyr Thr Thr Val Thr
        115                 120                 125

Thr Ile Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
            260                 265                 270

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

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
```

FIGURE 14A

```
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430

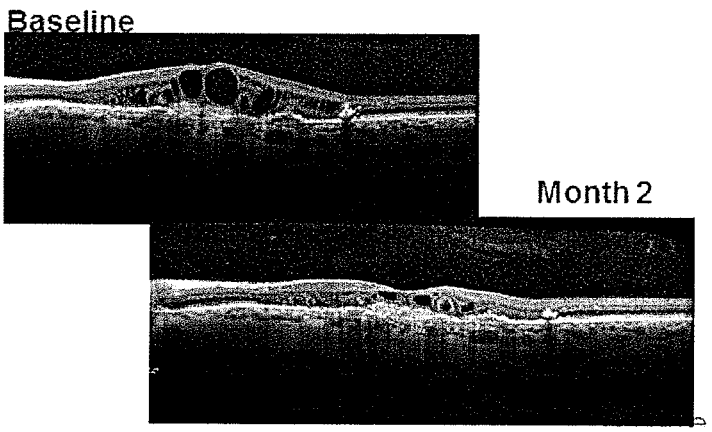
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475
```

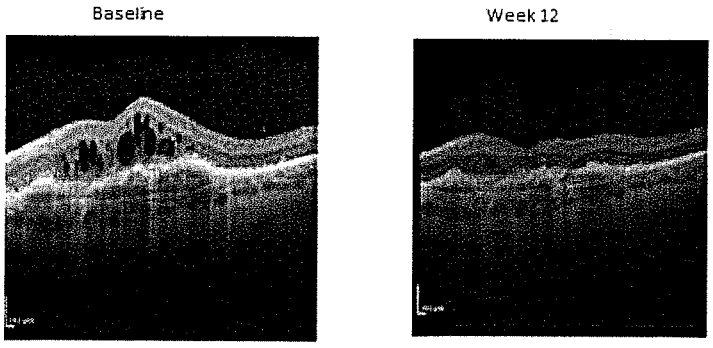
FIGURE 14B

A



B

FIGURE 15



A B

FIGURE 16