

# SEQUENCE LISTING

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<120> BISPECIFIC ANTIBODIES AND METHODS OF MAKING AND USING THEREOF

<130> SIBA003PCT

<160> 206

<170> PatentIn version 3.5

<210> 1

<211> 2103

<212> DNA

<213> Artificial Sequence

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| gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 240  |
| ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc  | 300  |
| tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc  | 360  |
| accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca | 420  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac  | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc  | 540  |
| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 600  |
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| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca  | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 780  |
| acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg  | 900  |
| taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
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| aagaaccagg | tcagcctgac | ctgcctggtc  | aaaggcttct | atcccagcga | catcgccgtg  | 1140 |
| gagtgggaga | gcaatgggca | gccggagaac  | aactacaaga | ccacgcctcc | cgtgctggac  | 1200 |
| tccgacggct | ccttcttcct | ctatagcaag  | ctcaccgtgg | acaagagcag | gtggcagcag  | 1260 |
| gggaacgtct | tctcatgctc | cgtgatgcat  | gaggctctgc | acaaccacta | cacgcagaag  | 1320 |
| agcctctccc | tgtctccggg | tggcggtgga  | gggtccggcg | gtggtggatc | cgaggtgcag  | 1380 |
| ctggtggagt | ctgggggagg | cttggtccag  | cctggggggg | ccctgagact | ctcctgtaca  | 1440 |
| gcctctggat | tctccctcag | tagctatgca  | atgagctggg | tcgccaggc  | tccaggggaag | 1500 |
| gggctggagt | acatcggcta | cattggtgat  | actactggca | tagcctacgc | gagctgggcg  | 1560 |
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| atctggggcc | aagggaccct | ggtcaccgtc  | tcgagcggtg | gaggcggatc | tggcggaggt  | 1740 |
| ggttccggcg | gtggcggctc | cggtggaggc  | ggctctgccc | ttgtgatgac | ccagtctcca  | 1800 |
| tcctccctgt | ctgcatctgt | aggagacaga  | gtcaccatca | cttgccaggc | cagtcagaac  | 1860 |
| atttacagca | atttagcctg | gtatcagcag  | aaaccaggga | aagttcctaa | gctcctgatc  | 1920 |
| tatcaggcct | ccactctggc | atctgggggtc | ccatctcggt | tcagtggcag | tggatatggg  | 1980 |
| acagatttca | ctctcaccat | cagcagcctg  | cagcctgaag | atgttgcaac | ttattactgt  | 2040 |
| caaggcgggt | attatagtgc | tgcccttaat  | actttcggcg | gagggaccaa | ggtggagatc  | 2100 |
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<400> 2

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| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr  
465 470 475 480

Ala Ser Gly Phe Ser Leu Ser Ser Tyr Ala Met Ser Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly Tyr Ile Gly Asp Thr Thr  
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Gly Ile Ala Tyr Ala Ser Trp Ala Asn Gly Arg Phe Thr Ile Ser Lys  
515 520 525

Asp Asn Thr Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Trp Ser Tyr Leu Asp  
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Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly  
565 570 575

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580 585 590

Ala Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
595 600 605

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
625 630 635 640

Tyr Gln Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
645 650 655

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
660 665 670

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ser Ala Ala  
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Leu Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
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gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300  
caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360  
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420  
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480  
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540  
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<220>  
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<400> 4

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala  
100 105 110

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys  
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<212> DNA  
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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360  
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
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acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaaccat ctcaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gaggagtctg ggggaggctt ggtccagcct ggggggtccc tgagactctc ctgtaccgcc  | 1440 |
| tctggaatcg accttaatac ctacgacatg atctgggtcc gccaggctcc aggcaagggg  | 1500 |
| ctagagtggg ttggaatcat tacttatagt ggtagtagat actacgcgaa ctgggcgaaa  | 1560 |
| ggccgattca ccatctccaa agacaatacc aagaacacgg tgtatctgca aatgaacagc  | 1620 |
| ctgagagctg aggacacggc tgtgtattac tgtgcgagag attatatgag tggttccac   | 1680 |
| ttgtggggcc aggggaaccct ggtcacgctc tcttccggtg gaggcggttc aggcggaggt | 1740 |
| ggaagtgggtg gtggcggctc tggaggcggc ggatctgcct atgatatgac ccagtctcca | 1800 |
| tcttccgtgt ctgcatctgt aggagacaga gtcacatca agtgtcaggc cagtgaggac   | 1860 |
| atttatagct tcttggcctg gtatcagcag aaaccaggga aagcccctaa gctcctgac   | 1920 |
| cattctgcat cctctctggc atctggggtc ccatcaaggt tcagcggcag tggatctggg  | 1980 |
| acagatttca ctctcaccat cagcagcctg cagcctgaag attttgcaac ttactattgt  | 2040 |
| caacagggtt atggtaaaaa taatgttgat aatgctttcg gcggaggac caaggtggag   | 2100 |
| atcaaa                                                             | 2106 |

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 <213> Artificial Sequence

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| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Ile | Ser | Tyr | Asp | Gly | Asn | Asn | Lys | Tyr | Tyr | Ala | Asp | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
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Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
370 375 380

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Glu Glu Ser Gly  
450 455 460

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala  
465 470 475 480

Ser Gly Ile Asp Leu Asn Thr Tyr Asp Met Ile Trp Val Arg Gln Ala  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Gly Ile Ile Thr Tyr Ser Gly Ser  
500 505 510

Arg Tyr Tyr Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp  
515 520 525

Asn Thr Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Met Ser Gly Ser His  
545 550 555 560

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly  
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
595 600 605

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe  
610 615 620

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
625 630 635 640

His Ser Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
645 650 655

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
660 665 670

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn  
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Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
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aactgggcca aaggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 1620  
caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgagag atcggcgttt 1680  
tcgttcgact acgccatgga cctctggggc cagggaaccc tggtcaccgt ctcgagcgg 1740  
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atccagatga ccagtcctcc ttccaccctg tctgcatctg taggagacag agtcaccatc 1860  
acttgccagg ccagtcagag cattagttcc cacttaaact ggtatcagca gaaaccaggg 1920  
aaagccccta agctcctgat ctataaggca tccactctgg catctggggg cccatcaagg 1980  
ttcagcggca gtggatctgg gacagaattt actctcacca tcagcagcct gcagcctgat 2040  
gattttgcaa cttattactg ccaacagggt tatagttggg gtaatgttga taatgttttc 2100  
ggcggaggga ccaaggtgga gatcaaa 2127

<210> 8  
<211> 709  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 8

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

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Ser Phe Ser Ser Gly Tyr Asp Met Cys Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala Cys Ile Ala Ala Gly  
500 505 510

Ser Ala Gly Ile Thr Tyr Asp Ala Asn Trp Ala Lys Gly Arg Phe Thr  
515 520 525

Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Ala Phe  
545 550 555 560

Ser Phe Asp Tyr Ala Met Asp Leu Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
595 600 605

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala  
610 615 620

Ser Gln Ser Ile Ser Ser His Leu Asn Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly  
645 650 655

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu  
660 665 670

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln  
675 680 685

Gln Gly Tyr Ser Trp Gly Asn Val Asp Asn Val Phe Gly Gly Gly Thr  
690 695 700

Lys Val Glu Ile Lys  
705

<210> 9  
<211> 2109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 9  
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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tgggtggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360  
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaaccat ctcaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg tggcggtgga gggctccggcg gtggtggatc acaggtgcag 1380

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ctggtggagt ctgggggagg cctggtccag cctgggggct ccctgagact ctcctgtaca   | 1440 |
| acttctggaa tcgaccttag tacctacgac atgatctggg tccgccaggc tccaggcaag   | 1500 |
| gggctagagt ggggtgggaat cattagttat gttggtaaca catactacgc gagctgggcg  | 1560 |
| aaaggccgat tcaccctctc caaagacaat acctcgacca cgggtgatct gcaaatgaac   | 1620 |
| agcctgagag ctgaggacac ggctgtgtat tactgtgcga gagattttat tagtggttcc   | 1680 |
| cacttgtggg gccagggaa cctggtcacc gtctcgagcg gtggaggcgg atctggcgga    | 1740 |
| ggtaggttccg gcgggtggcg ctccgggtgga ggcggttctg cctatgatat gacccagtct | 1800 |
| ccatcttccg tgtctgcatc tgtaggagac agagtcacca tcaattgtca ggccagtgag   | 1860 |
| agcattagta gcttcttatt ctggtatcag cagaaaccag ggaaagcccc taagctcctg   | 1920 |
| atcttttctg catccactct ggcatctggg gtcccatcaa ggttcagcgg cagtggatct   | 1980 |
| gggacagatt tcactctcac catcagcagc ctgcagcctg aagattttgc aacttactat   | 2040 |
| tgtcaacagg gttatagtaa aagtaatgtg gataatgctt tcggcggagg gaccaaggtg   | 2100 |
| gagatcaaa                                                           | 2109 |

<210> 10  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 10

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Ile | Ser | Tyr | Asp | Gly | Asn | Asn | Lys | Tyr | Tyr | Ala | Asp | Ser | Val |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr  
465 470 475 480

Thr Ser Gly Ile Asp Leu Ser Thr Tyr Asp Met Ile Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Ile Ile Ser Tyr Val Gly  
500 505 510

Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Leu Ser Lys  
515 520 525

Asp Asn Thr Ser Thr Thr Val Asp Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Phe Ile Ser Gly Ser  
545 550 555 560

His Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly  
565 570 575

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
580 585 590

Ser Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val  
595 600 605

Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser Ile Ser Ser  
610 615 620

Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
625 630 635 640

Ile Phe Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser  
645 650 655

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln  
660 665 670

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Lys Ser  
675 680 685

Asn Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 11  
<211> 2121

<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360  
accaagggcc catcggctct ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
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tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattc 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
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aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg tggcggtgga gggctccggc gtggtggatc agaggtgcag 1380  
ctggtggagt ctgggggagg cttggtccag cctggggggt ccctgagact ctcctgtgca 1440

gcctctggat tctccctcag tagctactgg atgagctggg tccgccaggc tccagggaag 1500  
 gggctggagt ggatcggagt cattgatact aatgtttata tatactacgc gaactgggca 1560  
 aaaggcagat tcaccatctc cagagacaat tccaagaaca cgctgtatct tcaaatgaac 1620  
 agcctgagag ccgaggacac ggctgtgtat tactgtgcga gatatgtggg taataatgat 1680  
 gattatatta acttgtgggg ccaggaacc ctggtcaccg tctcgagcgg tggaggcgga 1740  
 tctggcggag gtggttccgg cgggtggcggc tccggtggag gcggctctga catccagatg 1800  
 acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcacat cacttgccag 1860  
 tccagtcaga gtgtttataa tggctactgg ttatcctggg atcagcagaa accaggga 1920  
 gcccctaagc tcctgatcta tgggtgatcc actctggcat ctgggggtccc atcaaggttc 1980  
 agcggcagtg gatctgggac agaattcact ctacccatca gcagcctgca gcctgatgat 2040  
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 gggaccaagg tggagatcaa a 2121

<210> 12  
 <211> 707  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 12

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

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Ser Leu Ser Ser Tyr Trp Met Ser Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Asp Thr Asn Val  
500 505 510

Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Val Gly Asn Asn Asp  
545 550 555 560

Asp Tyr Ile Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
580 585 590

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser  
595 600 605

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser  
610 615 620

Val Tyr Asn Gly Tyr Trp Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys  
625 630 635 640

Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val  
645 650 655

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
660 665 670

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Leu Gly  
675 680 685

Ser Tyr Thr Ser Ser Thr Glu Asn Ser Phe Gly Gly Gly Thr Lys Val  
690 695 700

Glu Ile Lys  
705

<210> 13  
<211> 2112  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 13  
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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360  
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg tggcggtgga gggctccggcg gtggtggatc agaggtgcag 1380

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctggtggagt ctgggggagg cttggtccag cctgggggggt ccctgagact ctcctgtaca | 1440 |
| gtgtctggaa tcgacctcag tgtcatcaat atgggctggg tccgccaggc tccaggaag   | 1500 |
| gggctggagt ggatcggaac cattacttat gttggtaaca catattacgc gagctgggcg  | 1560 |
| aaaggcagat tcaccatctc caaaacctcg accacggtgg atcttaaaat caccagtccg  | 1620 |
| acaaccgagg acacggctgt gtattactgt gcgagagaat ctggtactat ttattacagt  | 1680 |
| tactttaact tgtggggcca agggaccctg gtcaccgtct cgagcgggtg aggcggatct  | 1740 |
| ggcggagggtg gttccggcgg tggcggctcc ggtggaggcg gctctgcatt cgaattgacc | 1800 |
| cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcaa gtgccaggcc  | 1860 |
| agtgaagca ttagcaacta cttatcctgg tatcagcaga ttccaggga agttcctaag    | 1920 |
| ctcctgatct attatgcatc caatctggca tctggggtcc catctcggtt cagtggcagt  | 1980 |
| ggatctggga cagatttcac tctcaccatc agcagcctgc agcctgaaga tgttgcaact  | 2040 |
| tattactgtc aaagctatta tgggtggtgg agtgcctata ctttcggcgg agggaccaag  | 2100 |
| gtggagatca aa                                                      | 2112 |

<210> 14  
 <211> 704  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 14

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Ile | Ser | Tyr | Asp | Gly | Asn | Asn | Lys | Tyr | Tyr | Ala | Asp | Ser | Val |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr  
465 470 475 480

Val Ser Gly Ile Asp Leu Ser Val Ile Asn Met Gly Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Thr Ile Thr Tyr Val Gly  
500 505 510

Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys  
515 520 525

Thr Ser Thr Thr Val Asp Leu Lys Ile Thr Ser Pro Thr Thr Glu Asp  
530 535 540

Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Gly Thr Ile Tyr Tyr Ser  
545 550 555 560

Tyr Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
580 585 590

Gly Gly Ser Ala Phe Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala  
595 600 605

Ser Val Gly Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Ser Ile  
610 615 620

Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys  
625 630 635 640

Leu Leu Ile Tyr Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg  
645 650 655

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
660 665 670

Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Gly  
675 680 685

Gly Gly Ser Ala Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
690 695 700

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<211> 2121

<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 15  
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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360  
accaagggcc catcggctct ccccttgga ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattc 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcgcgg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg tggcggtgga gggctccggc gtggtggatc agaggtgcag 1380  
ctggtggagt ctgggggagg cttggtccag cctggggggt ccctgagact ctcctgtgca 1440

|                                                                      |      |
|----------------------------------------------------------------------|------|
| gcctctggat tgcacttcag tagcggctac tggatatgct ggggccgcca ggctccaggg    | 1500 |
| aaggggctgg agttgatcgc atgcatttat gctggtacta gtggtagtagtac ttcctacgcg | 1560 |
| agctgggga gaggcagatt caccatctcc gaaacctcca agaacacggt gactcttcaa     | 1620 |
| atgaacagcc tgagagccga ggactcggct gtgtattact gtgcgagaaa tctttacact    | 1680 |
| tacaatagct tgtggggcca gggaaccctg gtcaccgtct cgagcgggtgg aggcggatct   | 1740 |
| ggcggaggtg gttccggcgg tggcgggctcc ggtggaggcg gctctgacat ccagatgacc   | 1800 |
| cagtctcctt ccaccctgtc tgcattctgta ggagacagag tcaccatcac ttgccagtcc   | 1860 |
| agtcagagtg tttatgataa caactgggta gcctgggtatc agcagaaaacc agggaaagcc  | 1920 |
| cctaagctcc tgatctatac agtatccact ctggcatctg ggggtcccatc aaggttcagc   | 1980 |
| ggcagtggat ctgggacaga attcactctc accatcagca gcctgcagcc tgatgatttt    | 2040 |
| gcaacttatt actgccaagg cacttattat agtagtggtt ggaactttgc tttcggcgga    | 2100 |
| gggaccaagg tggagatcaa a                                              | 2121 |

<210> 16  
 <211> 707  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 16

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Ile | Ser | Tyr | Asp | Gly | Asn | Asn | Lys | Tyr | Tyr | Ala | Asp | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Asp Phe Ser Ser Gly Tyr Trp Ile Cys Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Leu Ile Ala Cys Ile Tyr Ala Gly  
500 505 510

Thr Ser Gly Ser Thr Ser Tyr Ala Ser Trp Ala Arg Gly Arg Phe Thr  
515 520 525

Ile Ser Glu Thr Ser Lys Asn Thr Val Thr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Asn Leu Tyr Thr  
545 550 555 560

Tyr Asn Ser Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
580 585 590

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala  
595 600 605

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val  
610 615 620

Tyr Asp Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
625 630 635 640

Pro Lys Leu Leu Ile Tyr Thr Val Ser Thr Leu Ala Ser Gly Val Pro  
645 650 655

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile  
660 665 670

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

Tyr Tyr Ser Ser Gly Trp Asn Phe Ala Phe Gly Gly Gly Thr Lys Val  
690 695 700

Glu Ile Lys  
705

<210> 17  
<211> 2100  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 17  
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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360  
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg tggcggtgga gggctccggcg gtggtggatc acaggagcag 1380



Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Glu Gln Leu Leu Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr  
465 470 475 480

Ala Ser Gly Phe Ser Phe Ser Ser Tyr Trp Met Cys Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Cys Ile Thr Thr Gly Ser  
500 505 510

Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys Arg Arg Phe Thr Ile Ser  
515 520 525

Lys Asp Asn Ser Lys Asn Thr Val Thr Leu Gln Met Asn Ser Leu Arg  
530 535 540

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Ala Phe Asp Leu Trp  
545 550 555 560

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile  
580 585 590

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
595 600 605

Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Tyr Ser Tyr Leu Asn  
610 615 620

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly  
625 630 635 640

Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
645 650 655

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
660 665 670

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

Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 19  
<211> 2097  
<212> DNA  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 19

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| tcctgtgcag | cctctggatt  | caccttcagt | agctatacta  | tgacttgggt | ccgccaggct | 120  |
| ccaggcaagg | ggctggagtg  | ggtgacattt | atatcatatg  | atggaaacaa | taaatactac | 180  |
| gcagactccg | tgaagggccg  | attcaccatc | tccagagaca  | attccaagaa | cacgctgtat | 240  |
| ctgcaaatga | acagcctgag  | agctgaggac | acggctatat  | attactgtgc | gaggaccggc | 300  |
| tggctggggc | cctttgacta  | ctggggccag | ggaaccctgg  | tcaccgtctc | ctcagctagc | 360  |
| accaagggcc | catcgggtctt | ccccctggca | ccctcctcca  | agagcacctc | tgggggcaca | 420  |
| gcggccctgg | gctgcctggt  | caaggactac | ttccccgaac  | cggtgacggt | gtcgtggaac | 480  |
| tcaggcgccc | tgaccagcgg  | cgtgcacacc | ttcccggctg  | tcctacagtc | ctcaggactc | 540  |
| tactccctca | gcagcgtggt  | gaccgtgccc | tccagcagct  | tgggcaccca | gacctacatc | 600  |
| tgcaacgtga | atcacaagcc  | cagcaacacc | aaggtggaca  | agagagttga | gccccaatct | 660  |
| tgtgacaaaa | ctcacacatg  | cccaccgtgc | ccagcacctg  | aagccgcggg | ggcaccgtca | 720  |
| gtcttcctct | ttcccccaaa  | acccaaggac | accctcatga  | tctcccggac | ccctgaggtc | 780  |
| acatgcgtgg | tggtggacgt  | gagccacgaa | gaccctgagg  | tcaagttcaa | ctggtacgtg | 840  |
| gacggcgtgg | aggtgcataa  | tgccaagaca | aagccgcggg  | aggagcagta | caacagcacg | 900  |
| taccgtgtgg | tcagcgtcct  | caccgtcctg | caccaggact  | ggctgaatgg | caaggagtac | 960  |
| aagtgcgcgg | tctccaacaa  | agccctccca | gccccatcg   | agaaaaccat | ctccaaagcc | 1020 |
| aaagggcagc | cccgagaacc  | acaggtgtac | accctgcccc  | catcccggga | tgagctgacc | 1080 |
| aagaaccagg | tcagcctgac  | ctgcctggtc | aaaggcttct  | atcccagcga | catcgccgtg | 1140 |
| gagtgggaga | gcaatgggca  | gccggagaac | aactacaaga  | ccacgcctcc | cgtgctggac | 1200 |
| tccgacggct | ccttcttcct  | ctatagcaag | ctcaccgtgg  | acaagagcag | gtggcagcag | 1260 |
| gggaacgtct | tctcatgctc  | cgtgatgcat | gaggctctgc  | acaaccacta | cacgcagaag | 1320 |
| agcctctccc | tgtctccggg  | tggcggtgga | gggtccggcg  | gtggtggatc | acaggagcag | 1380 |
| gtgaaggaga | ccgggggagg  | cttggtacag | cctgggggggt | ccctgagact | ctcctgtgca | 1440 |
| gcctctggat | tcaccatcag  | cagctatgga | gtgagctggg  | tccgccaggc | tccagggaag | 1500 |

gggctggagt gggtcgcatt gatttttccc gggattgggt tcaaagacta cgcgagctgg 1560  
 gtgaatggcc ggttcacct ctccagcgac aacgcccaga aactgtgga actgcaaagt 1620  
 aacagcctga gagccgagga cacggccgta tattactgtg cgagagattt ggacttgtgg 1680  
 ggccagggaa ccctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740  
 ggcgggtggcg gctccggtgg aggcggctct gacatccaga tgaccagtc tccatcctcc 1800  
 ctgtctgcat ctgtaggaga cagagtcacc atcacttgcc agtccagtc gagtgtttat 1860  
 agtaactact tatcctggta tcagcagaaa ccagggaag ttcctaagct cctgatctat 1920  
 tatgcatcca ctctggcatc tgggggtcca tctcggttca gtggcagtgg atctgggaca 1980  
 gatttcactc tcaccatcag cagcctgcag cctgaagatg ttgcaactta ttactgtgca 2040  
 ggcggttata gtagtagtac tcgtgctttc ggcggaggga ccaaggtgga gatcaaa 2097

<210> 20  
 <211> 699  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 20

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Glu Gln Val Lys Glu Thr  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Thr Ile Ser Ser Tyr Gly Val Ser Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Phe Pro Gly Ile  
500 505 510

Gly Phe Lys Asp Tyr Ala Ser Trp Val Asn Gly Arg Phe Thr Leu Ser  
515 520 525

Ser Asp Asn Ala Gln Asn Thr Val Glu Leu Gln Met Asn Ser Leu Arg  
530 535 540

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Asp Leu Trp  
545 550 555 560

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile  
580 585 590

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
595 600 605

Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Tyr Ser Asn Tyr Leu  
610 615 620

Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr  
625 630 635 640

Tyr Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu  
660 665 670

Asp Val Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Ser Ser Ser Thr Arg  
675 680 685

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
690 695

<210> 21  
<211> 2130  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 21

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 60   |
| tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct  | 120  |
| ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac  | 180  |
| gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 240  |
| ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc  | 300  |
| tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc  | 360  |
| accaagggcc catcggctct ccccttgga ccctcctcca agagcacctc tgggggcaca   | 420  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc  | 540  |
| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattc  | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca  | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg  | 900  |
| taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcgcgg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag   | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tggcggtgga gggctccggc gtggtggatc agaggtgcag  | 1380 |
| ctgttggagt ctgggggagg cttggtacag cctgggggggt ccctgagact ctcctgtgca | 1440 |
| gcctctggat tcaccttag cagcagccac tggatatgct gggctcccca ggctccaggg   | 1500 |
| aaggggctgg agtggatcgc atgcatttat actggtagta ttgatgtctt ttactacgcg  | 1560 |
| agctgggcga aaggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg  | 1620 |

caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgagag agccgctaata 1680  
 actgatacta cctactttaaa cttgtggggc cagggaaccc tggtcaccgt ctcgagcggc 1740  
 ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggctctgcc 1800  
 tatgatatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 1860  
 aattgccagg ccagtcagag cattaacaac caactatcct ggtatcagca gaaaccaggg 1920  
 aaagttccta agctcctgat ctatggtgca tccactctgg catctggggc cccatctcgg 1980  
 ttcaccggca gtggatctgg gacagatttc actctcacca tcagcagcct gcagcctgaa 2040  
 gatgttgcaa cttattactg tcatgttcat tattgcagtg gtggtagttg tttttgggct 2100  
 ttcggcggag ggaccaaggt ggagatcaaa 2130

<210> 22  
 <211> 710  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 22

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser  
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Thr Phe Ser Ser Ser His Trp Ile Cys Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala Cys Ile Tyr Thr Gly  
500 505 510

Ser Ile Asp Val Phe Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr  
515 520 525

Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ala Asn  
545 550 555 560

Thr Asp Thr Thr Tyr Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

Gly Ser Gly Gly Gly Gly Ser Ala Tyr Asp Met Thr Gln Ser Pro Ser  
595 600 605

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala  
610 615 620

Ser Gln Ser Ile Asn Asn Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

Lys Val Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Leu Ala Ser Gly  
645 650 655

Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
660 665 670

Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys His  
675 680 685

Val His Tyr Cys Ser Gly Gly Ser Cys Phe Trp Ala Phe Gly Gly Gly  
690 695 700

Thr Lys Val Glu Ile Lys  
705 710

<210> 23

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized

<400> 23

ggtggaggcg gatctggcgg aggtgggtcc ggcggtggcg gctccggtgg aggcggctct 60

<210> 24

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 24

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser  
20

<210> 25

<211> 2100

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized

<400> 25

cagtcggtgg aggagtctgg gggaggcttg gtccagcctg gggggtccct gagactctcc 60

tgtaccgcct ctggaatcga ccttaatacc tacgacatga tctgggtccg ccaggctcca 120

ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac 180

tgggcgaaag gccgattcac catctcaaaa gacaatacca agaacacggt gtatctgcaa 240

atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt 300

ggttcccact tgtggggcca gggaaccctg gtcaccgtct cgagcgctag caccaagggc 360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa 660

|                                                                    |      |
|--------------------------------------------------------------------|------|
| actcacacat gcccaccgtg cccagcacct gaagccgcgg gggcaccgtc agtcttcctc  | 720  |
| ttccccccaa aaccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg   | 780  |
| gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg  | 840  |
| gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg  | 900  |
| gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcgcg  | 960  |
| gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag  | 1020 |
| ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag  | 1080 |
| gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag  | 1140 |
| agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc  | 1200 |
| tccttcttcc tctatagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc   | 1260 |
| ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc  | 1320 |
| ctgtctccgg gtggcggtag agggctccggc ggtggtggat cccaggtgca attggtggag | 1380 |
| tctggggggag gcgtggtcca gcctgggagg tccctgagac tctcctgtgc agcctctgga | 1440 |
| ttcaccttca gtagctatac tatgcactgg gtccgccagg ctccaggcaa ggggctggag  | 1500 |
| tgggtgacat ttatatcata tgatggaaac aataaatact acgcagactc cgtgaagggc  | 1560 |
| cgattcacca tctccagaga caattccaag aacacgctgt atctgcaa at gaacagcctg | 1620 |
| agagctgagg acacggctat atattactgt gcgaggaccg gctggctggg gccctttgac  | 1680 |
| tactggggcc aggggaaccct ggtcaccgtc tcgagcgggt gaggcgggtt aggcggaggt | 1740 |
| ggaagtgggt gtggcggctc tggaggcggc ggatctgaaa ttgtgttgac gcagtctcca  | 1800 |
| ggcaccctgt ctttgtctcc aggggaaaga gccaccctct cctgcagggc cagtcagagt  | 1860 |
| gttggcagca gctacttagc ctggtaccag cagaaacctg gccaggctcc caggctcctc  | 1920 |
| atctatgggt cattcagcag ggccactggc atcccagaca ggttcagtgg cagtgggtct  | 1980 |
| gggacagact tcactctcac catcagcaga ctggagcctg aagattttgc agtgtattac  | 2040 |
| tgtcagcagt atggtagctc accgtggacg ttcgccaag ggaccaaggt ggaaatcaaa   | 2100 |

<210> 26  
 <211> 700  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> synthesized

<400> 26

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

Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn Thr Tyr Asp  
20 25 30

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

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly  
50 55 60

Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Tyr Leu Gln  
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
85 90 95

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
165 170 175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly  
450 455 460

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
465 470 475 480

Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys  
500 505 510

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
515 520 525

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
530 535 540

Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly  
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
595 600 605

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
610 615 620

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
625 630 635 640

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
645 650 655

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
660 665 670

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
675 680 685

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 27  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 27  
gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60  
atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatccattct gcacacctc tggcatctgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300  
ttcggcggag ggaccaaggt ggagatcaaa cgtacgggtg ctgcaccatc tgtcttcatc 360  
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtgtg cctgctgaat 420  
aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480  
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540  
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600  
catcagggcc tgagctcgcc cgtcaciaag agcttcaaca ggggagagtg t 651

<210> 28  
<211> 217

<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 28

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

His Ser Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn  
85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 29  
<211> 2100  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 29  
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtacag cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagta catcggctac attggtgata ctactggcat agcctacgcg 180  
agctgggcga atggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt 240  
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggctgggtcc 300  
tacttagaca tctggggcca agggaccctg gtcaccgtct cgagcgctag caccaagggc 360  
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg 420  
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480  
ctgaccagcg gcgtgcacac cttcccggtg gtcctacagt cctcaggact ctactccctc 540  
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600  
aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa 660  
actcacacat gcccaccgtg cccagcacct gaagccgcgg gggcaccgtc agtcttcctc 720  
ttccccccaa aaccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg 780  
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840  
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900  
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcgcg 960  
gtctccaaca aagccctccc agccccatc gagaaaacca tctccaaagc caaagggcag 1020  
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggc caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140  
 agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200  
 tccttcttcc tctatagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260  
 ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320  
 ctgtctccgg gtggcgggtg agggctccggc ggtggtggat cccaggtgca attggtggag 1380  
 tctggggggag gcgtgggtcca gcctgggagg tccctgagac tctcctgtgc agcctctgga 1440  
 ttcaccttca gtagctatac tatgcactgg gtccgccagg ctccaggcaa ggggctggag 1500  
 tgggtgacat ttatatcata tgatggaaac aataaatact acgcagactc cgtgaagggc 1560  
 cgattcacca tctccagaga caattccaag aacacgctgt atctgcaa at gaacagcctg 1620  
 agagctgagg acacggctat atattactgt gcgaggaccg gctggctggg gccctttgac 1680  
 tactggggcc aggggaaccct ggtcaccgtc tcgagcgggtg gaggcggatc tggcggaggt 1740  
 gggtccggcg gtggcggctc cgggtggaggc gggttctgaaa ttgtgttgac gcagtctcca 1800  
 ggcaccctgt ctttgtctcc aggggaaaga gccaccctct cctgcagggc cagtcagagt 1860  
 gttggcagca gctacttagc ctggtaccag cagaaacctg gccaggctcc caggctcctc 1920  
 atctatggtg cattcagcag ggccactggc atcccagaca gggttcagtgg cagtgggtct 1980  
 gggacagact tcactctcac catcagcaga ctggagcctg aagattttgc agtgtattac 2040  
 tgtcagcagt atggtagctc accgtggacg ttcggccaag ggaccaaggt ggaaatcaaa 2100

<210> 30  
 <211> 700  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 30

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Leu Ser Ser Tyr  
 20 25 30

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

Gly Tyr Ile Gly Asp Thr Thr Gly Ile Ala Tyr Ala Ser Trp Ala Asn  
50 55 60

Gly Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Asp Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Trp Ser Tyr Leu Asp Ile Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
165 170 175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly  
450 455 460

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
465 470 475 480

Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys  
500 505 510

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
515 520 525

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
530 535 540

Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly  
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
595 600 605

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
610 615 620

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
625 630 635 640

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
645 650 655

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
660 665 670

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
675 680 685

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 31  
<211> 648  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 31  
gcccttgatga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc aggccagtca gaacatttac agcaatttag cctggatatca gcagaaacca 120  
gggaaagttc ctaagctcct gatctatcag gcctccactc tggcatctgg ggtcccatct 180  
cggttcagtg gcagtggata tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagatgttg caacttatta ctgtcaaggc gggtattata gtgctgccct taatactttc 300  
ggcggaggga ccaaggtgga gatcaaactg acgggtggctg caccatctgt cttcatcttc 360  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420  
ttctatccca gagaggccaa agtacagtgg aagggtgata acgccctcca atcgggtaac 480  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600  
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 648

<210> 32  
<211> 216  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 32

Ala Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile Tyr Ser Asn  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Gln Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ser Ala Ala  
85 90 95

Leu Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
100 105 110

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 33

<211> 2121

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized

<400> 33

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| tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag   | 120  |
| gctccagggg aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggatatcact  | 180  |
| tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg   | 240  |
| ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga   | 300  |
| tcggcgtttt cgttcgacta cgccatggac ctctggggcc agggaaaccct ggtcaccgtc  | 360  |
| tcgagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc   | 420  |
| tctggggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 480  |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag    | 540  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc   | 600  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt   | 660  |
| gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg   | 720  |
| ggggcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg    | 780  |
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   | 840  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag   | 900  |
| tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   | 960  |
| ggcaaggagt acaagtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc   | 1020 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   | 1080 |
| gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   | 1140 |
| gacatgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct    | 1200 |
| cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc   | 1260 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac   | 1320 |
| tacacgcaga agagcctctc cctgtctccg ggtggcgggtg gaggggtccgg cggtggtgga | 1380 |
| tcccagggtgc aattggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga  | 1440 |
| ctctcctgtg cagcctctgg attcaccttc agtagctata ctatgcactg ggtccgccag   | 1500 |

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp  
100 105 110

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser  
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala  
225 230 235 240

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
260 265 270

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
305 310 315 320

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro  
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
340 345 350

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
385 390 395 400

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
435 440 445

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His  
485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile  
500 505 510

Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met  
530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr  
545 550 555 560

Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly  
595 600 605

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala  
610 615 620

Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro  
625 630 635 640

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr  
645 650 655

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
660 665 670

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys  
675 680 685

Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val  
690 695 700

Glu Ile Lys  
705

<210> 35

<211> 651

<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 35  
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc aggccagtca gagcattagt tcccacttaa actggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatctataag gcatccactc tggcatctgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240  
gatgattttg caacttatta ctgccaacag gggttatagtt ggggtaatgt tgataatgtt 300  
ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360  
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420  
aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480  
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540  
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600  
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 36  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn  
85 90 95

Val Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr  
100 105 110

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 37  
<211> 2103  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 37  
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tcctgtacaa cttctggaat cgaccttagt acctacgaca tgatctgggt ccgccaggct 120

|                                                                      |      |
|----------------------------------------------------------------------|------|
| ccaggcaagg ggctagagtg ggtgggaatc attagttatg ttggtaacac atactacgcg    | 180  |
| agctgggcga aaggccgatt caccctctcc aaagacaata cctcgaccac ggtggatctg    | 240  |
| caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agattttatt    | 300  |
| agtggttccc acttgtgggg ccagggaacc ctggtcaccg tctcgagcgc tagcaccaag    | 360  |
| ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc    | 420  |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg gaactcaggc | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc    | 540  |
| ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac    | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac   | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaagccg cgggggcacc gtcagtcttc    | 720  |
| ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc       | 780  |
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc    | 840  |
| gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt     | 900  |
| gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc    | 960  |
| gcggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg      | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac     | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg    | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac    | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcagggaac     | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc    | 1320 |
| tccctgtctc cgggtggcgg tggagggtcc ggcggtgggtg gatcccaggt gcaattgggtg  | 1380 |
| gagtctgggg gaggcgtggt ccagcctggg aggtccctga gactctcctg tgcagcctct    | 1440 |
| ggattcacct tcagtagcta tactatgcac tgggtccgcc aggctccagg caaggggctg    | 1500 |
| gagtgggtga catttatatc atatgatgga aacaataaat actacgcaga ctccgtgaag    | 1560 |
| ggccgattca ccatctccag agacaattcc aagaacacgc tgtatctgca aatgaacagc    | 1620 |
| ctgagagctg aggacacggc tatatattac tgtgcgagga ccggctggct ggggcccttt    | 1680 |
| gactactggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcggg    | 1740 |

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ggtaggttccg gcggtggcgg ctccggtgga ggcggttctg aaattgtgtt gacgcagtct      1800
ccaggcaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag ggccagtcag      1860
agtgttggca gcagctactt agcctggtac cagcagaaac ctggccaggc tcccaggctc      1920
ctcatctatg gtgcattcag cagggccact ggcattccag acaggttcag tggcagtggg      1980
tctgggacag acttcactct caccatcagc agactggagc ctgaagattt tgcagtgtat      2040
tactgtcagc agtatggtag ctcaccgtgg acgttcggcc aagggaacaa ggtggaaatc      2100
aaa                                                                    2103

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<210> 38  
 <211> 701  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 38

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

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

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

Gly Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys  
 50 55 60

Gly Arg Phe Thr Leu Ser Lys Asp Asn Thr Ser Thr Thr Val Asp Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Asp Phe Ile Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val  
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
165 170 175

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly  
450 455 460

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser  
465 470 475 480

Gly Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro  
485 490 495

Gly Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn  
500 505 510

Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp  
515 520 525

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu  
530 535 540

Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe  
545 550 555 560

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly  
565 570 575

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly  
580 585 590

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro  
595 600 605

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser  
610 615 620

Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu  
625 630 635 640

Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe  
645 650 655

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu  
660 665 670

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser  
675 680 685

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 39  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 39  
gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60  
atcaattgtc aggccagtga gagcattagt agcttcttat cctggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatcttttct gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
 gaagattttg caacttacta ttgtcaacag ggttatagta aaagtaatgt ggataatgct 300  
 ttcggcggag ggaccaaggt ggagatcaaa cgtacgggtg ctgcaccatc tgtcttcac 360  
 ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat 420  
 aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480  
 aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540  
 accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600  
 catcagggcc tgagctcgcc cgtcacaaaag agcttcaaca ggggagagtg t 651

<210> 40  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 40

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser Ile Ser Ser Phe  
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Phe Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Lys Ser Asn  
 85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 41  
<211> 2112  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 41  
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt ctccctcagt agctactgga tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatcggagtc attgatacta atgtttatat atactacgcg 180  
aactgggcaa aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240  
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgagcag atatgtgggt 300  
aataatgatg attatattaa cttgtggggc cagggaaccc tggtcaccgt ctcgagcgct 360  
agcaccaagg gcccatcggc cttccccctg gcaccctcct ccaagagcac ctctgggggc 420  
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

|                                                                    |      |
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| aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga  | 540  |
| ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac  | 600  |
| atctgcaacg tgaatcacia gccagcaac accaaggtgg acaagagagt tgagcccaaa   | 660  |
| tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagccgc gggggcaccg  | 720  |
| tcagtcttcc tcttcccccc aaaaccaag gacaccctca tgatctcccg gaccctgag    | 780  |
| gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac | 840  |
| gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc  | 900  |
| acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag  | 960  |
| tacaagtgcg cgggtctcaa caaagccctc ccagccccc tcgagaaaac catctccaaa   | 1020 |
| gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg  | 1080 |
| accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc  | 1140 |
| gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgctgctg | 1200 |
| gactccgacg gtccttctt cctctatagc aagctcaccg tggacaagag caggtggcag   | 1260 |
| caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag  | 1320 |
| aagagcctct ccctgtctcc ggggtggcggg ggagggtccg gcggtggtgg atcccaggtg | 1380 |
| caattggtgg agtctggggg aggcgtggtc cagcctggga ggtccctgag actctcctgt  | 1440 |
| gcagcctctg gattcacctt cagtagctat actatgcact ggggtccgcca ggctccaggc | 1500 |
| aaggggctgg agtgggtgac atttatatca tatgatggaa acaataaata ctacgcagac  | 1560 |
| tccgtgaagg gccgattcac catctccaga gacaattcca agaacacgct gtatctgcaa  | 1620 |
| atgaacagcc tgagagctga ggacacggct atatattact gtgcgaggac cggctggctg  | 1680 |
| gggccctttg actactgggg ccagggaacc ctggtcaccg tctcgagcgg tggaggcgga  | 1740 |
| tctggcggag gtggttccgg cgggtggcggc tccggtggag gcggttctga aattgtgttg | 1800 |
| acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccaccct ctctgcagg   | 1860 |
| gccagtcaga gtgttggcag cagctactta gcctggtacc agcagaaacc tggccaggct  | 1920 |
| cccaggctcc tcatctatgg tgcattcagc agggccactg gcatcccaga caggttcagt  | 1980 |
| ggcagtgggt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt  | 2040 |
| gcagtgtatt actgtcagca gtatggtagc tcaccgtgga cgttcgcca agggaccaag   | 2100 |

gtggaaatca aa

2112

<210> 42  
<211> 704  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 42

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Tyr  
20 25 30

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

Gly Val Ile Asp Thr Asn Val Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu Trp Gly Gln Gly  
100 105 110

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
165 170 175

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

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys  
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp  
500 505 510

Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu  
545 550 555 560

Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
580 585 590

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
595 600 605

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
610 615 620

Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
625 630 635 640

Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro  
645 650 655

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
660 665 670

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr  
675 680 685

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 43  
<211> 654  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 43  
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc agtccagtca gagtgtttat aatggctact gggtatcctg gtatcagcag 120  
aaaccaggga aagcccctaa gctcctgata tatgggtgcat ccactctggc atctggggtc 180  
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240  
cagcctgatg attttgcaac ttattactgc ctaggcagtt atactagtag tactgagaac 300  
tctttcggcg gagggaccaa ggtggagatc aaacgtacgg tggctgcacc atctgtcttc 360  
atcttcccg catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420  
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480  
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600  
 acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 44  
 <211> 218  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 44

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val Tyr Asn Gly  
 20 25 30

Tyr Trp Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
 35 40 45

Leu Ile Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe  
 50 55 60

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu  
 65 70 75 80

Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Leu Gly Ser Tyr Thr Ser  
 85 90 95

Ser Thr Glu Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
 100 105 110

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

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

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 45  
<211> 2109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 45  
gaggtgcagc tgggtggagtc tggggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtacag tgtctggaat cgacctcagt gtcacataa tgggctgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatcgggaacc attacttatg ttggtaacac atattacgcg 180  
agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240  
accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tggtactatt 300  
tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagcgctagc 360  
accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
tcaggcggcc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg   | 900  |
| taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc     | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc   | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg   | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac   | 1200 |
| tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag    | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1320 |
| agcctctccc tgtctccggg tggcggtgga gggctccggcg gtggtggatc ccaggtgcaa  | 1380 |
| ttggtggagt ctggggggagg cgtgggtccag cctgggaggt ccctgagact ctcctgtgca | 1440 |
| gcctctggat tcaccttcag tagctatact atgactggg tccgccaggc tccaggcaag    | 1500 |
| gggctggagt gggtgacatt tatatcatat gatggaaaca ataaatacta cgcagactcc   | 1560 |
| gtgaagggcc gattcacat ctccagagac aattccaaga acacgtgta tctgcaaatg     | 1620 |
| aacagcctga gagctgagga cacggctata tattactgtg cgaggaccgg ctggctgggg   | 1680 |
| ccctttgact actggggcca gggaaccctg gtcaccgtct cgagcgggtg aggcggatct   | 1740 |
| ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gttctgaaat tgtgttgacg   | 1800 |
| cagtctccag gcaccctgtc tttgtctcca ggggaaagag ccaccctctc ctgcagggcc   | 1860 |
| agtcagagtg ttggcagcag ctacttagcc tggtaccagc agaaacctgg ccaggctccc   | 1920 |
| aggctcctca tctatggtgc attcagcagg gccactggca tcccagacag gttcagtggc   | 1980 |
| agtgggtctg ggacagactt cactctcacc atcagcagac tggagcctga agattttgca   | 2040 |
| gtgtattact gtcagcagta tggtagctca ccgtggacgt tcggccaagg gaccaaggtg   | 2100 |
| gaaatcaaa                                                           | 2109 |

<210> 46  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 46

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

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

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

Gly Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile  
65 70 75 80

Thr Ser Pro Thr Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
85 90 95

Ser Gly Thr Ile Tyr Tyr Ser Tyr Phe Asn Leu Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly  
500 505 510

Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser  
515 520 525

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg  
530 535 540

Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly  
545 550 555 560

Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
580 585 590

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu  
595 600 605

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val  
610 615 620

Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro  
625 630 635 640

Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp  
645 650 655

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
660 665 670

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly  
675 680 685

Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 47  
<211> 648  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 47  
gcattcgaat tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcaagtgcc aggccagtga aagcattagc aactacttat cctggtatca gcagattcca 120  
gggaaagttc ctaagctcct gatctattat gcatccaatc tggcatctgg ggtcccatct 180  
cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagatgttg caacttatta ctgtcaaagc tattatgggtg gtggtagtgc ctatactttc 300  
ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc 360  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420  
ttctatccca gagaggcaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540  
ctgacgctga gcaaagcaga ctacagaaaa cacaagtct acgcctgcga agtcacccat 600  
cagggcctga gctcgcccgt cacaagagc ttcaacaggg gagagtgt 648

<210> 48  
<211> 216  
<212> PRT  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 48

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

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Ser Ile Ser Asn Tyr  
20 25 30

Leu Ser Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Gly Gly Gly Ser  
85 90 95

Ala Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
100 105 110

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 49  
<211> 2109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 49  
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120  
gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180  
tcctacgcga gctgggagcag aggcagattc accatctccg aaacctcaa gaacacgggtg 240  
actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300  
ctttacactt acaatagctt gtggggccag ggaaccctgg tcaccgtctc gagcgctagc 360  
accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattc 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag   | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1320 |
| agcctctccc tgtctccggg tggcgggtgga gggctccggcg gtggtggatc ccaggtgcaa | 1380 |
| ttggtggagt ctgggggagg cgtgggtccag cctgggaggt ccctgagact ctcctgtgca  | 1440 |
| gcctctggat tcaccttcag tagctatact atgcactggg tccgccaggc tccaggcaag   | 1500 |
| gggctggagt gggtgacatt tatatcatat gatggaaaca ataaatacta cgcagactcc   | 1560 |
| gtgaagggcc gattcacat ctccagagac aattccaaga acacgtgta tctgcaaatg     | 1620 |
| aacagcctga gagctgagga cacggctata tattactgtg cgaggaccgg ctggctgggg   | 1680 |
| ccctttgact actggggcca gggaaccctg gtcaccgtct cgagcgggtg aggcggatct   | 1740 |
| ggcggagggtg gttccggcgg tggcgggtcc ggtggaggcg gttctgaaat tgtgttgacg  | 1800 |
| cagtctccag gcaccctgtc tttgtctcca ggggaaagag ccaccctctc ctgcagggcc   | 1860 |
| agtcagagtg ttggcagcag ctacttagcc tggtaccagc agaaacctgg ccaggctccc   | 1920 |
| aggctcctca tctatggtgc attcagcagg gccactggca tcccagacag gttcagtggc   | 1980 |
| agtgggtctg ggacagactt cactctcacc atcagcagac tggagcctga agattttgca   | 2040 |
| gtgtattact gtcagcagta tggtagctca ccgtggacgt tcggccaagg gaccaaggtg   | 2100 |
| gaaatcaaa                                                           | 2109 |

<210> 50  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 50

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Asp | Phe | Ser | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Trp | Ile | Cys | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Ile Ala Cys Ile Tyr Ala Gly Thr Ser Gly Ser Thr Ser Tyr Ala Ser  
50 55 60

Trp Ala Arg Gly Arg Phe Thr Ile Ser Glu Thr Ser Lys Asn Thr Val  
65 70 75 80

Thr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Asn Leu Tyr Thr Tyr Asn Ser Leu Trp Gly Gln Gly Thr  
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

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

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser  
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser  
450 455 460

Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala  
465 470 475 480

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln  
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly  
500 505 510

Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser  
515 520 525

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg  
530 535 540

Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly  
545 550 555 560

Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
580 585 590

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu  
595 600 605

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val  
610 615 620

Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro  
625 630 635 640

Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp  
645 650 655

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
660 665 670

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly  
675 680 685

Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695 700

<210> 51  
<211> 657  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 51  
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc agtccagtca gagtgtttat gataacaact ggtagcctg gtatcagcag 120  
aaaccagggga aagcccctaa gctcctgatac tatacagtat ccactctggc atctgggggtc 180  
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240  
cagcctgatg attttgcaac ttattactgc caaggcactt attatagtag tggttggaac 300  
tttgctttcg gcggaggag caaggtggag atcaaagcta cggtaggctgc accatctgtc 360  
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420  
ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgccctccaa 480  
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540  
agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600  
gtcaccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 52  
<211> 219  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 52

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val Tyr Asp Asn  
20 25 30

Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
35 40 45

Leu Ile Tyr Thr Val Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe  
50 55 60

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu  
65 70 75 80

Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Thr Tyr Tyr Ser  
85 90 95

Ser Gly Trp Asn Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 53

<211> 2094

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized

<400> 53

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| caggagcagc  | tggttgagtc  | tgggggaggc  | ttggtacagc  | ctgggggggtc | cctgagactc  | 60   |
| tcctgtacag  | cctctggatt  | ctccttttagc | agctactgga  | tgtgctgggt  | ccgccaggct  | 120  |
| ccagggaagg  | ggctggagtg  | gatcggatgc  | attacgactg  | gtagtggttag | cacttactac  | 180  |
| gcgagctggg  | cgaagcgccg  | gttcaccatc  | tccaaagaca  | attccaagaa  | cacggtgact  | 240  |
| ctgcaaatga  | acagcctgag  | agccgaggac  | acggccgtat  | attactgtac  | gagagcattt  | 300  |
| gacttgtggg  | gccagggaac  | cctgggtcacc | gtctcgagcg  | ctagcaccaa  | gggcccacgc  | 360  |
| gtcttcccc   | tggcaccctc  | ctccaagagc  | acctctgggg  | gcacagcggc  | cctgggctgc  | 420  |
| ctgggtcaagg | actacttccc  | cgaaccggtg  | acgggtgtcgt | ggaactcagg  | cgccctgacc  | 480  |
| agcggcgtgc  | acaccttccc  | ggctgtccta  | cagtcctcag  | gactctactc  | cctcagcagc  | 540  |
| gtgggtgaccg | tgccctccag  | cagcttgggc  | accagacct   | acatctgcaa  | cgtgaatcac  | 600  |
| aagcccagca  | acaccaaggt  | ggacaagaga  | gttgagccca  | aatcttgtga  | caaaactcac  | 660  |
| acatgcccac  | cgtgcccagc  | acctgaagcc  | gcgggggcac  | cgtcagtctt  | cctcttcccc  | 720  |
| ccaaaacca   | aggacaccct  | catgatctcc  | cggacccctg  | aggtcacatg  | cgtgggtggtg | 780  |
| gacgtgagcc  | acgaagacct  | tgaggtcaag  | ttcaactggt  | acgtggacgg  | cgtggaggtg  | 840  |
| cataatgcca  | agacaaagcc  | gcgggaggag  | cagtacaaca  | gcacgtaccg  | tgtggtcagc  | 900  |
| gtcctcaccg  | tcctgcacca  | ggactggctg  | aatggcaagg  | agtacaagtg  | cgcggtctcc  | 960  |
| aacaaagccc  | tcccagcccc  | catcgagaaa  | accatctcca  | aagccaaagg  | gcagccccga  | 1020 |
| gaaccacagg  | tgtacaccct  | gccccatcc   | cgggatgagc  | tgaccaagaa  | ccaggtcagc  | 1080 |
| ctgacctgcc  | tgggtcaaagg | cttctatccc  | agcgacatcg  | ccgtggagtg  | ggagagcaat  | 1140 |
| gggcagccgg  | agaacaacta  | caagaccacg  | cctcccgtgc  | tggactccga  | cggctccttc  | 1200 |
| ttcctctata  | gcaagctcac  | cgtggacaag  | agcaggtggc  | agcaggggaa  | cgtcttctca  | 1260 |
| tgctccgtga  | tgcatgaggc  | tctgcacaac  | cactacacgc  | agaagagcct  | ctccctgtct  | 1320 |
| ccgggtggcg  | gtggaggggtc | cggcggtggt  | ggatcccagg  | tgcaattggt  | ggagtctggg  | 1380 |
| ggaggcgtgg  | tccagcctgg  | gaggtccctg  | agactctcct  | gtgcagcctc  | tggattcacc  | 1440 |
| ttcagtagct  | atactatgca  | ctgggtccgc  | caggctccag  | gcaaggggct  | ggagtgggtg  | 1500 |
| acatttatat  | catatgatgg  | aaacaataaa  | tactacgcag  | actccgtgaa  | gggccgattc  | 1560 |

accatctcca gagacaattc caagaacacg ctgtatctgc aaatgaacag cctgagagct 1620  
 gaggacacgg ctatatatta ctgtgcgagg accggctggc tggggccctt tgactactgg 1680  
 ggccagggaa ccctgggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740  
 ggcggtggcg gctccggtgg aggcggttct gaaatttgtt tgacgcagtc tccaggcacc 1800  
 ctgtctttgt ctccagggga aagagccacc ctctcctgca gggccagtca gagtgttggc 1860  
 agcagctact tagcctggta ccagcagaaa cctggccagg ctcccaggct cctcatctat 1920  
 ggtgcattca gcagggccac tggcatcca gacaggttca gtggcagtgg gtctgggaca 1980  
 gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgtt ttactgtcag 2040  
 cagtatggta gtcaccgtg gacgttcggc caagggacca aggtggaaat caaa 2094

<210> 54  
 <211> 698  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 54

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
 20 25 30

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

Gly Cys Ile Thr Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala  
 50 55 60

Lys Arg Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Thr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Thr Arg Ala Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
130 135 140

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

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
165 170 175

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

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
195 200 205

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
275 280 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser  
305 310 315 320

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

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

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly  
435 440 445

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val  
450 455 460

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr  
465 470 475 480

Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly  
485 490 495

Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr  
500 505 510

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys  
515 520 525

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala  
530 535 540

Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp  
545 550 555 560

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile  
580 585 590

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
595 600 605

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu  
610 615 620

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
625 630 635 640

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser  
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
660 665 670

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr  
675 680 685

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695

<210> 55  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 55  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atcacttgcc aggccagtca gagcatttac agctacttaa actggtatca gcagaaacca | 120 |
| gggaaagccc ctaagctcct gatctatggg gcatccaatc tggcatctgg ggtcccatca | 180 |
| aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct | 240 |
| gaagattttg caacttacta ctgtcaaagc agttgggtga gtggtgctgt tggtaatgct | 300 |
| ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcac  | 360 |
| ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat  | 420 |
| aacttctatc ccagagaggc caaagtacag tggaagggtg ataacgccct ccaatcgggt | 480 |
| aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc | 540 |
| accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc | 600 |
| catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t          | 651 |

<210> 56  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 56

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Gln | Ala | Ser | Gln | Ser | Ile | Tyr | Ser | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Gly | Ala | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Ser | Ser | Trp | Leu | Ser | Gly | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

Val Gly Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr  
100 105 110

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 57  
<211> 2094  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 57  
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tcctgtgcag cctctggatt caccatcagc agctatggag tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtcgcattg atttttcccg ggattggttt caaagactac 180  
gcgagctggg tgaatggccg gttcacctc tccagcgaca acgccagaa cactgtggaa 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatttg 300  
gacttgtggg gccaggaac cctggtcacc gtctcgagcg ctagcaccaa gggcccatcg 360

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| gtcttcccc   | tggcaccctc  | ctccaagagc | acctctgggg  | gcacagcggc | cctgggctgc  | 420  |
| ctgggtcaagg | actacttccc  | cgaaccggtg | acgggtgtcgt | ggaactcagg | cgccctgacc  | 480  |
| agcggcgtgc  | acaccttccc  | ggctgtccta | cagtcctcag  | gactctactc | cctcagcagc  | 540  |
| gtggtgaccg  | tgccctccag  | cagcttgggc | accagacct   | acatctgcaa | cgtgaatcac  | 600  |
| aagcccagca  | acaccaaggt  | ggacaagaga | gttgagccca  | aatcttgtga | caaaactcac  | 660  |
| acatgcccac  | cgtgcccagc  | acctgaagcc | gcgggggcac  | cgtcagtctt | cctcttcccc  | 720  |
| ccaaaacca   | aggacaccct  | catgatctcc | cggacccttg  | aggtcacatg | cgtggtggtg  | 780  |
| gacgtgagcc  | acgaagaccc  | tgaggtcaag | ttcaactggt  | acgtggacgg | cgtggaggtg  | 840  |
| cataatgcca  | agacaaagcc  | gcgggaggag | cagtacaaca  | gcacgtaccg | tgtggtcagc  | 900  |
| gtcctcaccg  | tcctgcacca  | ggactggctg | aatggcaagg  | agtacaagtg | cgcggtctcc  | 960  |
| aacaaagccc  | tcccagcccc  | catcgagaaa | accatctcca  | aagccaaagg | gcagccccga  | 1020 |
| gaaccacagg  | tgtacaccct  | gccccatcc  | cgggatgagc  | tgaccaagaa | ccaggtcagc  | 1080 |
| ctgacctgcc  | tgggtcaaagg | cttctatccc | agcgacatcg  | ccgtggagtg | ggagagcaat  | 1140 |
| gggcagccgg  | agaacaacta  | caagaccacg | cctcccgtgc  | tggactccga | cggctccttc  | 1200 |
| ttcctctata  | gcaagctcac  | cgtggacaag | agcaggtggc  | agcaggggaa | cgtctttctca | 1260 |
| tgctccgtga  | tgcatgaggc  | tctgcacaac | cactacacgc  | agaagagcct | ctccctgtct  | 1320 |
| ccgggtggcg  | gtggaggggtc | cggcggtggt | ggatcccagg  | tgcaattggt | ggagtctggg  | 1380 |
| ggaggcgtgg  | tccagcctgg  | gaggtccctg | agactctcct  | gtgcagcctc | tggattcacc  | 1440 |
| ttcagtagct  | atactatgca  | ctgggtccgc | caggctccag  | gcaaggggct | ggagtgggtg  | 1500 |
| acatttatat  | catatgatgg  | aaacaataaa | tactacgcag  | actccgtgaa | gggccgattc  | 1560 |
| accatctcca  | gagacaattc  | caagaacacg | ctgtatctgc  | aatgaacag  | cctgagagct  | 1620 |
| gaggacacgg  | ctatatatta  | ctgtgcgagg | accggctggc  | tggggccctt | tgactactgg  | 1680 |
| ggccagggaa  | ccctggtcac  | cgtctcgagc | ggtggaggcg  | gatctggcgg | aggtggttcc  | 1740 |
| ggcgggtggcg | gctccggtgg  | aggcggttct | gaaatttgtgt | tgacgcagtc | tccaggcacc  | 1800 |
| ctgtctttgt  | ctccagggga  | aagagccacc | ctctcctgca  | gggccagtca | gagtgttggc  | 1860 |
| agcagctact  | tagcctggta  | ccagcagaaa | cctggccagg  | ctcccaggct | cctcatctat  | 1920 |
| ggtgcattca  | gcagggccac  | tggcatccca | gacaggttca  | gtggcagtgg | gtctgggaca  | 1980 |

gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgtg ttactgtcag 2040

cagtatggta gctcaccgtg gacgttcggc caagggacca aggtggaaat caaa 2094

<210> 58

<211> 698

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 58

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Ser Tyr  
20 25 30

Gly Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val  
50 55 60

Asn Gly Arg Phe Thr Leu Ser Ser Asp Asn Ala Gln Asn Thr Val Glu  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
130 135 140

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

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
165 170 175

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

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
195 200 205

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
275 280 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser  
305 310 315 320

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

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

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly  
435 440 445

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val  
450 455 460

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr  
465 470 475 480

Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly  
485 490 495

Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr  
500 505 510

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys  
515 520 525

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala  
530 535 540

Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp  
545 550 555 560

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile  
580 585 590

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
595 600 605

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu  
610 615 620

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
625 630 635 640

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser  
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
660 665 670

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr  
675 680 685

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
690 695

<210> 59  
<211> 648  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 59  
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atcacttgcc agtccagtc gagtggttat agtaactact tatcctggta tcagcagaaa 120  
ccagggaag ttcctaagct cctgatctat tatgcatcca ctctggcatc tgggggtcca 180  
tctcggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 240  
cctgaagatg ttgcaactta ttactgtgca ggcgggttata gtagtagtac tcgtgctttc 300  
ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc 360  
ccgcatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420  
ttctatcca gagaggcaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc  | 540 |
| ctgacgctga gcaaagcaga ctacagagaaa cacaaagtct acgcctgcga agtcacccat | 600 |
| cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt              | 648 |

<210> 60  
 <211> 216  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Gln | Ser | Ser | Pro | Ser | Val | Tyr | Ser | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Leu | Ser | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Val | Pro | Lys | Leu | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Tyr | Ala | Ser | Thr | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Glu | Asp | Val | Ala | Thr | Tyr | Tyr | Cys | Ala | Gly | Gly | Tyr | Ser | Ser | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Ala | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Thr | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 61  
<211> 2121  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 61  
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gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180  
tactacgcga gctgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240  
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300  
gccgctaata ctgatactac ctactttaac ttgtggggcc agggaaccct ggtcaccgtc 360  
tcgagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 420  
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480  
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 540  
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600  
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660  
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 720  
ggggcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 780

|                                                                     |      |
|---------------------------------------------------------------------|------|
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   | 840  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag   | 900  |
| tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   | 960  |
| ggcaaggagt acaagtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc   | 1020 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   | 1080 |
| gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   | 1140 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   | 1200 |
| cccgtgctgg actccgacgg ctcttcttctc ctctatagca agctcaccgt ggacaagagc  | 1260 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac   | 1320 |
| tacacgcaga agagcctctc cctgtctccg ggtggcgggtg gaggggtccgg cggtggtgga | 1380 |
| tcccaggtgc aattggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga   | 1440 |
| ctctcctgtg cagcctctgg attcaccttc agtagctata ctatgcactg ggtccgccag   | 1500 |
| gctccaggca aggggctgga gtgggtgaca tttatatcat atgatggaaa caataaatac   | 1560 |
| tacgcagact ccgtgaaggg ccgattcacc atctccagag acaattcaa gaacacgctg    | 1620 |
| tatctgcaaa tgaacagcct gagagctgag gacacggcta tatattactg tgcgaggacc   | 1680 |
| ggctggctgg ggccctttga ctactggggc cagggaaccc tggtcaccgt ctcgagcgg    | 1740 |
| ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggttctgaa   | 1800 |
| attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc   | 1860 |
| tcctgcaggg ccagtcagag tggtggcagc agctacttag cctggtacca gcagaaacct   | 1920 |
| ggccaggctc ccaggctcct catctatggt gcattcagca gggccactgg catcccagac   | 1980 |
| aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct   | 2040 |
| gaagattttg cagtgtatta ctgtcagcag tatggtagct caccgtggac gttcggccaa   | 2100 |
| gggaccaagg tggaaatcaa a                                             | 2121 |

<210> 62

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 62

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser  
20 25 30

His Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Ala Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu Trp  
100 105 110

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser  
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala  
225 230 235 240

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
260 265 270

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
305 310 315 320

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro  
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
340 345 350

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
385 390 395 400

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
435 440 445

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His  
485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile  
500 505 510

Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met  
530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr  
545 550 555 560

Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly  
595 600 605

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala  
610 615 620

Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro  
625 630 635 640

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr  
645 650 655

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
660 665 670

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys  
675 680 685

Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val  
690 695 700

Glu Ile Lys  
705

<210> 63  
<211> 654  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 63  
gcctatgata tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcaattgcc aggccagtca gagcattaac aaccaactat cctggtatca gcagaaacca 120  
gggaaagttc ctaagctcct gatctatggg gcatccactc tggcatctgg ggtcccatct 180  
cggttcaccg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagatgttg caacttatta ctgtcatgtt cattattgca gtggtggttag ttgttttttg 300  
gctttcggcg gagggaccaa ggtggagatc aaacgtacgg tggctgcacc atctgtcttc 360  
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420  
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480  
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540  
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600  
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 64  
<211> 218  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 64

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asn Asn Gln  
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Thr Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys His Val His Tyr Cys Ser Gly Gly  
85 90 95

Ser Cys Phe Trp Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
100 105 110

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

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

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

<210> 65  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 65  
atgaaacacc tgtggttctt cctcctcctg gtggcagctc ccagatgggt cctgtcc 57

<210> 66  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 66

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser

<210> 67  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 67  
atggctgtct tggggctgct cttctgcctg gtgacattcc caagctgtgt cctatcc 57

<210> 68  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 68

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Leu | Gly | Leu | Leu | Phe | Cys | Leu | Val | Thr | Phe | Pro | Ser | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

Val Leu Ser

<210> 69  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 69  
atgaggggccc ctgctcagtt tcttggcttc ttgcttttct ggattccagc ctccagaagt 60

<210> 70  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 70

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | Pro | Ala | Gln | Phe | Leu | Gly | Phe | Leu | Leu | Phe | Trp | Ile | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

Ala Ser Arg Ser  
20

<210> 71  
<211> 738  
<212> DNA  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 71

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| caggtgcaat tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 60  |
| tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct  | 120 |
| ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac  | 180 |
| gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 240 |
| ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc  | 300 |
| tggctggggc cttttgacta ctggggccag ggaaccctgg tcaccgtctc gagcggtgga  | 360 |
| ggcggatctg gcggagggtg ttccggcggt ggcggctccg gtggaggcgg ttctgaaatt  | 420 |
| gtgttgacgc agtctccagg caccctgtct ttgtctccag gggaaagagc caccctctcc  | 480 |
| tgcagggcca gtcagagtgt tggcagcagc tacttagcct ggtaccagca gaaacctggc  | 540 |
| caggctccca ggctcctcat ctatggtgca ttcagcaggg ccactggcat cccagacagg  | 600 |
| ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa  | 660 |
| gattttgcag tgtattactg tcagcagtat ggtagctcac cgtggacgtt cggccaaggg  | 720 |
| accaaggtgg aaatcaaa                                                | 738 |

<210> 72

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 72

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Ile | Ser | Tyr | Asp | Gly | Asn | Asn | Lys | Tyr | Tyr | Ala | Asp | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln  
130 135 140

Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser  
145 150 155 160

Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln  
165 170 175

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser  
180 185 190

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr  
195 200 205

Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val  
210 215 220

Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly  
225 230 235 240

Thr Lys Val Glu Ile Lys  
245

<210> 73  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 73

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| gaggtgcagc  | tggtggagtc | tgggggaggc | ttggtccagc  | ctgggggggtc | cctgagactc | 60  |
| tcctgtacag  | cctctggatt | ctccctcagt | agctatgcaa  | tgagctgggt  | ccgccaggct | 120 |
| ccagggaagg  | ggctggagta | catcggctac | attggtgata  | ctactggcat  | agcctacgcg | 180 |
| agctgggcga  | atggcagatt | caccatctcc | aaagacaata  | ccaagaacac  | ggtggatctt | 240 |
| caaatgaaca  | gcctgagagc | cgaggacacg | gctgtgtatt  | actgtgcgag  | aggctggtcc | 300 |
| tacttagaca  | tctggggcca | agggaccctg | gtcaccgtct  | cgagcgggtg  | aggcggatct | 360 |
| ggcggagggtg | gttccggcgg | tggcggctcc | ggtggaggcg  | gctctgccct  | tgtgatgacc | 420 |
| cagtctccat  | cctccctgtc | tgcattctgt | ggagacagag  | tcaccatcac  | ttgccaggcc | 480 |
| agtcagaaca  | tttacagcaa | tttagcctgg | tatcagcaga  | aaccagggaa  | agttcctaag | 540 |
| ctcctgatct  | atcaggcctc | cactctggca | tctgggggtcc | catctcggtt  | cagtggcagt | 600 |
| ggatatggga  | cagatttcac | tctcaccatc | agcagcctgc  | agcctgaaga  | tgttgcaact | 660 |
| tattactgtc  | aaggcggtta | ttatagtgtc | gcccttaata  | ctttcggcgg  | agggaccaag | 720 |
| gtggagatca  | aa         |            |             |             |            | 732 |

<210> 74

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 74

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Thr | Ala | Ser | Gly | Phe | Ser | Leu | Ser | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Met | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Tyr | Ile |
|     |     |     |     |     |     |     | 35  |     | 40  |     |     | 45  |     |     |     |

Gly Tyr Ile Gly Asp Thr Thr Gly Ile Ala Tyr Ala Ser Trp Ala Asn  
50 55 60

Gly Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Asp Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Trp Ser Tyr Leu Asp Ile Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
115 120 125

Gly Ser Gly Gly Gly Gly Ser Ala Leu Val Met Thr Gln Ser Pro Ser  
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala  
145 150 155 160

Ser Gln Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
165 170 175

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

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

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

Gly Gly Tyr Tyr Ser Ala Ala Leu Asn Thr Phe Gly Gly Gly Thr Lys  
225 230 235 240

Val Glu Ile Lys

<210> 75

<211> 750

<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 75  
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120  
gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180  
tcctacgcga gctgggcgag aggcagattc accatctccg aaacctcaa gaacacggtg 240  
actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300  
ctttacactt acaatagctt gtggggccag ggaaccctgg tcaccgtctc gagcgggtgga 360  
ggcggatctg gcggaggtgg ttccggcggg ggcggctccg gtggaggcgg ctctgacatc 420  
cagatgacc agtctccttc caccctgtct gcatctgtag gagacagagt caccatcact 480  
tgccagtcca gtcagagtgt ttatgataac aactggttag cctggtatca gcagaaacca 540  
gggaaagccc ctaagctcct gatctataca gtatccactc tggcatctgg ggtcccatca 600  
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 660  
gatgattttg caacttatta ctgccaaggc acttattata gtagtggttg gaactttgct 720  
ttcggcggag ggaccaaggt ggagatcaaa 750

<210> 76  
<211> 250  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 76

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Ser Gly  
20 25 30

Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu  
35 40 45

Ile Ala Cys Ile Tyr Ala Gly Thr Ser Gly Ser Thr Ser Tyr Ala Ser  
50 55 60

Trp Ala Arg Gly Arg Phe Thr Ile Ser Glu Thr Ser Lys Asn Thr Val  
65 70 75 80

Thr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Asn Leu Tyr Thr Tyr Asn Ser Leu Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln  
130 135 140

Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
145 150 155 160

Cys Gln Ser Ser Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala Trp Tyr  
165 170 175

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

Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
195 200 205

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala  
210 215 220

Thr Tyr Tyr Cys Gln Gly Thr Tyr Tyr Ser Ser Gly Trp Asn Phe Ala  
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 77  
<211> 729  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 77  
caggagcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtacag cctctggatt ctcttttagc agctactgga tgtgctgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatcggatgc attacgactg gtagtggttag cacttactac 180  
gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300  
gacttgtggg gccagggaac cctgggtcacc gtctcgagcg gtggaggcgg atctggcgga 360  
ggtggttccg gcggtggcgg ctccggtgga ggcggctctg acatccagat gaccagtcct 420  
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcca ggccagtcag 480  
agcatttaca gctacttaaa ctggtatcag cagaaaccag ggaaagcccc taagctcctg 540  
atctatggtg catccaatct ggcatctggg gtcccatcaa gggttcagtgg cagtggatct 600  
gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660  
tgtcaaagca gttggttgag tgggtgctgtt ggtaatgctt tcggcggagg gaccaagggtg 720  
gagatcaaa 729

<210> 78  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 78

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
20 25 30

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

Gly Cys Ile Thr Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala  
50 55 60

Lys Arg Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Thr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Thr Arg Ala Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln  
145 150 155 160

Ser Ile Tyr Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
165 170 175

Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Leu Ala Ser Gly Val Pro  
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Ser  
210 215 220

Trp Leu Ser Gly Ala Val Gly Asn Ala Phe Gly Gly Gly Thr Lys Val  
225 230 235 240

Glu Ile Lys

<210> 79  
<211> 759  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 79  
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag 120  
gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180  
tactacgcga gctggggcga aggccggttc accatctcca gagacaattc caagaacacg 240  
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300  
gccgctaata ctgatactac ctactttaac ttgtggggcc agggaaccct ggtcaccgtc 360  
tcgagcggtg gaggcggatc tggcggaggt ggttccggcg gtggcggctc cggtggaggc 420  
ggctctgcct atgatatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 480  
gtcaccatca attgccaggc cagtcagagc attaacaacc aactatcctg gtatcagcag 540  
aaaccaggga aagttcctaa gtcctgatc tatggtgcat ccactctggc atctgggggtc 600  
ccatctcggg tcaccggcag tggatctggg acagatttca ctctcaccat cagcagcctg 660  
cagcctgaag atgttgcaac ttattactgt catgttcatt attgcagtgg tggtagttgt 720  
ttttgggctt tcggcggagg gaccaagggt gagatcaaa 759

<210> 80  
<211> 253  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 80

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser  
20 25 30

His Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Ala Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Tyr  
130 135 140

Asp Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
145 150 155 160

Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asn Asn Gln Leu Ser  
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Gly  
180 185 190

Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Thr Gly Ser Gly  
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
210 215 220

Val Ala Thr Tyr Tyr Cys His Val His Tyr Cys Ser Gly Gly Ser Cys  
225 230 235 240

Phe Trp Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 81  
<211> 735  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 81  
cagtcggtgg aggagtctgg gggaggcttg gtccagcctg ggggggtccct gagactctcc 60  
tgtaccgcct ctggaatcga ccttaatacc tacgacatga tctgggtccg ccaggctcca 120  
ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac 180  
tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa 240  
atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt 300  
ggttcccact tgtggggcca gggaaccctg gtcaccgtct cttccggtgg aggcggttca 360  
ggcggaggtg gaagtgggtg tggcggctct ggaggcggcg gatctgccta tgatatgacc 420  
cagtcctcat cttccgtgtc tgcattctga ggagacagag tcaccatcaa gtgtcaggcc 480  
agtgaggaca tttatagctt cttggcctgg tatcagcaga aaccagggaag agcccctaag 540  
ctcctgatcc attctgcatc ctctctggca tctgggttcc catcaagggt cagcggcagt 600  
ggatctggga cagatttcac tctcaccatc agcagcctgc agcctgaaga ttttgcaact 660  
tactattgtc aacagggtta tggtaaaaat aatgttgata atgctttcgg cggagggacc 720  
aaggtggaga tcaaa 735

<210> 82  
<211> 245  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 82

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

Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn Thr Tyr Asp  
20 25 30

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

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly  
50 55 60

Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Tyr Leu Gln  
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
85 90 95

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
115 120 125

Gly Ser Gly Gly Gly Gly Ser Ala Tyr Asp Met Thr Gln Ser Pro Ser  
130 135 140

Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Lys Cys Gln Ala  
145 150 155 160

Ser Glu Asp Ile Tyr Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
165 170 175

Lys Ala Pro Lys Leu Leu Ile His Ser Ala Ser Ser Leu Ala Ser Gly  
180 185 190

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

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
210 215 220

Gln Gly Tyr Gly Lys Asn Asn Val Asp Asn Ala Phe Gly Gly Gly Thr  
225 230 235 240

Lys Val Glu Ile Lys  
245

<210> 83  
<211> 528  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 83  
aaagacaata cctcgaccac ggtggatctg caaatgaaca gcctgagagc tgaggacacg 60  
gctgtgtatt actgtgcgag agattttatt agtggttccc acttgtgggg ccagggaacc 120  
ctggtcaccg tctcgagcgg tggaggcgga tctggcggag gtggttccgg cggaggcggc 180  
tccggtggag gcggttctgc ctatgatatg acccagtctc catcttccgt gtctgcatct 240  
gtaggagaca gagtcaccat caattgtcag gccagtgaga gcattagtag cttcttatcc 300  
tggtatcagc agaaaccagg gaaagcccct aagctcctga tcttttctgc atccactctg 360  
gcatctgggg tcccatcaag gttcagcggc agtggatctg ggacagattt cactctcacc 420  
atcagcagcc tgcagcctga agattttgca acttactatt gtcaacaggg ttatagtaaa 480  
agtaatgtgg ataatgcttt cggcggaggg accaaggtgg agatcaaa 528

<210> 84  
<211> 246  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 84

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

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

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

Gly Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Leu Ser Lys Asp Asn Thr Ser Thr Thr Val Asp Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Asp Phe Ile Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly  
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Tyr Asp Met Thr Gln Ser Pro  
130 135 140

Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln  
145 150 155 160

Ala Ser Glu Ser Ile Ser Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro  
165 170 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
210 215 220

Gln Gln Gly Tyr Ser Lys Ser Asn Val Asp Asn Ala Phe Gly Gly Gly  
225 230 235 240

Thr Lys Val Glu Ile Lys  
245

<210> 85  
<211> 756  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 85  
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60  
tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120  
gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggatcact 180  
tacgacgca actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240  
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300  
tcggcgtttt cgttcgacta cgccatggac ctctggggcc agggaaacct ggtcaccgtc 360  
tcgagcggtg gaggcggatc tggcggaggt ggttccggcg gtggcggctc cggtggaggc 420  
ggctctgaca tccagatgac ccagtctcct tccaccctgt ctgcatctgt aggagacaga 480  
gtcaccatca cttgccaggc cagtcagagc attagttccc acttaaactg gtatcagcag 540  
aaaccaggga aagcccctaa gctcctgac tataaggcat ccactctggc atctggggtc 600  
ccatcaaggt tcagcggcag tggatctggg acagaattta ctctcaccat cagcagcctg 660  
cagcctgatg attttgcaac ttattactgc caacagggtt atagttgggg taatgttgat 720  
aatgttttcg gcggaggggac caaggtggag atcaaa 756

<210> 86  
<211> 252  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 86

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Gly  
20 25 30

Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile  
130 135 140

Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg  
145 150 155 160

Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His Leu Asn  
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys  
180 185 190

Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
195 200 205

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp  
210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn Val Asp  
225 230 235 240

Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 87  
<211> 750  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 87  
gaggtgcagc tgggtggagtc tggggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt ctccctcagt agctactgga tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatcggagtc attgatacta atgtttatat atactacgcg 180  
aactgggcaa aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240  
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag atatgtgggt 300  
aataatgatg attatattaa cttgtggggc cagggaaccc tggtcaccgt ctcgagcgggt 360  
ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggctctgac 420  
atccagatga cccagtctcc ttccaccctg tctgcatctg taggagacag agtcaccatc 480  
acttgccagt ccagtcagag tgtttataat ggctactgggt taccctggta tcagcagaaa 540  
ccagggaaag cccctaagct cctgatctat ggtgcatcca ctctggcatc tgggggtccca 600  
tcaaggttca gcggcagtg atctgggaca gaattcactc tcaccatcag cagcctgcag 660  
cctgatgatt ttgcaactta ttactgccta ggcagttata ctagtagtac tgagaactct 720  
ttcggcggag ggaccaaggt ggagatcaaa 750

<210> 88  
<211> 250  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 88

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Tyr  
20 25 30

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

Gly Val Ile Asp Thr Asn Val Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr  
130 135 140

Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
145 150 155 160

Thr Cys Gln Ser Ser Gln Ser Val Tyr Asn Gly Tyr Trp Leu Ser Trp  
165 170 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala  
180 185 190

Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser  
195 200 205

Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe  
210 215 220

Ala Thr Tyr Tyr Cys Leu Gly Ser Tyr Thr Ser Ser Thr Glu Asn Ser  
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 89  
<211> 741  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 89  
gaggatgcagc tggatggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
tcctgtacag tgtctggaat cgacctcagt gtcacataa tgggctgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatcgggaacc attacttatg ttggtaacac atattacgcg 180  
agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240  
accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tgggtactatt 300  
tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagcgggtgga 360  
ggcggatctg gcggaggtgg ttccggcggt ggcggctccg gtggaggcgg ctctgcattc 420  
gaattgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcaag 480  
tgccaggcca gtgaaagcat tagcaactac ttatcctggt atcagcagat tccagggaaa 540  
gttcctaagc tcctgatcta ttatgcatcc aatctggcat ctgggggtccc atctcggttc 600  
agtggcagtg gatctgggac agatttcact ctcacatca gcagcctgca gcctgaagat 660  
gttgcaactt attactgtca aagctattat ggtgggtgga gtgcctatac tttcggcgga 720  
gggaccaagg tggagatcaa a 741

<210> 90  
<211> 247  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 90

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

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

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

Gly Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile  
65 70 75 80

Thr Ser Pro Thr Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
85 90 95

Ser Gly Thr Ile Tyr Tyr Ser Tyr Phe Asn Leu Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Phe Glu Leu Thr Gln  
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Lys  
145 150 155 160

Cys Gln Ala Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln  
165 170 175

Ile Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Leu  
180 185 190

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr  
210 215 220

Tyr Cys Gln Ser Tyr Tyr Gly Gly Gly Ser Ala Tyr Thr Phe Gly Gly  
225 230 235 240

Gly Thr Lys Val Glu Ile Lys  
245

<210> 91  
<211> 354  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 91  
caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60  
tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct 120  
ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 92  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 92

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser  
115

<210> 93  
<211> 324  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 93  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttggc agcagctact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300  
caagggacca aggtggaaat caaa 324

<210> 94  
<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 94

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
20 25 30

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

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 95  
<211> 345  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 95  
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60  
tcctgtacag cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagta catcggctac attggtgata ctactggcat agcctacgcg 180  
agctgggcga atggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt 240  
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgagag aggctggtcc 300  
tacttagaca tctggggcca agggaccctg gtcaccgtct cgagc 345

<210> 96  
<211> 115  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 96

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Leu Ser Ser Tyr  
20 25 30

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

Gly Tyr Ile Gly Asp Thr Thr Gly Ile Ala Tyr Ala Ser Trp Ala Asn  
50 55 60

Gly Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Asp Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Trp Ser Tyr Leu Asp Ile Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 97  
<211> 327  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 97  
gcccttgtga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc aggccagtca gaacatttac agcaatttag cctggtatca gcagaaacca 120  
gggaaagttc ctaagctcct gatctatcag gcctccactc tggcatctgg ggtcccatct 180  
cggttcagtg gcagtggata tgggacagat ttactctca ccatcagcag cctgcagcct 240  
gaagatgttg caacttatta ctgtcaaggc gggtattata gtgctgccct taatactttc 300  
ggcggaggga ccaaggtgga gatcaaa 327

<210> 98  
<211> 109  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 98

Ala Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile Tyr Ser Asn  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Gln Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ser Ala Ala  
85 90 95

Leu Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 99  
<211> 354  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 99

gaggtgcagc tgggtggagtc tggggggaggc ttggtccagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggagcag aggcagattc accatctccg aaacctccaa gaacacggtg 240

actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300  
ctttacactt acaatagctt gtggggccag ggaaccctgg tcaccgtctc gagc 354

<210> 100  
<211> 118  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 100

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Ser Gly  
20 25 30

Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu  
35 40 45

Ile Ala Cys Ile Tyr Ala Gly Thr Ser Gly Ser Thr Ser Tyr Ala Ser  
50 55 60

Trp Ala Arg Gly Arg Phe Thr Ile Ser Glu Thr Ser Lys Asn Thr Val  
65 70 75 80

Thr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Asn Leu Tyr Thr Tyr Asn Ser Leu Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser  
115

<210> 101  
<211> 336  
<212> DNA  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 101

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc  | 60  |
| atcacttgcc agtccagtca gagtgtttat gataacaact ggtagcctg gtatcagcag  | 120 |
| aaaccaggga aagcccctaa gtcctgatac tacaagctat ccactctggc atctggggtc | 180 |
| ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg | 240 |
| cagcctgatg attttgcaac ttattactgc caaggcactt attatagtag tggttggaac | 300 |
| tttgctttcg gcggaggac caaggtggag atcaaa                            | 336 |

<210> 102

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 102

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Thr | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Gln | Ser | Ser | Gln | Ser | Val | Tyr | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Trp | Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Tyr | Thr | Val | Ser | Thr | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Asp | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gly | Thr | Tyr | Tyr | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Trp | Asn | Phe | Ala | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 103  
<211> 339  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 103  
caggagcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtacag cctctggatt ctcttttagc agctactgga tgtgctgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatcggatgc attacgactg gtagtggtag cacttactac 180  
gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300  
gacttgtggg gccagggaac cctgggtcacc gtctcgagc 339

<210> 104  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 104

Gln Glu Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
20 25 30  
Trp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45  
Gly Cys Ile Thr Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala  
50 55 60  
Lys Arg Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Thr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Thr Arg Ala Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ser

<210> 105  
<211> 330  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 105  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc aggccagtca gagcatttac agctacttaa actggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatctatggg gcatccaatc tggcatctgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaaagc agttgggtga gtggtgctgt tggtaatgct 300  
ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 106  
<211> 110  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 106

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Tyr Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Gly Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Ser Trp Leu Ser Gly Ala  
85 90 95

Val Gly Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 107  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 107  
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag 120  
gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180  
tactacgcga gctgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240  
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300  
gccgctaata ctgatactac ctactttaac ttgtggggcc agggaaccct ggtcaccgtc 360  
tcgagc 366

<210> 108  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 108

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser  
20 25 30

His Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Ala Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 109  
<211> 333  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 109  
gcctatgata tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcaattgcc aggccagtca gagcattaac aaccaactat cctggtatca gcagaaacca 120  
gggaaagttc ctaagctcct gatctatggg gcatccactc tggcatctgg ggtcccatct 180  
cggttcaccg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagatgttg caacttatta ctgtcatgtt cattattgca gtggtggttag ttgttttttg 300  
gctttcggcg gagggaccaa ggtggagatc aaa 333

<210> 110  
<211> 111  
<212> PRT  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 110

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asn Asn Gln  
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Thr Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys His Val His Tyr Cys Ser Gly Gly  
85 90 95

Ser Cys Phe Trp Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 111

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized

<400> 111

cagtcggtgg aggagtctgg gggaggcttg gtccagcctg gggggtcctt gagactctcc 60  
tgtaccgcct ctggaatcga ccttaatacc tacgacatga tctgggtccg ccaggctcca 120  
ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac 180  
tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa 240  
atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt 300  
ggttcccact tgtggggcca gggaaccctg gtcaccgtct cttcc 345

<210> 112  
<211> 115  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 112

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

Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn Thr Tyr Asp  
20 25 30

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

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly  
50 55 60

Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Tyr Leu Gln  
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
85 90 95

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 113  
<211> 330  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 113

gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120  
 gggaaagccc ctaagctcct gatccattct gcatactctc tggcatctgg ggtcccatca 180  
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
 gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300  
 ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 114  
 <211> 110  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 114

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

His Ser Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn  
 85 90 95

Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105 110

<210> 115  
 <211> 348  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> synthesized

<400> 115

caggtgcagc tggtaggagtc tgggggaggc ctggtccagc ctgggggctc cctgagactc 60

tcctgtacaa cttctggaat cgaccttagt acctacgaca tgatctgggt ccgccaggct 120

ccaggcaagg ggctagagt ggtgggaatc attagttatg ttggtaacac atactacgcg 180

agctgggcga aaggccgatt caccctctcc aaagacaata cctcgaccac ggtggatctg 240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agattttatt 300

agtggttccc acttgtgggg ccagggaacc ctggtcaccg tctcgagc 348

<210> 116

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 116

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

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

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

Gly Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Leu Ser Lys Asp Asn Thr Ser Thr Thr Val Asp Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Asp Phe Ile Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser  
115

<210> 117  
<211> 330  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 117  
gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60  
atcaattgtc aggccagtga gagcattagt agcttcttat cctggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatcttttct gcatccactc tggcatctgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagattttg caacttacta ttgtcaacag ggttatagta aaagtaatgt ggataatgct 300  
ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 118  
<211> 110  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 118

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser Ile Ser Ser Phe  
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Phe Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Lys Ser Asn  
85 90 95

Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 119  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 119  
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120  
gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggatatcact 180  
tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240  
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300  
tcggcgtttt cgttcgacta cgccatggac ctctggggcc aggggaaccct ggtcaccgtc 360  
tcgagc 366

<210> 120  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 120

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Gly  
20 25 30

Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 121  
<211> 330  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 121  
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc aggccagtca gagcattagt tcccacttaa actggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatctataag gcatccactc tggcatctgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240  
gatgattttg caacttatta ctgccaacag gggttatagtt ggggtaatgt tgataatggt 300  
ttcggcggag ggaccaaggt ggagatcaaaa 330

<210> 122  
<211> 110  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 122

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn  
85 90 95

Val Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 123

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized

<400> 123

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gaggtgcagc | tggtggagtc | tgggggaggc | ttggtccagc | ctgggggggtc | cctgagactc | 60  |
| tcctgtgcag | cctctggatt | ctccctcagt | agctactgga | tgagctgggt  | ccgccaggct | 120 |
| ccagggaagg | ggctggagtg | gatcggagtc | attgatacta | atgtttatat  | atactacgcg | 180 |
| aactgggcaa | aaggcagatt | caccatctcc | agagacaatt | ccaagaacac  | gctgtatctt | 240 |
| caaatgaaca | gcctgagagc | cgaggacacg | gctgtgtatt | actgtgcgag  | atatgtgggt | 300 |
| aataatgatg | attatattaa | cttgtggggc | cagggaaccc | tggtcaccgt  | ctcgagc    | 357 |

<210> 124

<211> 119

<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 124

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Tyr  
20 25 30

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

Gly Val Ile Asp Thr Asn Val Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> 125  
<211> 333  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 125

gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtccagtca gagtgtttat aatggctact ggttatcctg gtatcagcag 120

aaaccagggga aagcccctaa gctcctgata tatggtgcat ccactctggc atctgggggc 180

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg | 240 |
| cagcctgatg attttgcaac ttattactgc ctaggcagtt atactagtag tactgagaac | 300 |
| tctttcggcg gagggaccaa ggtggagatc aaa                              | 333 |

<210> 126  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 126

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Thr | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Gln | Ser | Ser | Gln | Ser | Val | Tyr | Asn | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Trp | Leu | Ser | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Tyr | Gly | Ala | Ser | Thr | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Asp | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Leu | Gly | Ser | Tyr | Thr | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Glu | Asn | Ser | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |

<210> 127  
 <211> 354  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 127  
 gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60  
 tcctgtacag tgtctggaat cgacctcagt gtcatcaata tgggctgggt ccgccaggct 120  
 ccagggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180  
 agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240  
 accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tgggtactatt 300  
 tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gaggc 354

<210> 128  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 128  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Ile Asp Leu Ser Val Ile  
 20 25 30  
 Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys  
 50 55 60  
 Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile  
 65 70 75 80  
 Thr Ser Pro Thr Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
 85 90 95  
 Ser Gly Thr Ile Tyr Tyr Ser Tyr Phe Asn Leu Trp Gly Gln Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ser  
 115

<210> 129  
<211> 327  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 129  
gcattcgaat tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcaagtgcc aggccagtga aagcattagc aactacttat cctggtatca gcagattcca 120  
gggaaagttc ctaagctcct gatctattat gcatccaatc tggcatctgg ggtcccatct 180  
cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagatgttg caacttatta ctgtcaaagc tattatgggtg gtggtagtgc ctatactttc 300  
ggcggaggga ccaaggtgga gatcaaa 327

<210> 130  
<211> 109  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 130

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

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Ser Ile Ser Asn Tyr  
20 25 30

Leu Ser Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Gly Gly Gly Ser  
85 90 95

Ala Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 131  
<211> 339  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 131  
caggagcagg tgaaggagac cgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt caccatcagc agctatggag tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtcgcattg atttttcccg ggattggttt caaagactac 180  
gcgagctggg tgaatggccg gttcacctc tccagcgaca acgcccagaa cactgtggaa 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatttg 300  
gacttgtggg gccagggaac cctggtcacc gtctcgagc 339

<210> 132  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 132

Gln Glu Gln Val Lys Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Ser Tyr  
20 25 30

Gly Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val  
50 55 60

Asn Gly Arg Phe Thr Leu Ser Ser Asp Asn Ala Gln Asn Thr Val Glu  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ser

<210> 133  
<211> 327  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 133  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc agtccagtc gagtggttat agtaactact taccctggta tcagcagaaa 120  
ccagggaaag ttcctaagct cctgatctat tatgcatcca ctctggcatc tgggggtccca 180  
tctcggttca gtggcagtg atctgggaca gatttcactc tcaccatcag cagcctgcag 240  
cctgaagatg ttgcaactta ttactgtgca ggcgggttata gtagtagtac tcgtgctttc 300  
ggcggaggga ccaaggtgga gatcaaa 327

<210> 134  
<211> 109  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 134

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Tyr Ser Asn  
20 25 30

Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu  
35 40 45

Ile Tyr Tyr Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln  
65 70 75 80

Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Ser Ser Ser  
85 90 95

Thr Arg Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 135  
<211> 987  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 135  
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 120  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 240  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300  
aaatcttggt acaaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga 360  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 420  
gaggtcacat gcgtgggtgtt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540  
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600  
gagtacaagt gcaaggctctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720  
 ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840  
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 900  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960  
 cagaagagcc tctccctgtc tccgggt 987

<210> 136  
 <211> 329  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized

<400> 136

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80

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

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

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

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

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

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

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

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

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

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

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
260 265 270

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
325

<210> 137  
<211> 987  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 137  
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 120  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 240  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300  
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc cgcgggggca 360  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 420  
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540  
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600  
gagtacaagt gcgcggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660  
aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720  
ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 780  
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840  
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 900  
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960  
cagaagagcc tctccctgtc tccgggt 987

<210> 138  
<211> 329  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 138

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
65 70 75 80

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

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

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

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

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

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

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

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

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

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

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
260 265 270

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly  
325

<210> 139  
<211> 726  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 139  
caggagcagg tgaaggagac cgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt caccatcagc agctatggag tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtcgcattg atttttcccg ggattggttt caaagactac 180  
gcgagctggg tgaatggccg gttcacctc tccagcgaca acgcccagaa cactgtggaa 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatttg 300  
gacttgtggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcgga 360  
ggtaggttccg gcggtggcgg ctccggtgga ggcggctctg acatccagat gacccagtct 420  
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcca gtccagtccg 480

agtgtttata gtaactactt atcctggtat cagcagaaac cagggaaagt tcctaagctc 540  
 ctgatctatt atgcatccac tctggcatct ggggtcccat ctcggttcag tggcagtgga 600  
 tctgggacag atttcactct caccatcagc agcctgcagc ctgaagatgt tgcaacttat 660  
 tactgtgcag gcggttatag tagtagtact cgtgctttcg gcggaggagac caaggtggag 720  
 atcaaa 726

<210> 140  
 <211> 242  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized

<400> 140

Gln Glu Gln Val Lys Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Ser Tyr  
 20 25 30

Gly Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val  
 50 55 60

Asn Gly Arg Phe Thr Leu Ser Ser Asp Asn Ala Gln Asn Thr Val Glu  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro  
145 150 155 160

Ser Val Tyr Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys  
165 170 175

Val Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser Gly Val  
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly  
210 215 220

Gly Tyr Ser Ser Ser Thr Arg Ala Phe Gly Gly Gly Thr Lys Val Glu  
225 230 235 240

Ile Lys

<210> 141  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 141

Ser Ser Tyr Thr Met His  
1 5

<210> 142  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 142

Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15

Gly

<210> 143

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized

<400> 143

Thr Gly Trp Leu Gly Pro Phe Asp Tyr  
1 5

<210> 144

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized

<400> 144

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

<210> 145

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized

<400> 145

Gly Ala Phe Ser Arg Ala Thr  
1 5

<210> 146

<211> 9

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 146

Gln Gln Tyr Gly Ser Ser Pro Trp Thr  
1 5

<210> 147  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 147

Asn Thr Tyr Asp Met Ile  
1 5

<210> 148  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 148

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly  
1 5 10 15

<210> 149  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 149

Asp Tyr Met Ser Gly Ser His Leu  
1 5

<210> 150  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 150

Gln Ala Ser Glu Asp Ile Tyr Ser Phe Leu Ala  
1 5 10

<210> 151  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesized

<400> 151

Ser Ala Ser Ser Leu Ala Ser  
1 5

<210> 152  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 152

Gln Gln Gly Tyr Gly Lys Asn Asn Val Asp Asn Ala  
1 5 10

<210> 153  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 153

Asn Thr Tyr Asp Met Ile  
1 5

<210> 154  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 154

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly  
1 5 10 15

<210> 155  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 155

Asp Tyr Met Ser Gly Ser His Leu  
1 5

<210> 156  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 156

Gln Ala Ser Glu Asp Ile Tyr Ser Phe Leu Ala  
1 5 10

<210> 157  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 157

Ser Ala Ser Ser Leu Ala Ser  
1 5

<210> 158  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 158

Gln Gln Gly Tyr Gly Lys Asn Asn Val Asp Asn Ala  
1 5 10

<210> 159  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 159

Ser Gly Tyr Asp Met Cys  
1 5

<210> 160  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized

<400> 160

Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn Trp Ala  
1 5 10 15

Lys Gly

<210> 161  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>

<223> synthesized

<400> 161

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Phe | Ser | Phe | Asp | Tyr | Ala | Met | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 162

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 162

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Ser | Gln | Ser | Ile | Ser | Ser | His | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 163

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 163

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Ser | Thr | Leu | Ala | Ser |
| 1   |     |     |     | 5   |     |     |

<210> 164

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized

<400> 164

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Gly | Tyr | Ser | Trp | Gly | Asn | Val | Asp | Asn | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

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Ser Thr Tyr Asp Met Ile  
1 5

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Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly  
1 5 10 15

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Asp Phe Ile Ser Gly Ser His Leu  
1 5

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Gln Ala Ser Glu Ser Ile Ser Ser Phe Leu Ser  
1 5 10

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Ser Ala Ser Thr Leu Ala Ser  
1 5

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Gln Gln Gly Tyr Ser Lys Ser Asn Val Asp Asn Ala  
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Ser Ser Tyr Trp Met Ser  
1 5

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Val Ile Asp Thr Asn Val Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys Gly  
1 5 10 15

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Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu  
1 5 10

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<400> 174

Gln Ser Ser Gln Ser Val Tyr Asn Gly Trp Leu Ser  
1 5 10

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Gly Ala Ser Thr Leu Ala Ser  
1 5

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Leu Gly Ser Tyr Thr Ser Ser Thr Glu Asn Ser  
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Ser Val Ile Asn Met Gly  
1 5

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Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly  
1 5 10 15

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Glu Ser Gly Thr Ile Tyr Tyr Ser Tyr Phe Asn Leu  
1 5 10

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Gln Ala Ser Glu Ser Ile Ser Asn Tyr Leu Ser  
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Tyr Ala Ser Asn Leu Ala Ser  
1 5

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Gln Ser Tyr Tyr Gly Gly Gly Ser Ala Tyr Thr  
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Ser Gly Tyr Trp Ile Cys  
1 5

<210> 184

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<400> 184

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ile | Tyr | Ala | Gly | Thr | Ser | Gly | Ser | Thr | Ser | Tyr | Ala | Ser | Trp | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Arg Gly

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<211> 8

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<213> Artificial Sequence

<220>

<223> synthesized

<400> 185

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Tyr | Thr | Tyr | Asn | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |

<210> 186

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<223> synthesized

<400> 186

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Ser | Gln | Ser | Val | Tyr | Asp | Asn | Asn | Trp | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 187

<211> 7

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<223> synthesized

<400> 187

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Ser | Thr | Leu | Ala | Ser |
| 1   |     |     |     | 5   |     |     |

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Gln Gly Thr Tyr Tyr Ser Ser Gly Trp Asn Phe Ala  
1 5 10

<210> 189  
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<220>  
<223> synthesized

<400> 189

Ser Ser Tyr Trp Met Cys  
1 5

<210> 190  
<211> 17  
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Cys Ile Thr Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys  
1 5 10 15

Arg

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<400> 191

Ala Phe Asp Leu  
1

<210> 192

<211> 11

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Gln Ala Ser Gln Ser Ile Tyr Ser Tyr Leu Asn  
1 5 10

<210> 193

<211> 7

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<400> 193

Gly Ala Ser Asn Leu Ala Ser  
1 5

<210> 194

<211> 12

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Gln Ser Ser Trp Leu Ser Gly Ala Val Gly Asn Ala  
1 5 10

<210> 195

<211> 6

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<213> Artificial Sequence

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Ser Ser Tyr Gly Val Ser  
1 5

<210> 196

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

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Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val Asn  
1 5 10 15

Gly

<210> 197

<211> 4

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Asp Leu Asp Leu  
1

<210> 198

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Gln Ser Ser Pro Ser Val Tyr Ser Asn Tyr Leu Ser  
1 5 10

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<400> 199

Tyr Ala Ser Thr Leu Ala Ser  
1 5

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Ala Gly Gly Tyr Ser Ser Ser Thr Arg Ala  
1 5 10

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<220>  
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<400> 201

Ser Ser His Trp Ile Cys  
1 5

<210> 202  
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<212> PRT  
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<220>  
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<400> 202

Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser Trp Ala  
1 5 10 15

Lys Gly

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Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu  
1 5 10

<210> 204  
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<220>  
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<400> 204

Gln Ala Ser Gln Ser Ile Asn Asn Gln Leu Ser  
1 5 10

<210> 205  
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<220>  
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<400> 205

Gly Ala Ser Thr Leu Ala Ser  
1 5

<210> 206  
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<212> PRT  
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 206

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Val | His | Tyr | Cys | Ser | Gly | Gly | Ser | Cys | Phe | Trp | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |